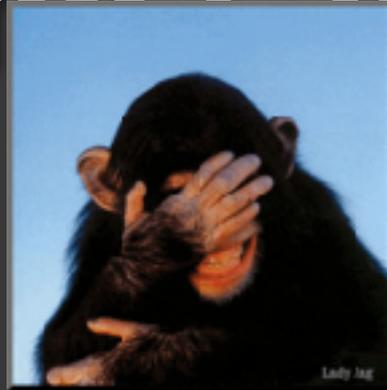
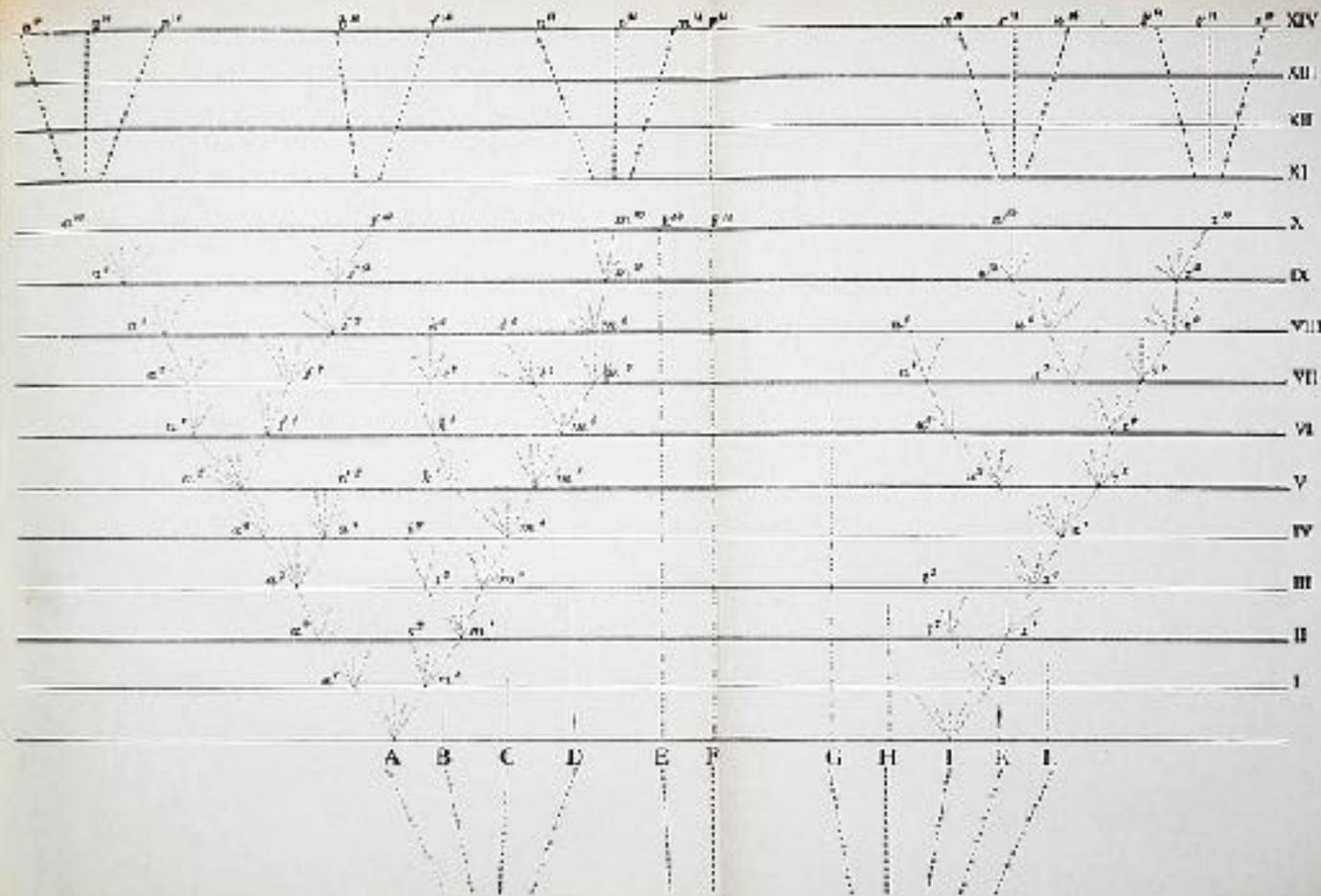
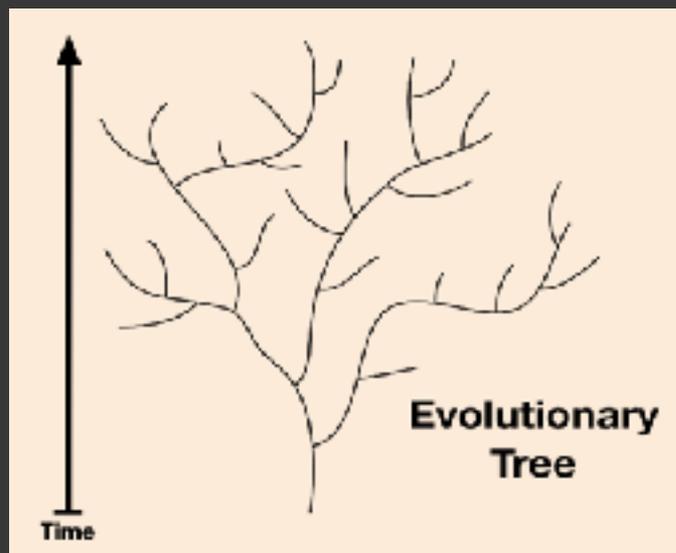


# Monkey Business in the Chimp Genome

Jeffrey Tomkins, PhD







# Created after their kind



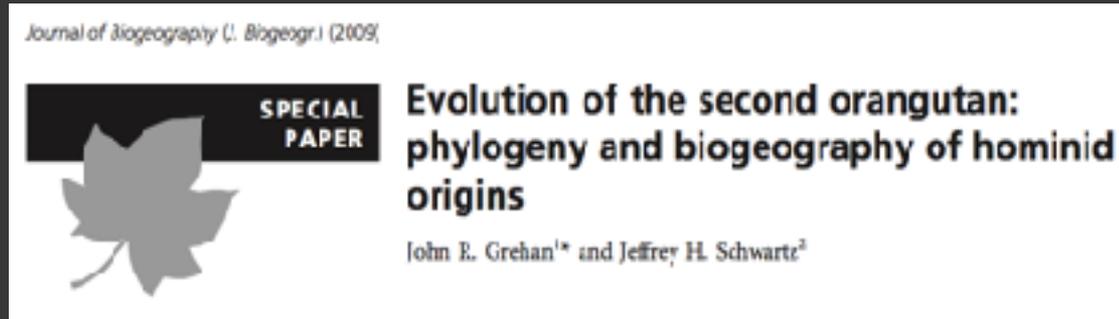
**Chimpanzee was chosen as the closest living ancestor to human**





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

# Morphological and molecular mosaics between humans and apes





Alpha motif protein 11



ACAP3

“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*

“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.

**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.



INDEX

**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.**

## ARTICLES

## 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*). In an overview, we have generated a large-scale catalogue of the genetic differences between the human and chimpanzee species diverged from our common ancestor, identifying 90 single-nucleotide changes, five million insertion/deletion events, and various chromosomal catalogues to explore the magnitude and regional variation of mutational forces shaping the divergence of positive and negative selection acting on both genes. In particular, we find that human and chimpanzee protein-coding genes are highly correlated and dominated by the same mutations. We also use the chimpanzee genome as an outgroup to investigate the identity signatures of selective forces in recent human evolution.



((% alignment Identity x amount aligned) / 2004 human genome size) x 100

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

# Cherry Picking the data...





AN GENO

articles

# Initial sequencing and analysis of the human genome

International Human Genome Sequencing Consortium\*

*The paper has been published in the journal Nature*

The human genome is the most extraordinary treasure of life on earth. We present the results of an international collaboration to sequence and analyze the human genome. We also present an initial analysis of the data.



...the human genome is the most extraordinary treasure of life on earth. We present the results of an international collaboration to sequence and analyze the human genome. We also present an initial analysis of the data.

## The Sequence of the Human Genome

J. Craig Venter,<sup>1\*</sup> Mark D. Adams,<sup>1</sup> Eugene W. Myers,<sup>2</sup> Peter W. U.,<sup>3</sup> Richard J. Muzel,<sup>1</sup>  
 Conger G. Sutton,<sup>1</sup> Hamilton O. Smith,<sup>1</sup> Mark Yancelli,<sup>1</sup> Cheryl A. Evans,<sup>1</sup> Robert A. Holt,<sup>1</sup>  
 Joanne D. Cooney,<sup>1</sup> Peter Amanatides,<sup>1</sup> Richard M. Bellor,<sup>1</sup> Daniel H. Haan,<sup>1</sup>  
 Jennifer Russ Wortman,<sup>1</sup> Qiang Zhang,<sup>1</sup> Chinnasa E. Kodra,<sup>1</sup> Xiaosun H. Zhou,<sup>1</sup> Liu Chen,<sup>1</sup>  
 Marlan Skupski,<sup>1</sup> Gangadharan Sub  
 George L. Gabor Nikles,<sup>6</sup> Catherine Ntzo  
 Victor A. McKusick,<sup>6</sup> Nertea Zinder,<sup>7</sup> A  
 Carolyn Slayman,<sup>10</sup> Michael Hankapfner,<sup>11</sup> Bar  
 Michael Flanigan,<sup>1</sup> Eiliana Flores,<sup>1</sup> Aaron Halp  
 Clark Hobarry,<sup>1</sup> Knut Reinert,<sup>1</sup> Karis Remingt  
 Willem Bonazzi,<sup>5</sup> Rhonda Brandes,<sup>3</sup> Michela C

104270 | December 22, 2000 | 929-930 | www.nature.com

nature

## ARTICLES



Zuoming Deng,<sup>1</sup> Yale  
 Wei E. Gabrielian,<sup>1</sup> Wei  
 J. Helman,<sup>5</sup> Maureen E  
 Yidong Lai,<sup>3</sup> Zhanya Li  
 Arkulav,<sup>3</sup> Natalia Milh  
 Beena Neelam,<sup>1</sup> Deb  
 Hui,<sup>3</sup> Jingtan Sun,<sup>3</sup> Zhi  
 Wides,<sup>11</sup> Chuanlin Xia  
 Jangyu Zhang,<sup>3</sup> Qi Zha  
 Shaying Zhao,<sup>12</sup> De  
 Sibyl Crauchik,<sup>1</sup> Treve  
 Holly Baden,<sup>1</sup> Mary Bar  
 Center,<sup>1</sup> Ming Lai Ch  
 Susanna Oletz,<sup>3</sup> Kristin  
 Brit Hart,<sup>1</sup> Issun Hava

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

The Chimpanzee Sequencing and Analysis Consortium\*

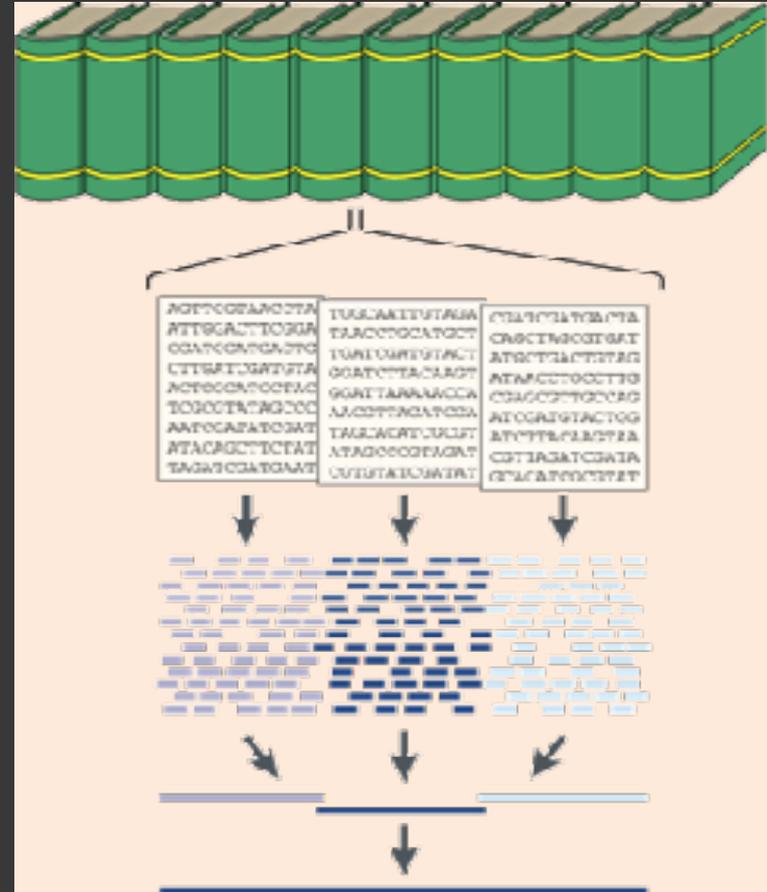
Here we present a draft genome sequence of the common chimpanzee (*Pan troglodytes*). In an genome, we have compiled a large-scale catalog of the genome's differences from the human and chimpanzee species diverged from our common ancestor, including approximately 1.5 million single-nucleotide changes, five million insertion/deletion events, and variations in chromosome structure. To explore the magnitude and regional variation of mutational forces shaping the genome, we calculated the ratio of non-synonymous to synonymous substitutions (dN/dS) for all protein-coding genes. In particular, we find that human and chimpanzee protein-coding genes are highly correlated and dominated by the dN/dS ratio. We also use the chimpanzee genome as an outgroup to investigate and identify signatures of selective sweeps in recent human evolution.





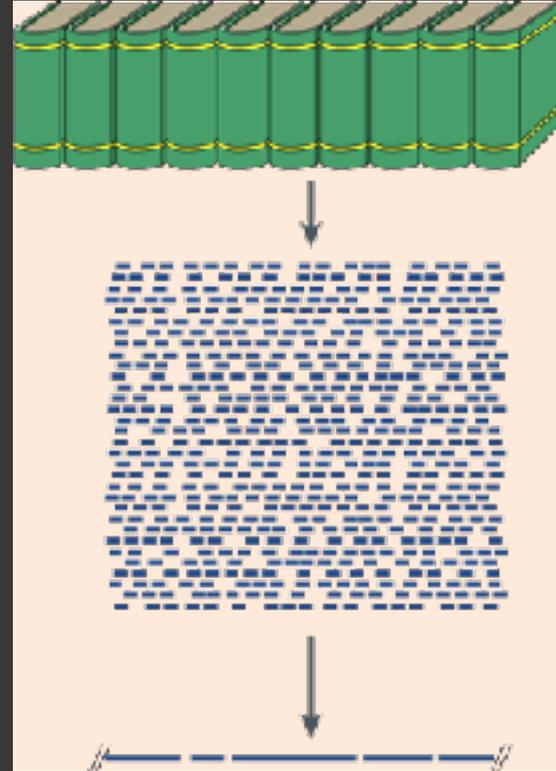
# Human Genome Sequencing Project

Page-by-page sequencing strategy

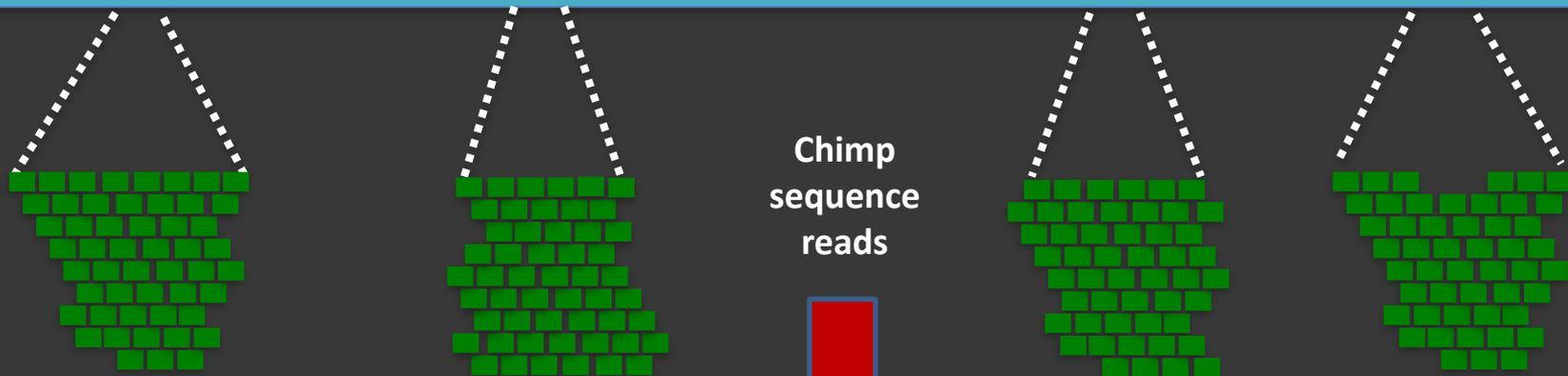


# Chimp - All-at-once sequencing strategy

- Shred the whole book(s) into small pieces of paper
- Decipher the words on each fragment
- Look for overlaps to assemble everything at once



Human chromosome (reference sequence)



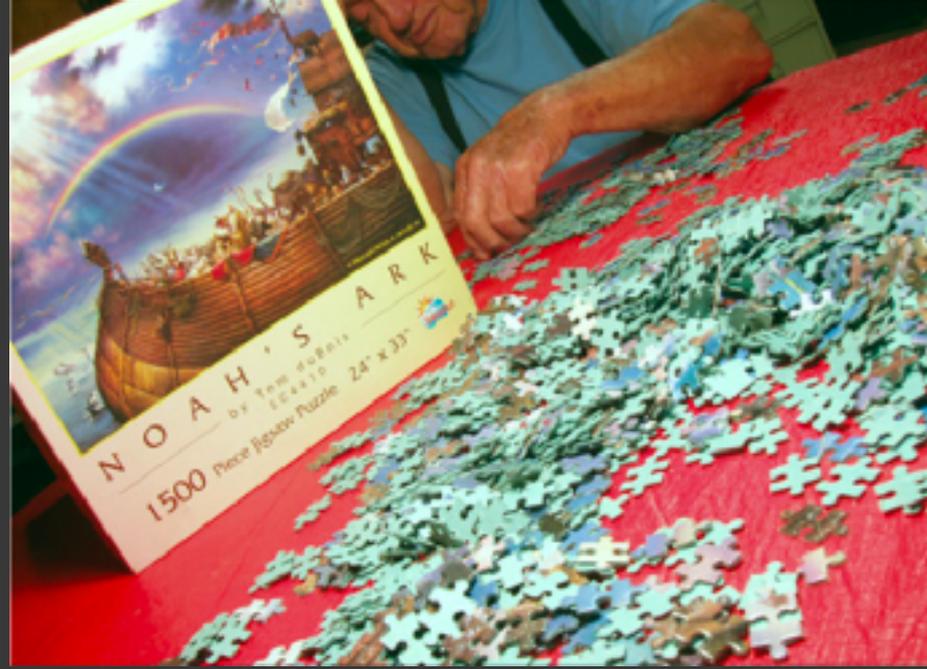
Chimp  
sequence  
reads



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. Kronenberg<sup>1</sup>, Ian T. Fiddes<sup>2\*</sup>, David Gordon<sup>1,2\*</sup>, Shwetha Murali<sup>1,2\*</sup>, Stuart Cantalieris<sup>1\*</sup>, Olivia S. Meyerson<sup>1,4</sup>, Jas...

“...nonhuman primate genomes have not been finished to the same standard as the human reference genome and typically carry hundreds of thousands of gaps precisely over these regions of complex genetic variation.”



Published as: *N Engl J Med*. 2019 July 04; 381(1): 61–74.

**Genetic Variation, Comparative Genomics, and the Diagnosis of Disease**

Evan E. Eichler, Ph.D.

# 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](mailto: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

TTAAGCTC CACCCTTACAGCTAAACGGC

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

Chimp

TAAGTTC A CACCCTTACAGCTAAACGGC

**27/28 bases match**

***96% similarity***



Answers Research Journal 9 (2016):294–298.

[www.answersingenesis.org/arj/v9/101\\_chimpanzee\\_human\\_DNA.pdf](http://www.answersingenesis.org/arj/v9/101_chimpanzee_human_DNA.pdf)

ARJ

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

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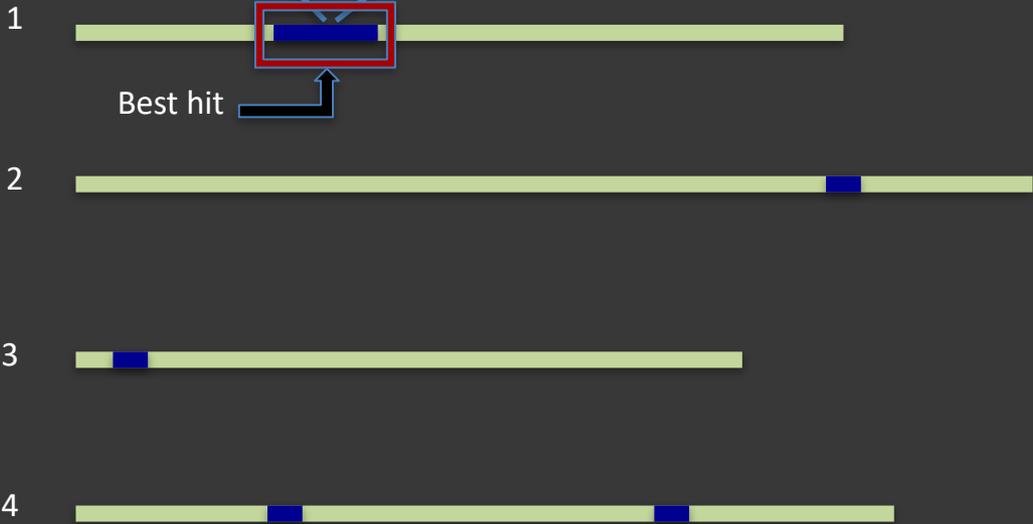
**Jeffrey P. Tomkins**, Institute for Creation Research, 1806 Royal Lane, Dallas, Texas 75229.

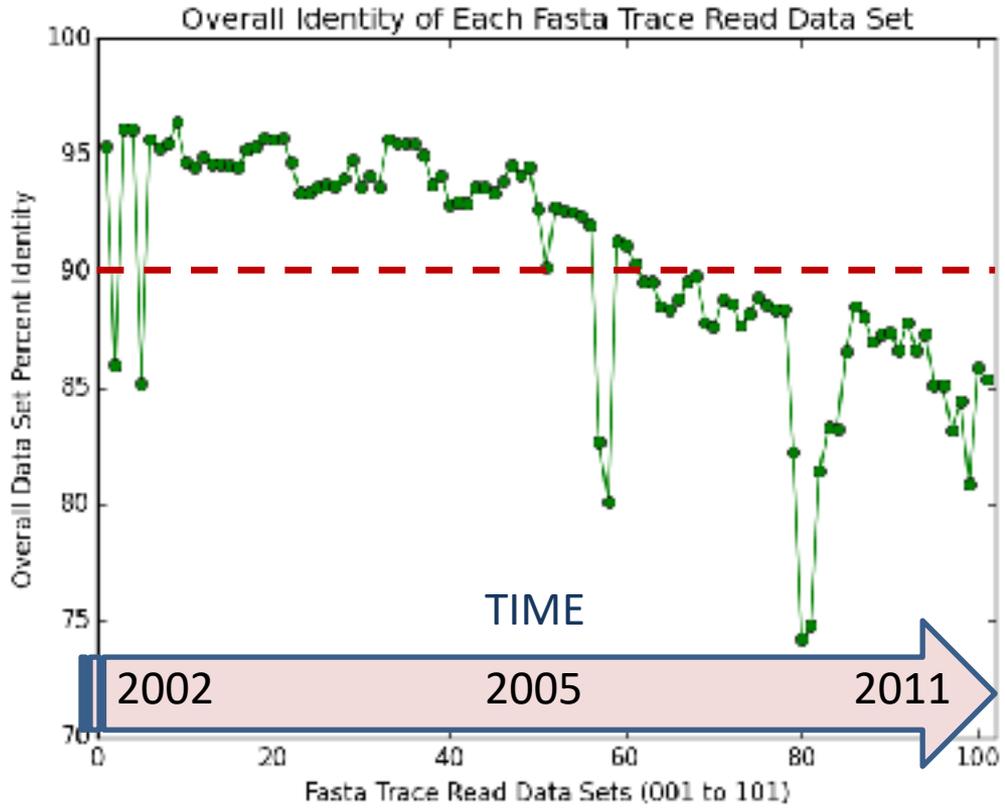
Sampled 25,000 DNA sequences at random from each of 101 data sets – total 2.5 million.

DNA sequences were on average 704 bases long

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

Chromosome





Years

DNA similarity

2002-2004

92%

**Contamination**

2005-2011

85%

## *New research at ICR...*

- 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%**



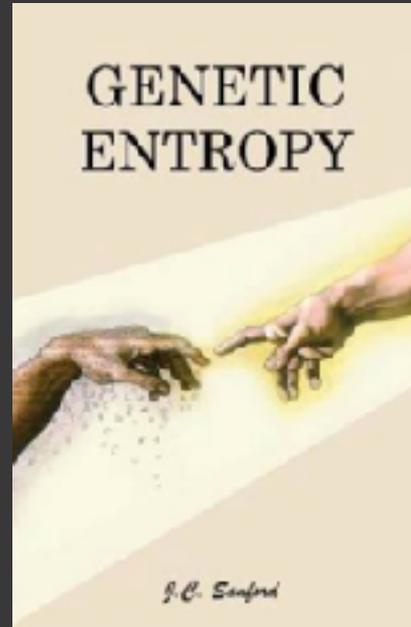
**Richard Buggs, PhD**  
**Professor of Evolutionary Genomics**

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

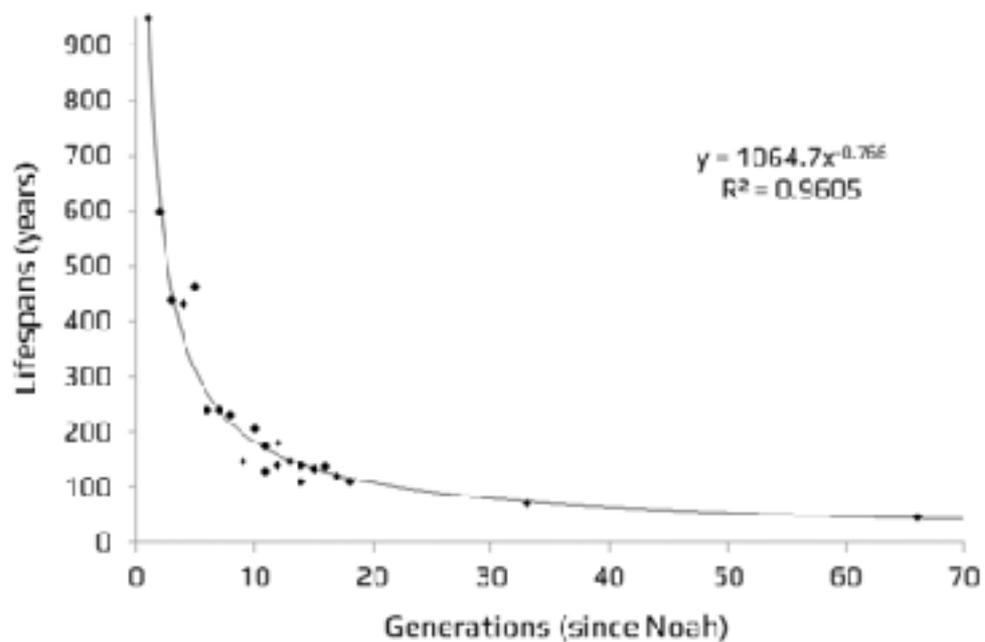
## The evolutionary problem with 84%

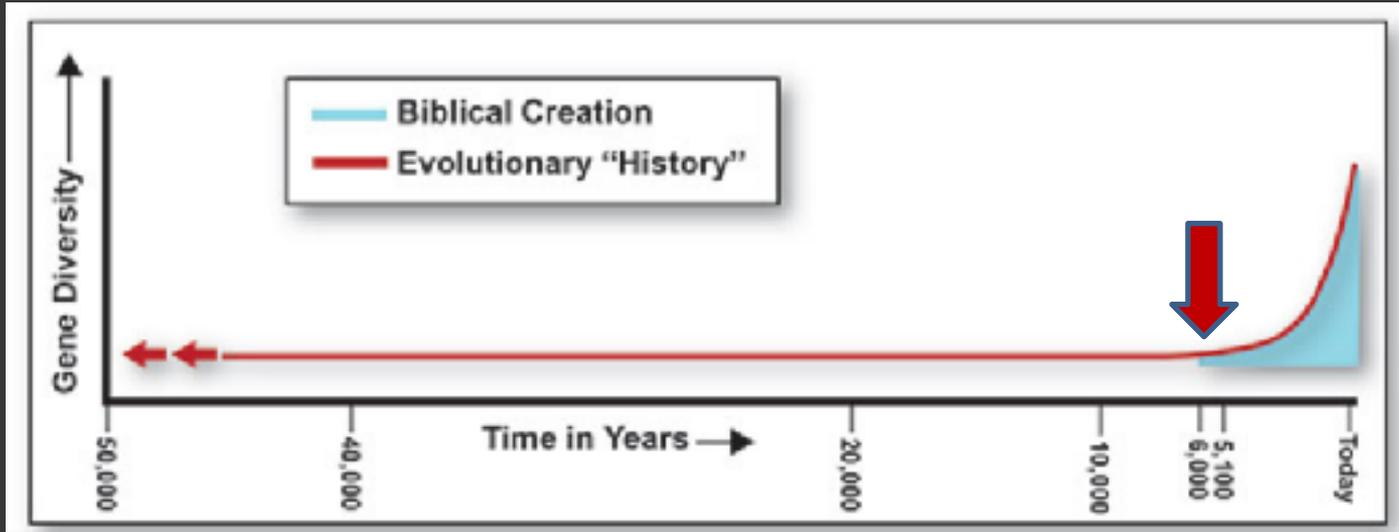
Theoretical evolutionists need a 98.5 to 99% genome similarity to explain human evolution with known mutation rates in 3 to 6 million years time since a common ancestor with chimps.

# The human genome is devolving not evolving



### Declining Lifespans of Noah and His Descendants



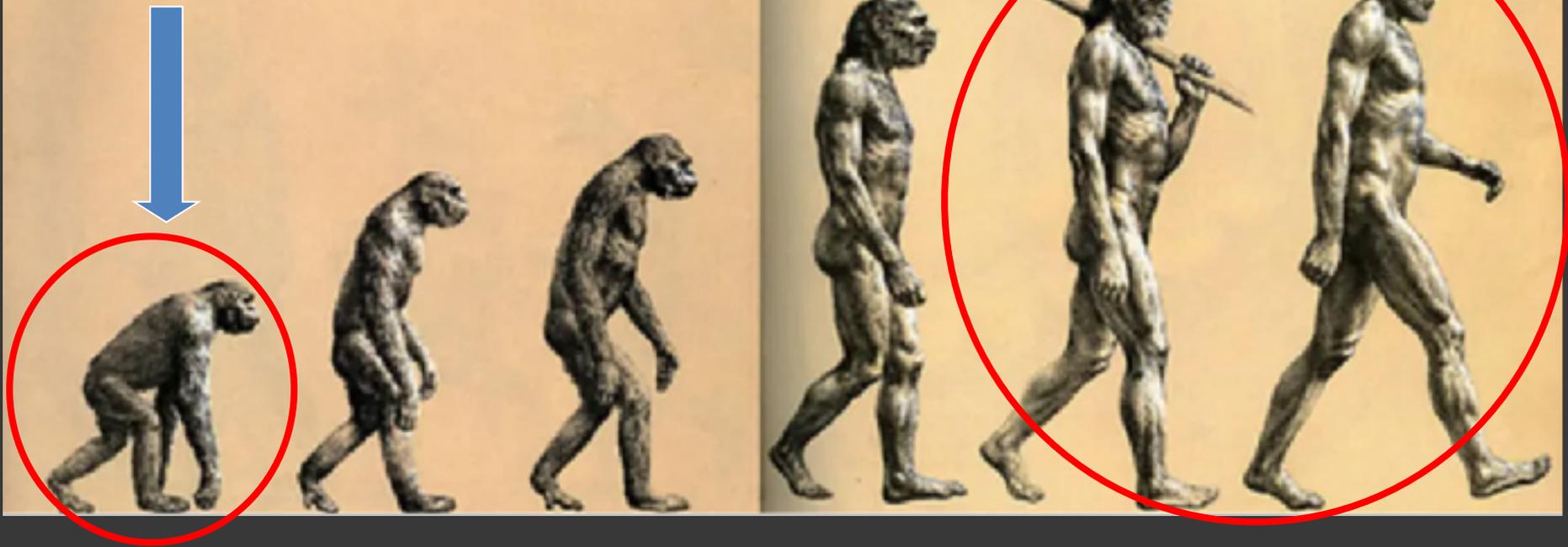


Tennessen, J.A. *et al.*, Evolution and functional impact of rare coding variation from deep sequencing of human exomes, *Science* **337**:64–69, 2012 | doi:10.1126/science.1219240.

Fu, W. *et al.*, Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants, *Nature* **493**:216–220, 2013 | doi:10.1038/nature11690.

All Apes

Humans





## 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

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Review

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Cite this article: Kimbel WH, Yilmore B.

From *Australopithecus* to *Homo*:  
the transition that wasn't<sup>†</sup>

William H. Kimbel<sup>1</sup> and Brian Yilmore<sup>2,3</sup>

<sup>†</sup>Institute of Human Origins, and School of Human Evolution and Social Change, Arizona State University  
Tempe, AZ 85287, USA

<sup>2</sup>Department of Anthropology, University of Nevada Las Vegas, Las Vegas, NV 89154, USA

<sup>3</sup>Department of Anthropology, University College London, London, UK WC1H 0RN

DOI: 10.1098/rstb.2015.0218

2016

# Neanderthal

- Sloping forehead
- Pronounced brow ridge



## *Homo erectus*



# What About the Neanderthals and So-Called Primitive Traits?



## Humans bred with this mysterious species more than once, new study shows

"This is a breakthrough paper," one expert in ancient DNA says of the new findings, which identified Denisovan genes in Southeast Asia.

Mar 15, 2018



## Your Neanderthal DNA might actually be doing you some good

Prehistoric hanky-panky between archaic hominids and our ancestors may have helped us survive as modern humans.

Oct 19, 2016



## Ancient humans may have been mothers to some Neanderthals earlier than we thought

*The latest discovery adds another clue to the mystery of human and Neanderthal evolution*

By Rachel Becker | @RA.Becks | Jul 4, 2017, 3:09pm EDT

## Pronounced Brow Ridge





Rugby players with a pronounced supraorbital ridge and sloping forehead

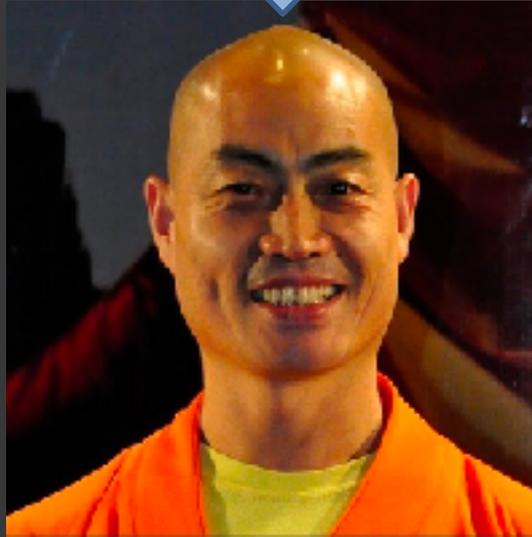
- Sloping forehead
- Pronounced brow ridge



**Nikolay Valuev**

**Former professional boxer, Current Member of Russian Parliament**

## Pronounced Sagittal Crest





Human variation NOT evolution

## **Genesis 1:27**

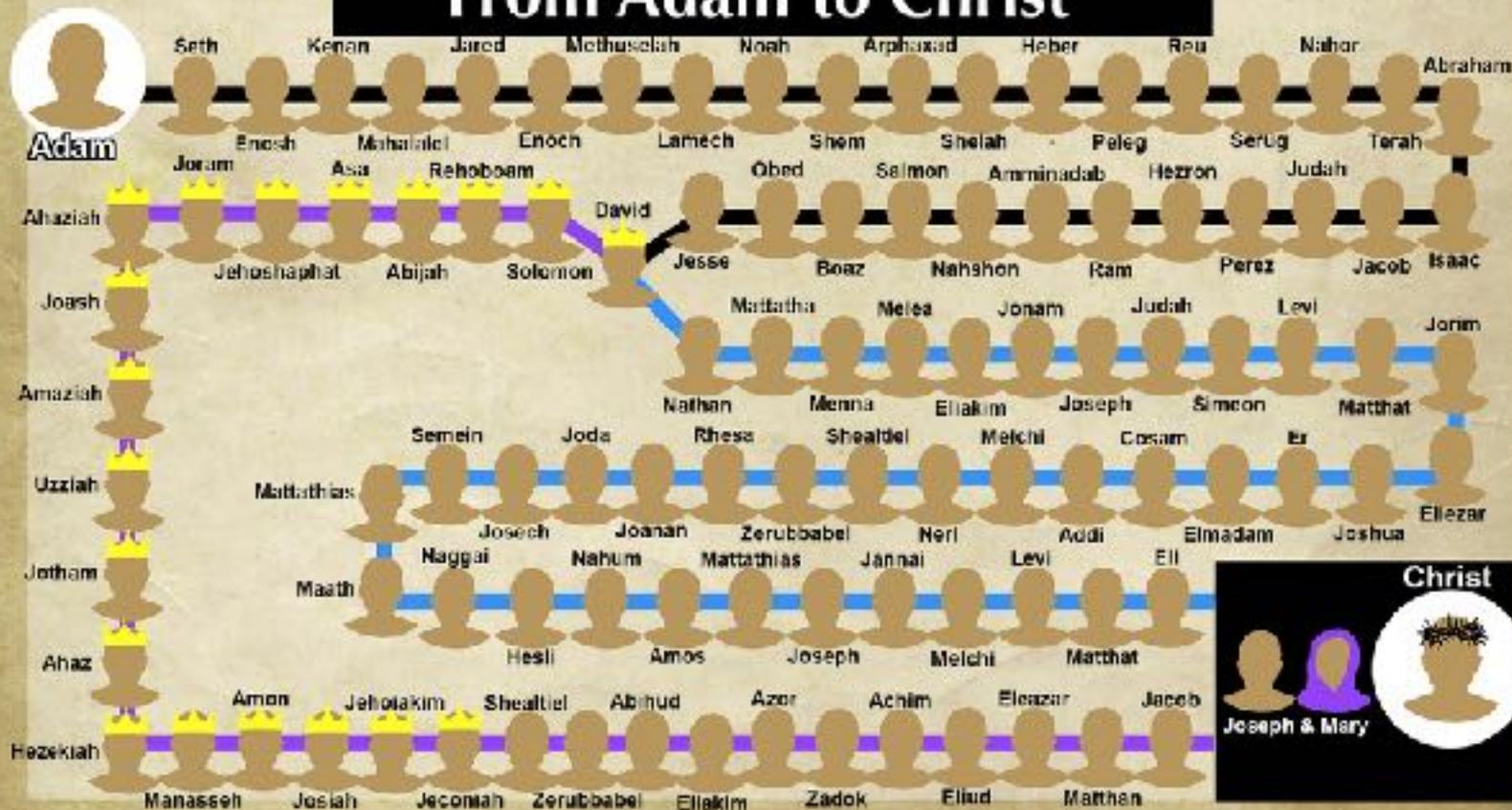
**So God created man in His own image; in the image of God He created him; male and female He created them.**

# A “Historical” Adam?

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



# From Adam to Christ

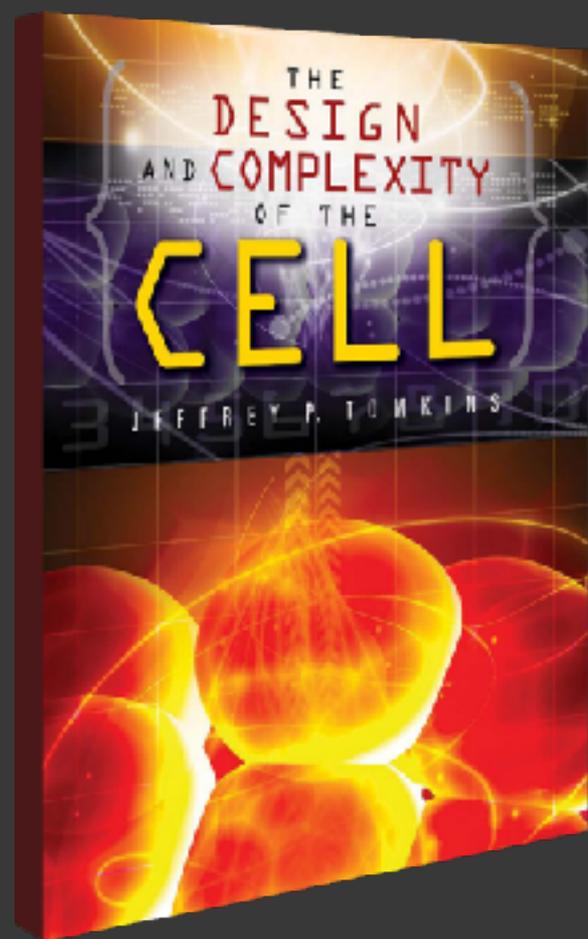
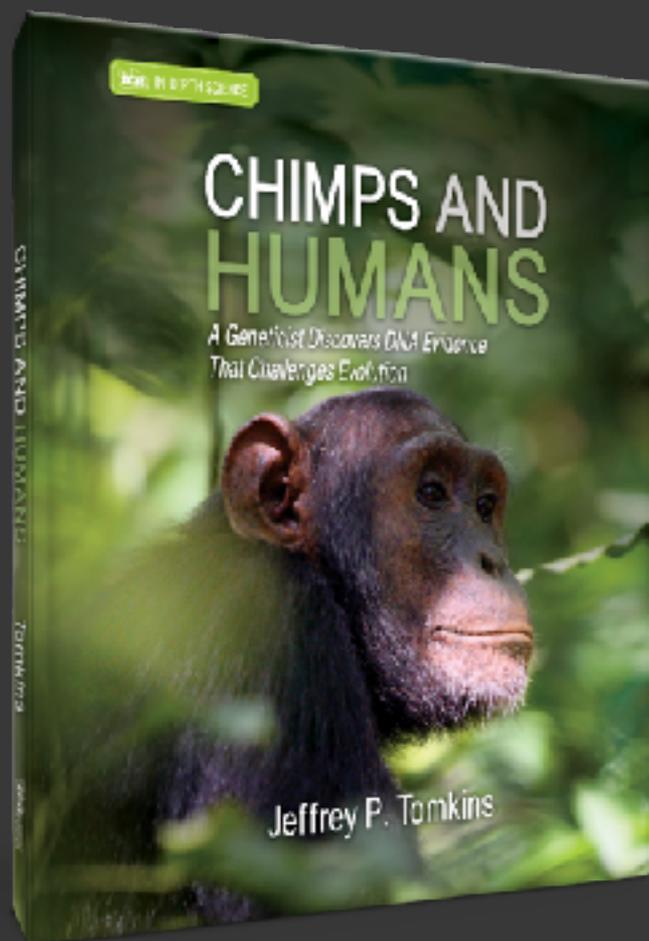


### **Romans 5:12**

**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.**



SECOND EDITION

# CREATION BASICS & BEYOND

An In-Depth Look at Science, Origins, and Evolution



Henry M. Morris, B.S., Ph.D. • Jerry L. Bergman, Ph.D.  
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# ACTS & FACTS

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SEPTEMBER | OCTOBER  
2022



Natural Selection's  
Death-Driven Worldview

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Youngest Rocky Mountains

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Evolutionary Dinosaur  
Myths Debunked

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The Venus Flytrap's Snap

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