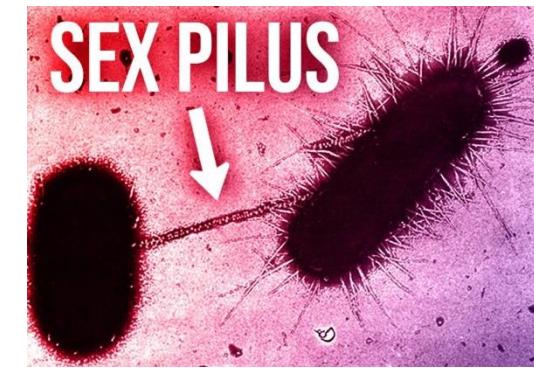




1 - A EMERGÊNCIA DO GÊNERO *HOMO*

2 - EXTENDED OR STANDARD (HUMAN) EVOLUTION?



3 - ANCESTRAL COMUM E ILS?

1 - A EMERGÊNCIA DO GÊNERO *HOMO*



- *Homo habilis*
- *Homo rudolfensis*
- *Homo georgicus*

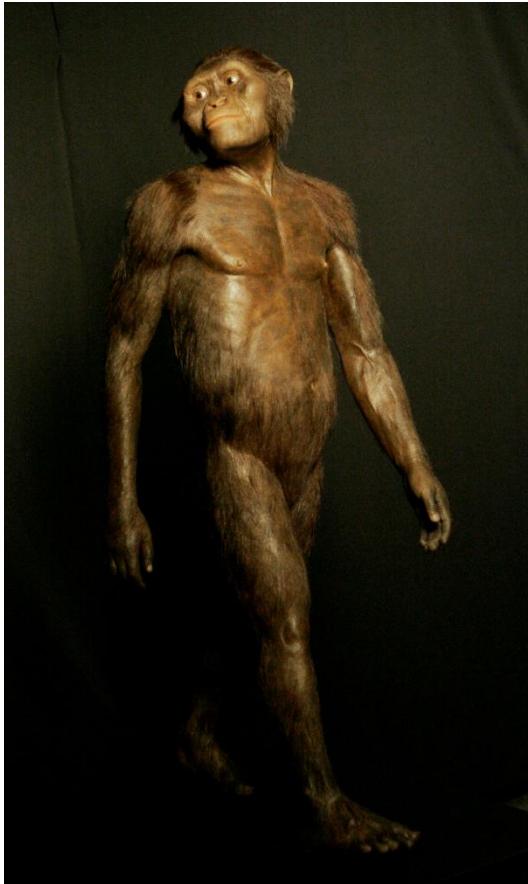
Emerging *Homo*

*"no-man's-land, a grey zone between the aped-sized brains of *Australopithecus africanus* and the moderately enlarged brains of *Homo erectus*"* (Tobias, 1991>515)

The point during human evolution where hominins become closer to us than to the last common ancestral

7ma

Australopithecus



2.8-1.9 ma

present

Homo

Emergence of genus *Homo*



Crossing the Rubicon



Emerging *Homo*

The emergence of the...

- ... suborder Anthropoidea
- ... infraorder Catarrhine (Old World higher primates)
- ... superfamily Hominoidea (apes and people)
- ... family Hominidae (great apes and people)
- ... tribe Hominini (people + ancestrals after LCA with *Pan*)**
- ... genus *Homo* (hominins that are closer to people than to LCA with *Pan*)**
- ... species *sapiens* (modernity?)

Emerging *Homo*

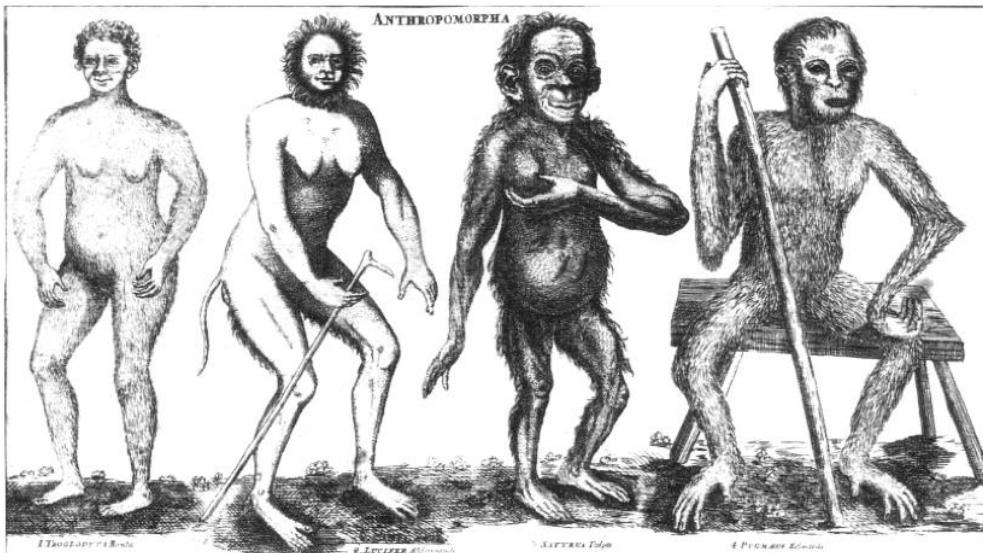
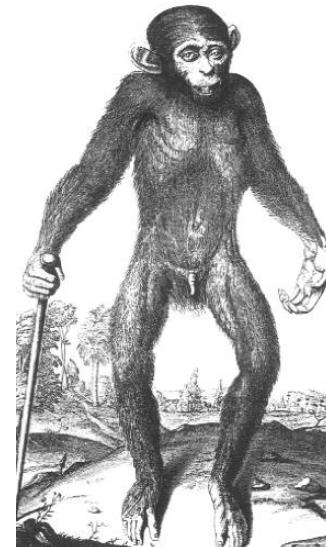
What is in a genus? Before the hominin fossil record.

Carolus Linnaeus (1758) defined the genus *Homo* in *Systema Naturae* (no type-specimen)

Six sub-groups: *H. sylvestris*, *H. troglodytes*, *H. sapiens* and four geographic variants from Africa, America, Asia and Europa.

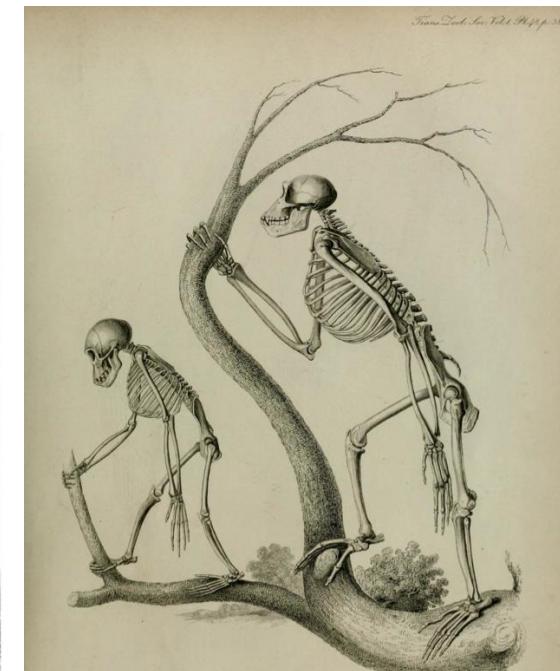
"At what distance from man shall we place the great apes, which resemble him so perfectly in bodily conformation?"
(Buffon, apud Watson et al., 2001).

- The contact of Europeans with **great apes** stimulated consideration on the boundaries of our genus.
- Darwin considered: bipedalism, canine reduction, brain growth, tool use, increased meat consumption, slower ontogeny.



Homo sylvestris,
Tyson (1699)

Symia satyrus, *Homo caudatus*, from Hoppius (1763)



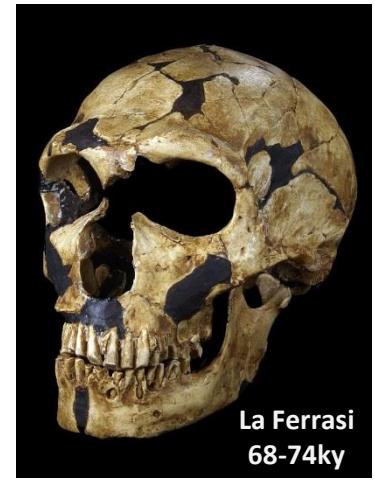
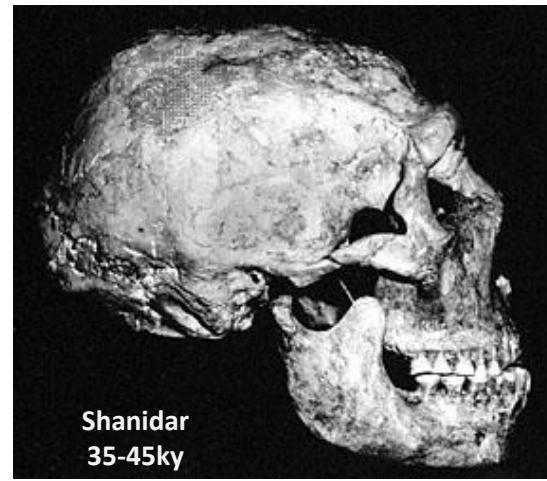
Symia troglodytes, from Owen (1835)

Emerging *Homo*

What is in a genus? The fossils come to scene.

In the next 200 years the genera expanded to include:

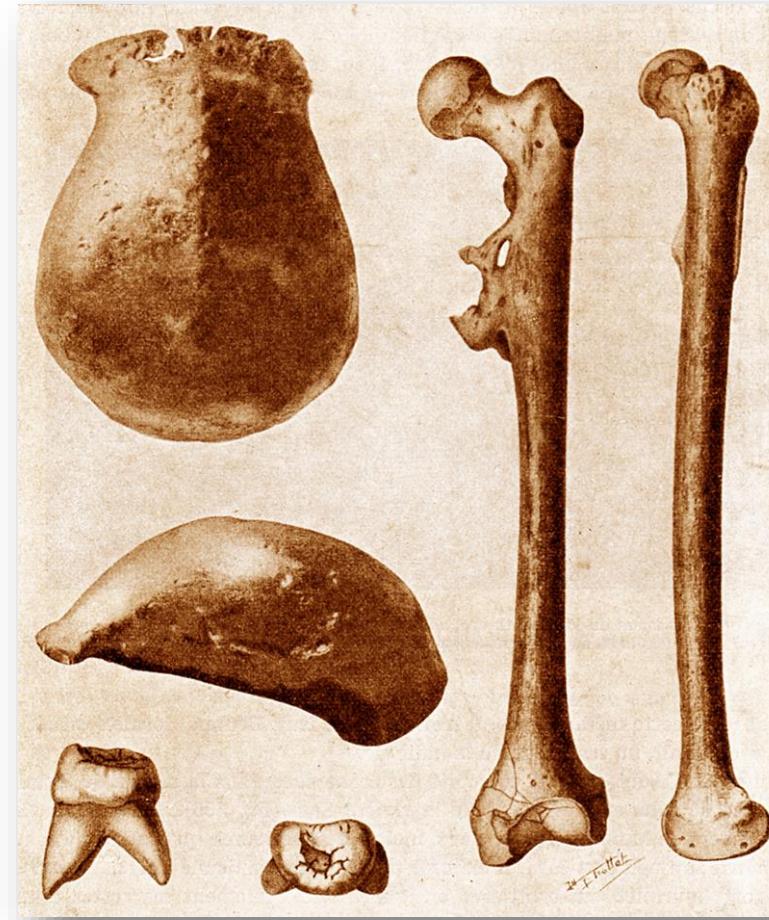
Homo neanderthalensis (King, 1864), *Homo heidelbergensis* (Schoetensack 1908)



Emerging *Homo*

What is in a genus? The fossils come to scene.

Homo erectus (Dubois 1892; Mayr 1944)* (1.9-0.07 Ma)
[*Sinanthropus*, *Pithecanthropus*, *Atlanthropus*]



Emerging *Homo*

What is in a genus? The fossils come to scene.

Australopithecus africanus (Dart 1924) (3.0 - 2.4 Mya)



Sts 5



Sts 71



Taung



Sts 52



Stw 505



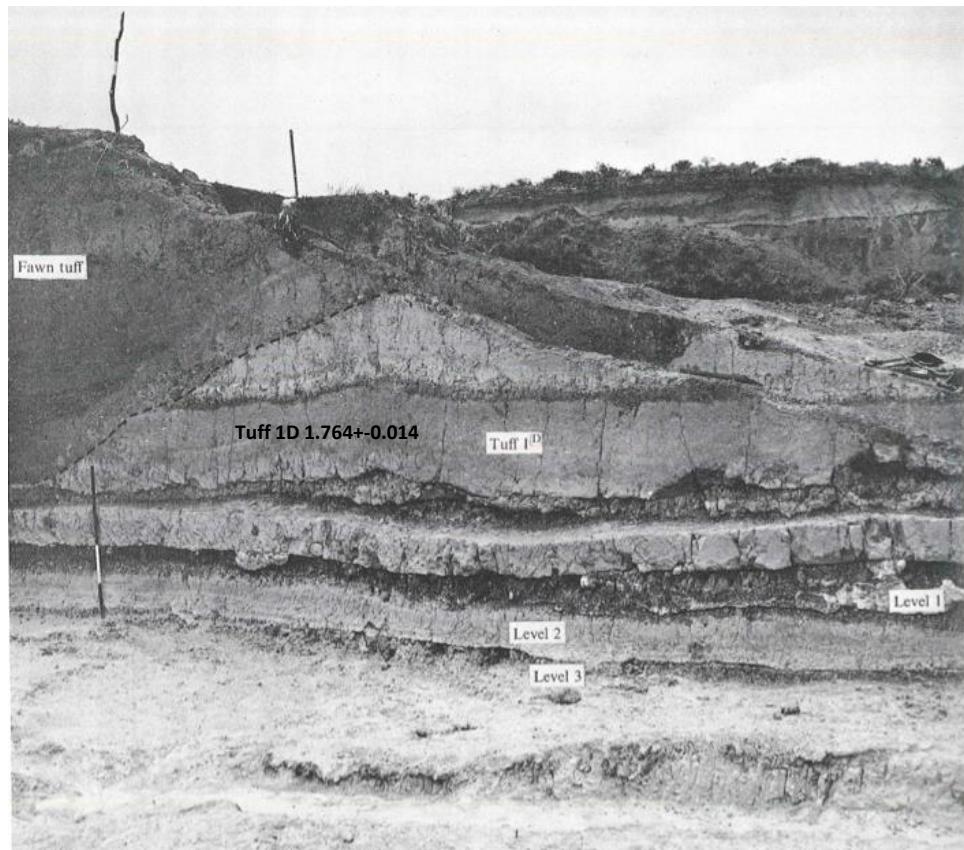
MLD 37/38

Emerging *Homo*

What is in a genus? The fossils come to scene.

Homo/Australopithecus habilis (Leakey et al. 1964) (ca. 2.3-1.6)

* Most revolutionary discovery of human evolution.



Emerging *Homo*

What is in a genus? The fossils come to scene.

Homo/Australopithecus habilis (Leakey et al. 1964) (ca. 2.3-1.6)

* Most revolutionary discovery of human evolution?

No. 4927 April 4, 1964

NATURE

7

A NEW SPECIES OF THE GENUS *HOMO* FROM OLDFUVAI GORGE

By Dr. L. S. B. LEAKY

Coryndon Museum, Centre for Prehistory and Palaeontology

PROF. P. V. TOBIAS

University of Witwatersrand, Johannesburg

AND

DR. J. R. NAPIER

Unit of Primatology and Human Evolution, Royal Free Hospital Medical School,
University of London

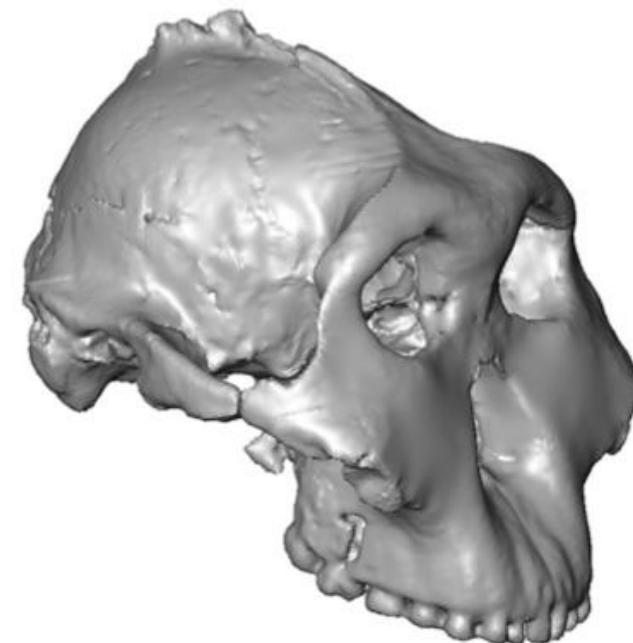
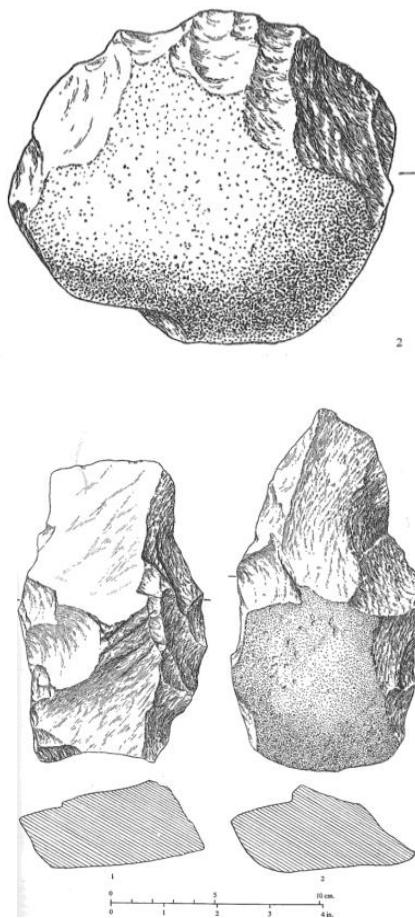


Emerging *Homo*

What is in a genus? The fossils come to scene.

Homo/Australopithecus habilis (Leakey et al. 1964) (ca. 2.3-1.6)

* Most revolutionary discovery of human evolution.

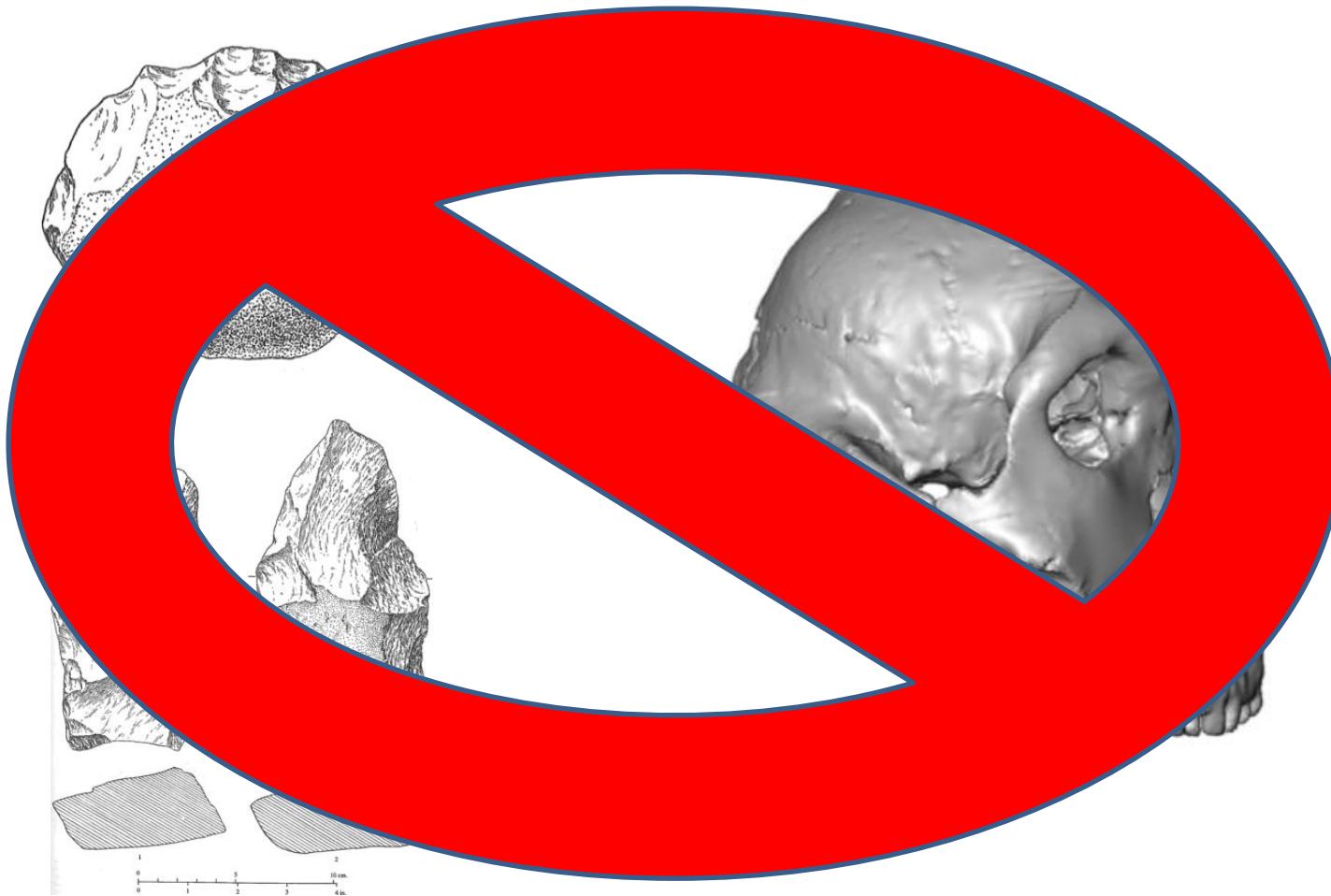


Emerging *Homo*

What is in a genus? The fossils come to scene.

Homo/Australopithecus habilis (Leakey et al. 1964) (ca. 2.3-1.6)

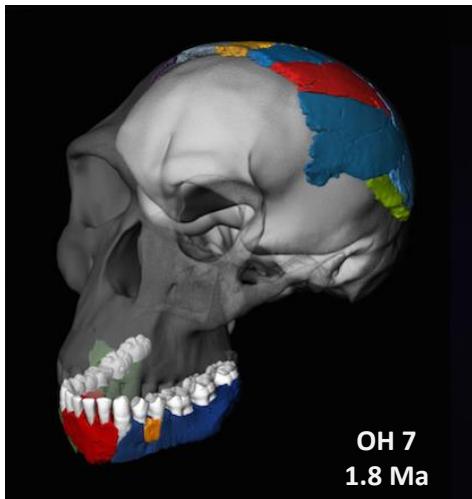
* Most revolutionary discovery of human evolution.



Emerging *Homo*

What is in a genus? The fossils come to scene.

Homo/Australopithecus habilis (Leakey et al. 1964) (ca. 2.3-1.6)

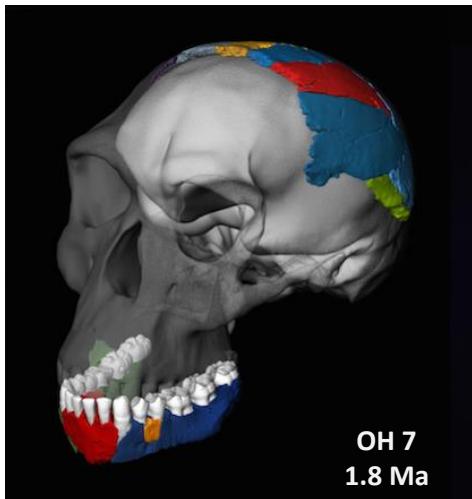


Homo
Australopithecus *habilis*

Emerging *Homo*

What is in a genus? The fossils come to scene.

Homo/Australopithecus habilis (Leakey et al. 1964) (ca. 2.3-1.6)

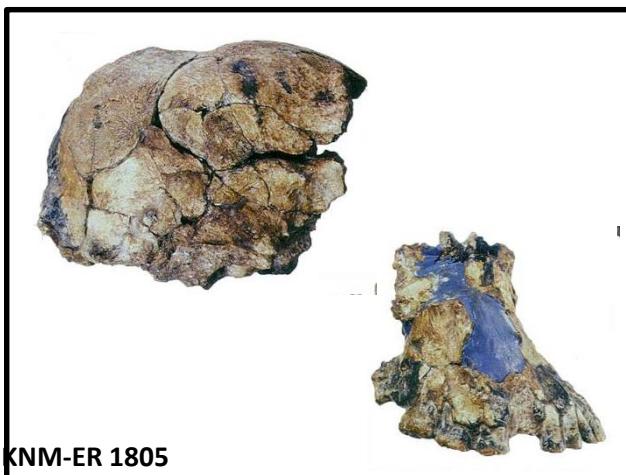
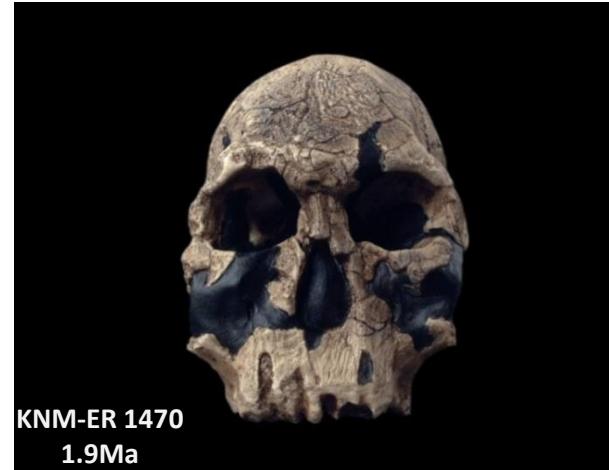


Homo
Australopithecus *habilis*

Emerging *Homo*

What is in a genus? The fossils come to scene.

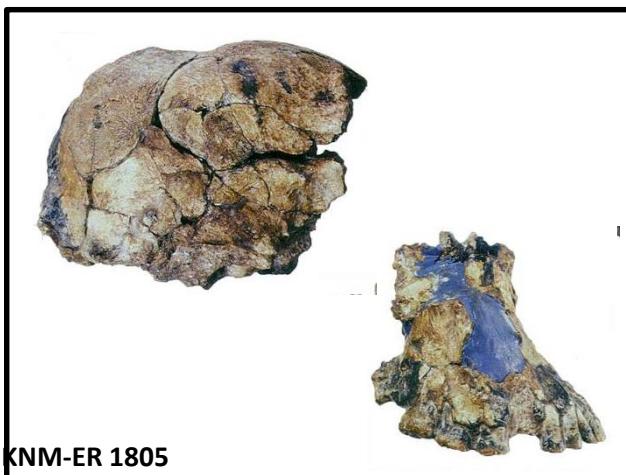
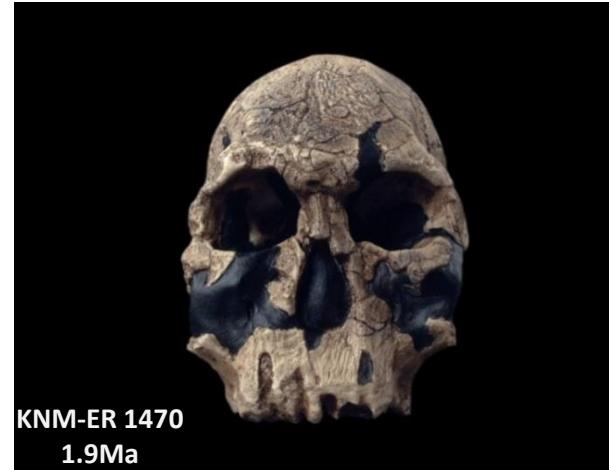
Homo/Australopithecus habilis (Leakey et al. 1964) (ca. 2.3-1.6)



Emerging *Homo*

What is in a genus? The fossils come to scene.

Homo/Australopithecus habilis (Leakey et al. 1964) (ca. 2.3-1.6)



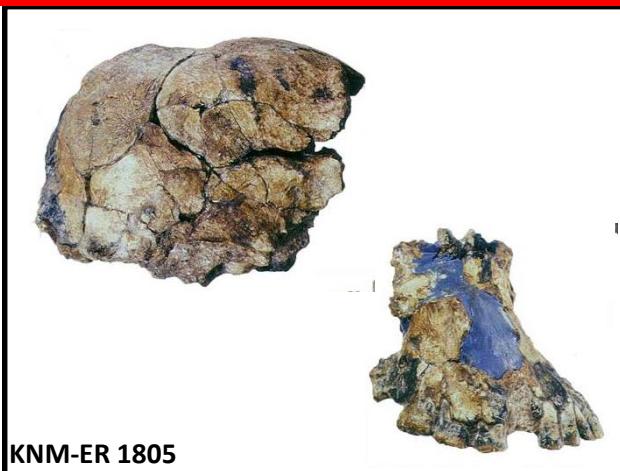
Emerging *Homo*

What is in a genus? The fossils come to scene.

Homo/Australopithecus habilis (Leakey et al. 1964) (ca. 2.3-1.6)



Wood (1991:83) -> KNM-ER-1805 enjoyed a more diverse taxonomic career than any other fossil from Koobi Fora.



KNM-ER 1805

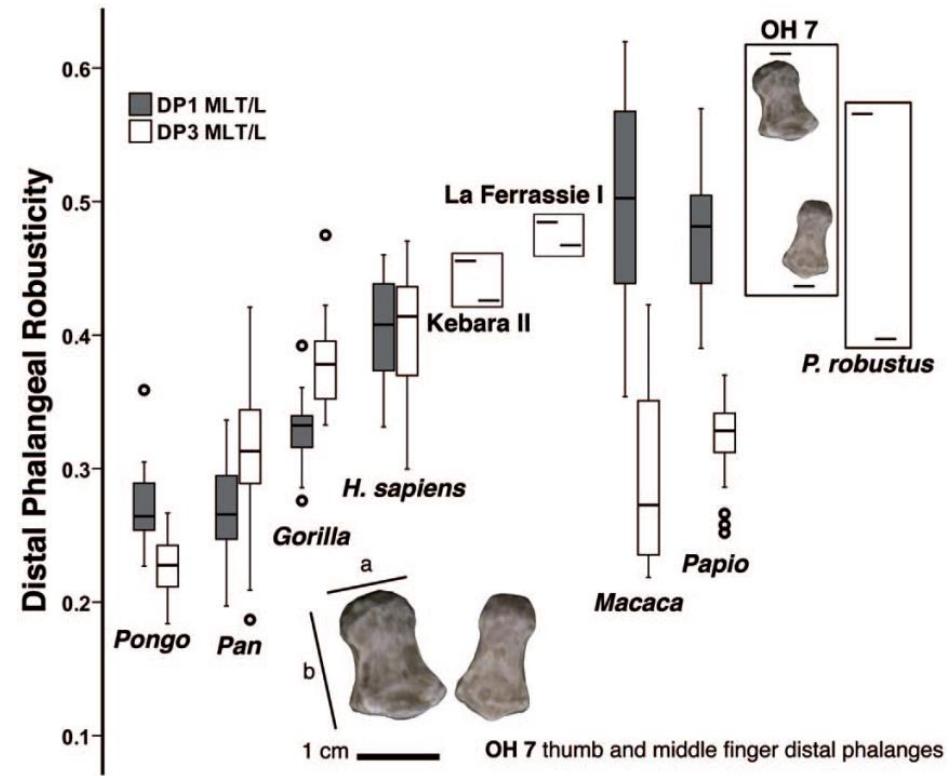
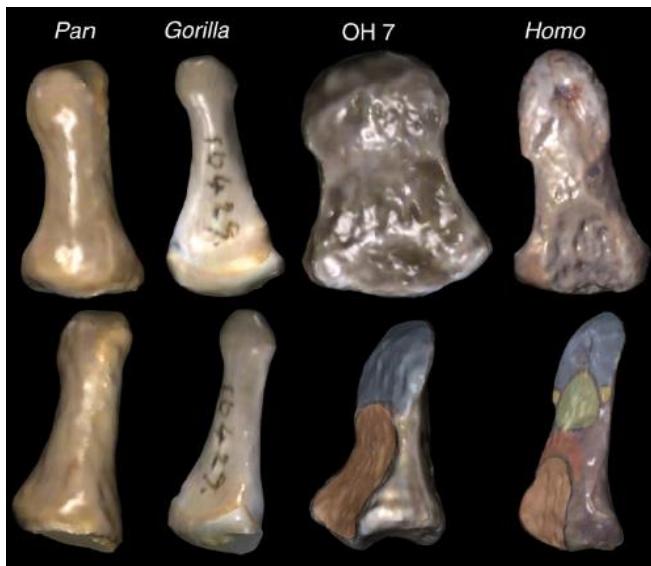


KNM-ER 62000 (1.8Ma)

Emerging *Homo*

The OH 7 hand (1.84 Mya)

- The pollical distal phalanx does not display ungual spines and there is no ridge for insertion of the *flexor pollicis longus*.
- The absence of an ungual fossa indicate limited palmar pad compartmentalization and, as such, of a restricted precision-grip capability.
- Extremely robust pollical distal phalanx compared to other distal phalanx.
- The OH7 trapezium is more similar to Gorilla than it is to modern humans.
- Better classified as *Paranthropus*?



Emerging *Homo*

The *Paranthropus* hand

- Relatively small size of the distal joint surfaces in relation to the cross-sectional area of the diaphysis.
- Overall the *Paranthropus* phalanges resemble those of *Theropithecus* in having relatively reduced second digit.
 - Exploitation of savannah resources, which may have consisted of small vegetable food items, harvested individually, and probably requiring a continuous feeding to satisfy caloric needs.
- Just indicative of arboreality?



Emerging *Homo*

Descendência de “*Habilis*”?



Table 1 | Relative fleshy-foot length in LB1, humans and apes*

Species	N	Mean	Standard deviation	Range
<i>Homo sapiens</i> †	34	54.2	2.5	49.3–58.9
<i>Homo sapiens</i> (pygmy)‡	10	54.5	2.1	50.7–56.7
<i>Homo floresiensis</i> (LB1)	1	70.0	—	67.5–72.9§
<i>Pan paniscus</i>	8	73.9	3.2	68.4–77.2
<i>Pan troglodytes</i>	36	82.5	4.9	72.3–95.9

N, sample size.

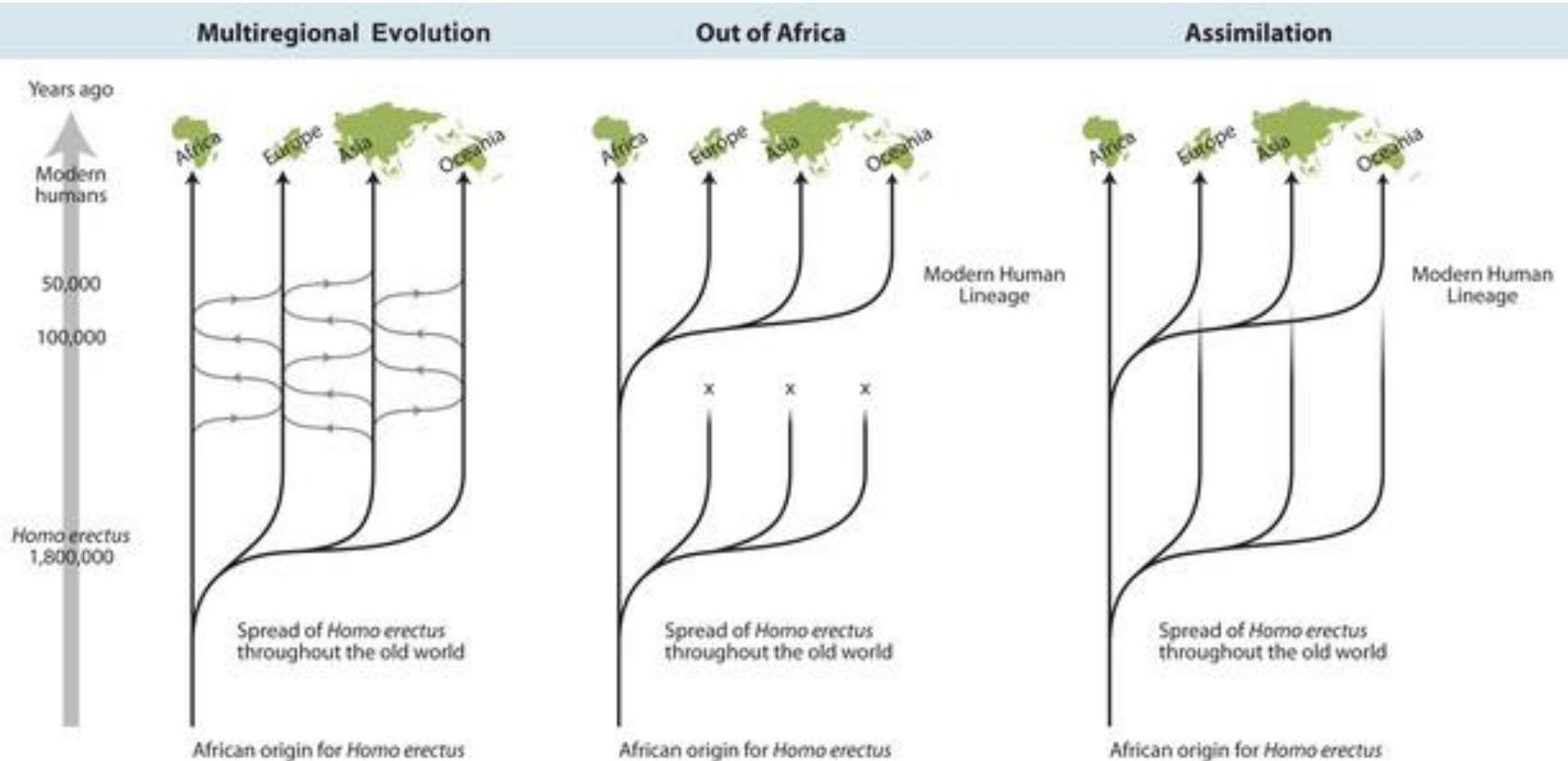
* $100 \times (\text{fleshy-foot length} / \text{femur length})$.

2 - EXTENDED OR STANDARD (HUMAN) EVOLUTION?



Extended or standard (human) evolution?

O multi-regionalismo



Extended or standard (human) evolution?

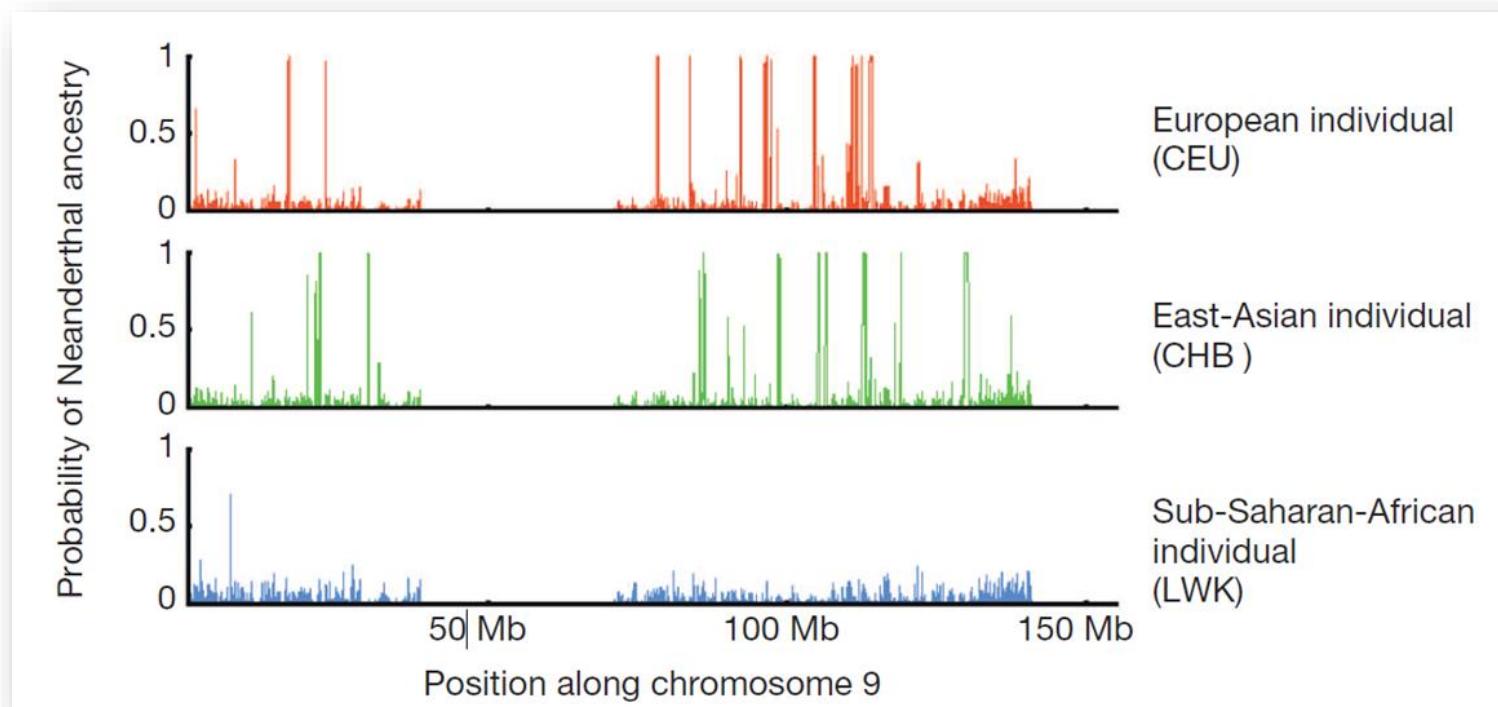
Interações além *Sapiens*: Neanderthal, Denisovano e além...



Extended or standard (human) evolution?

Ancestralidade neandertal em humanos

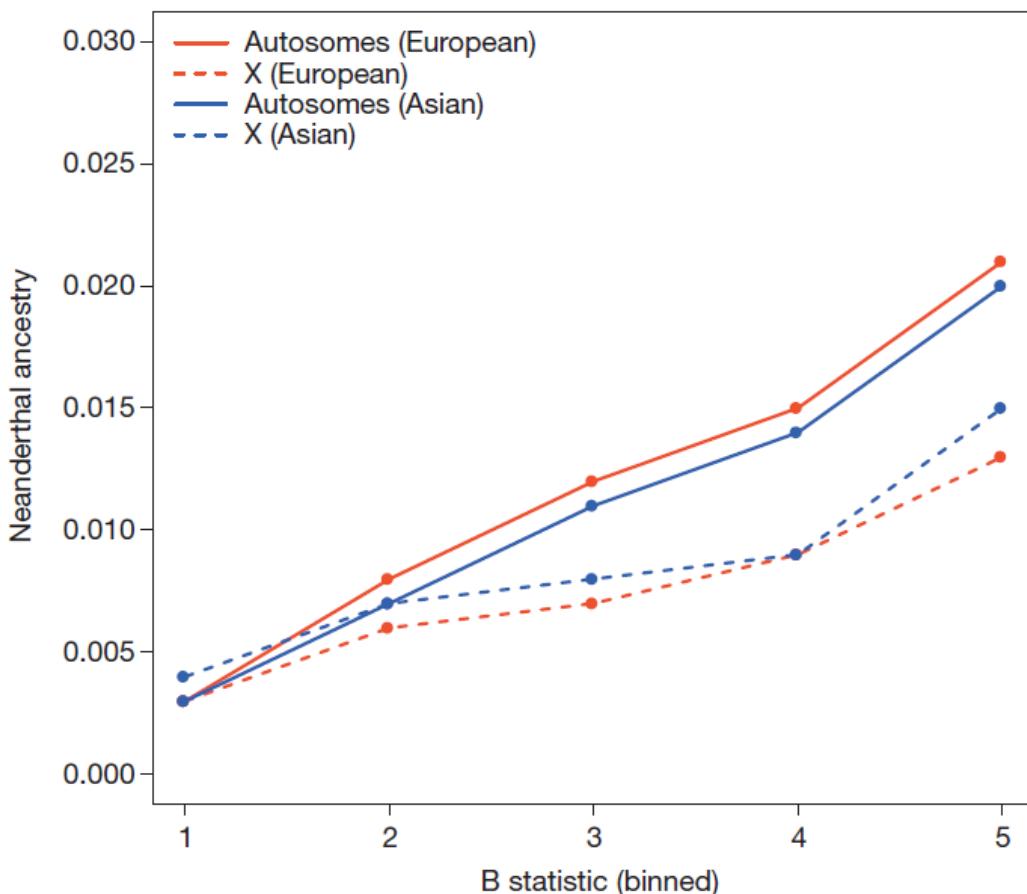
- Em busca de haplótipos Neandertais em 1000 genomas Europeus e Asiáticos
- A feição mais surpreendente dos mapas de introgressão são os longos ‘desertos’ de ancestralidade Neandertal. -> numa escala de 10Mb nos autossomos, existem 4 e 14 janelas em populações Européias e Asiáticas, respectivamente, com ancestralidade Neandertal <0,1%.



Extended or standard (human) evolution?

Ancestralidade neandertal em humanos

- Em busca de haplótipos Neandertais em 1000 genomas Europeus e Asiáticos
- A feição mais surpreendente dos mapas de introgressão são os longos ‘desertos’ de ancestralidade Neandertal. -> numa escala de 10Mb nos autossomos, existem 4 e 14 janelas em populações Européias e Asiáticas, respectivamente, com ancestralidade Neandertal <0,1%.



Seleção negativa?

Estatística B: indica relevância funcional de áreas do genoma (relação inversa).

Ancestralidade Neandertal é drasticamente menor em áreas altamente funcionais (i.e. com muitos genes).

Extended or standard (human) evolution?

Ancestralidade neandertal em humanos

- Em busca de haplótipos Neandertais em 1000 genomas Europeus e Asiáticos
- **No cromosso X a ausência de ancestralidade Neandertal é particularmente marcante (20% dos autossomos)**
- Genes que se expressão preferencialmente nos testículos estão particularmente ausentes da ancestralidade Neandertal

Table
Region
Europe (%)
East Asia (%)
Americas (%)
Africa (%)

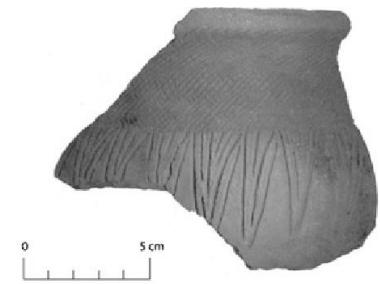
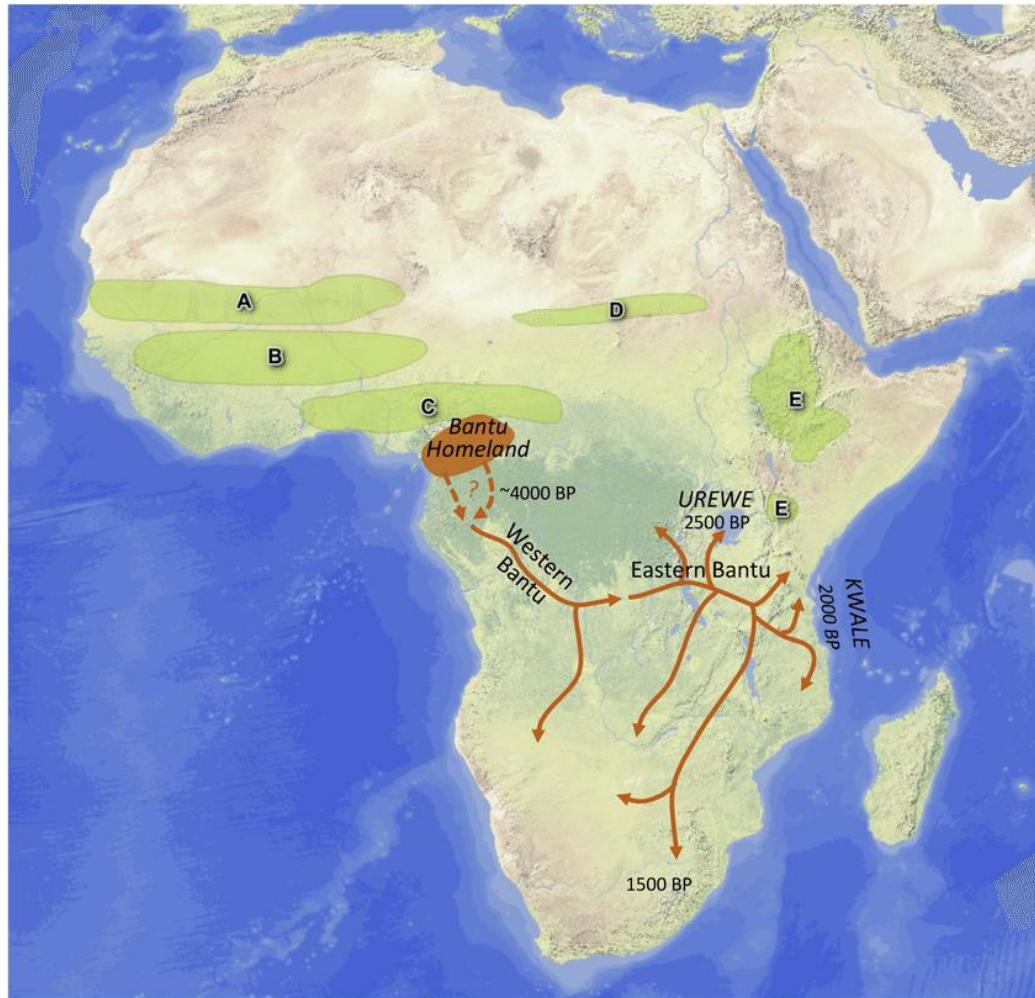
500 mil anos de divergência
=
limite da compatibilidade biológica

Extended or standard (human) evolution?



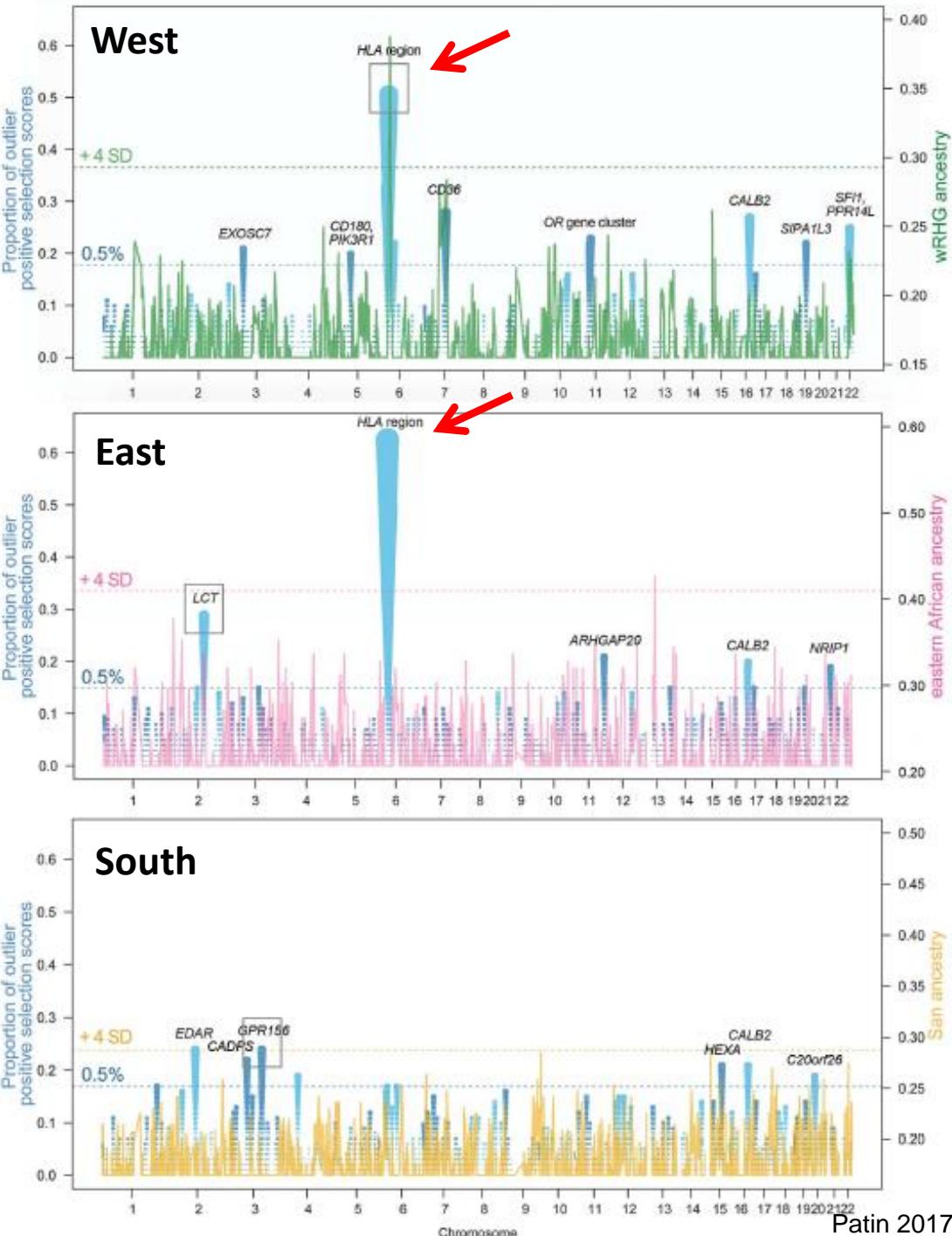
Extended or standard (human) evolution?

A genética da expansão Bantu



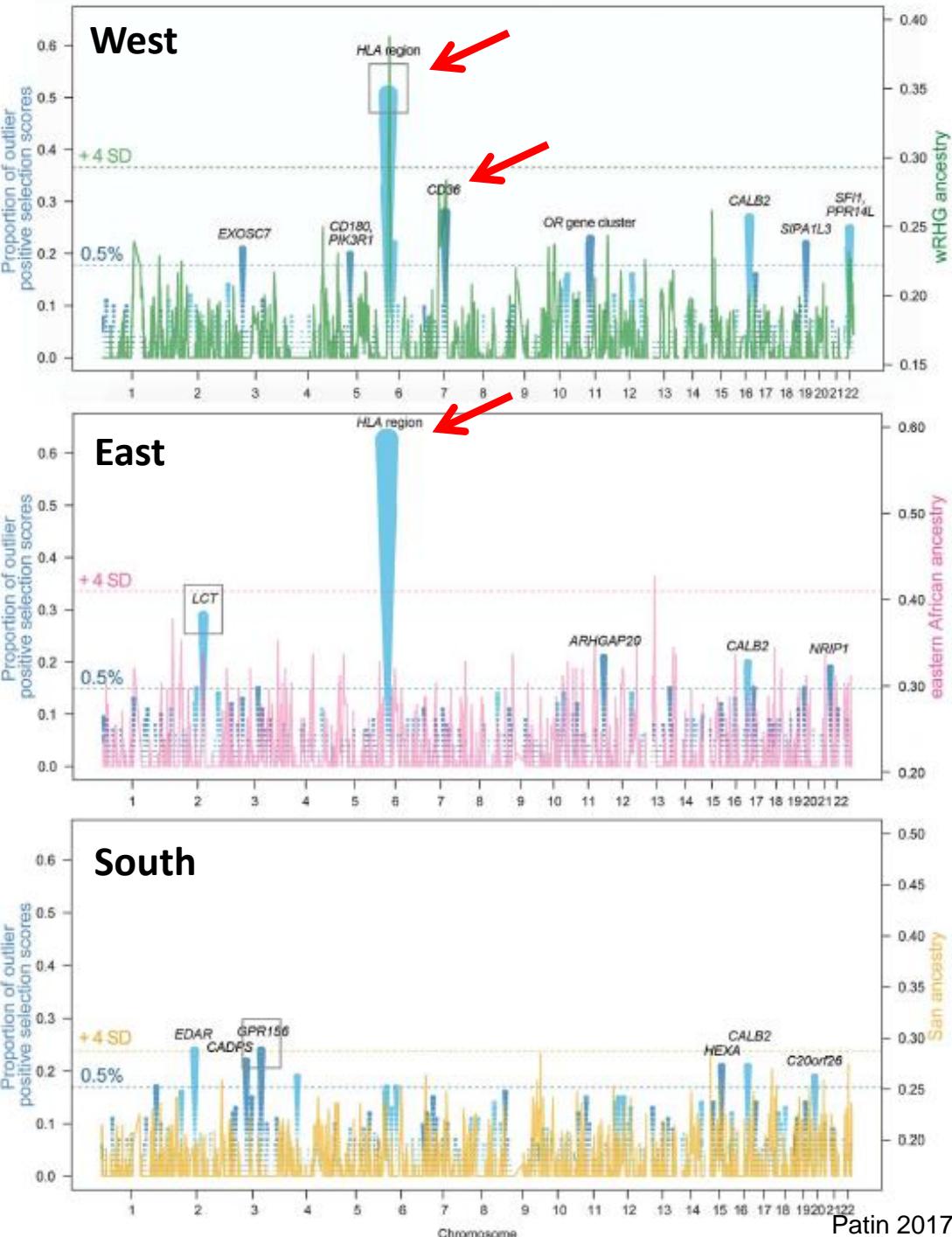
Adaptações ‘Bantu’?

- HLA [W,E] -> Sistema imune.



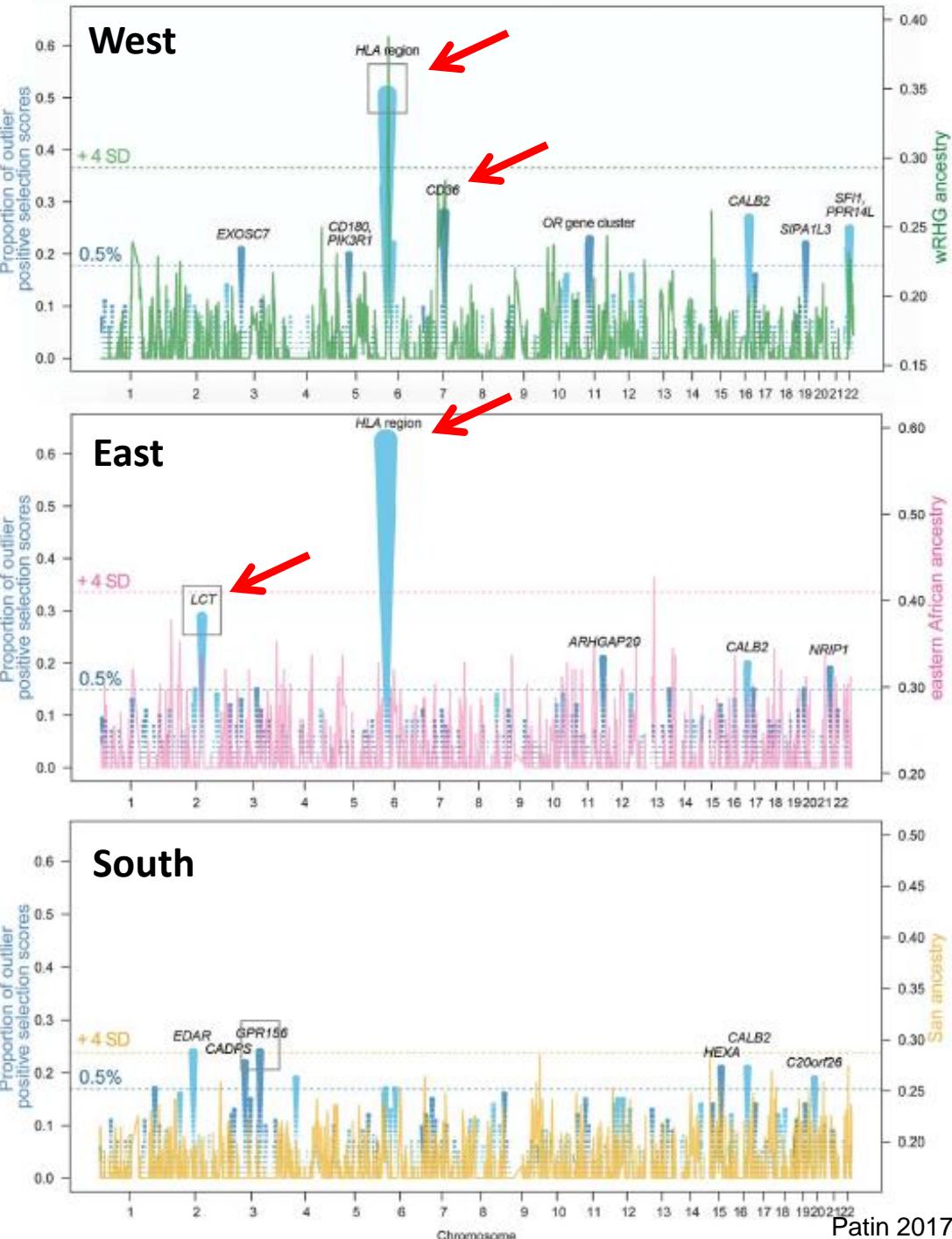
Adaptações ‘Bantu’?

- HLA [W,E] -> Sistema imune.
- CD36 [W] -> Susceptibilidade à malária.



Adaptações ‘Bantu’?

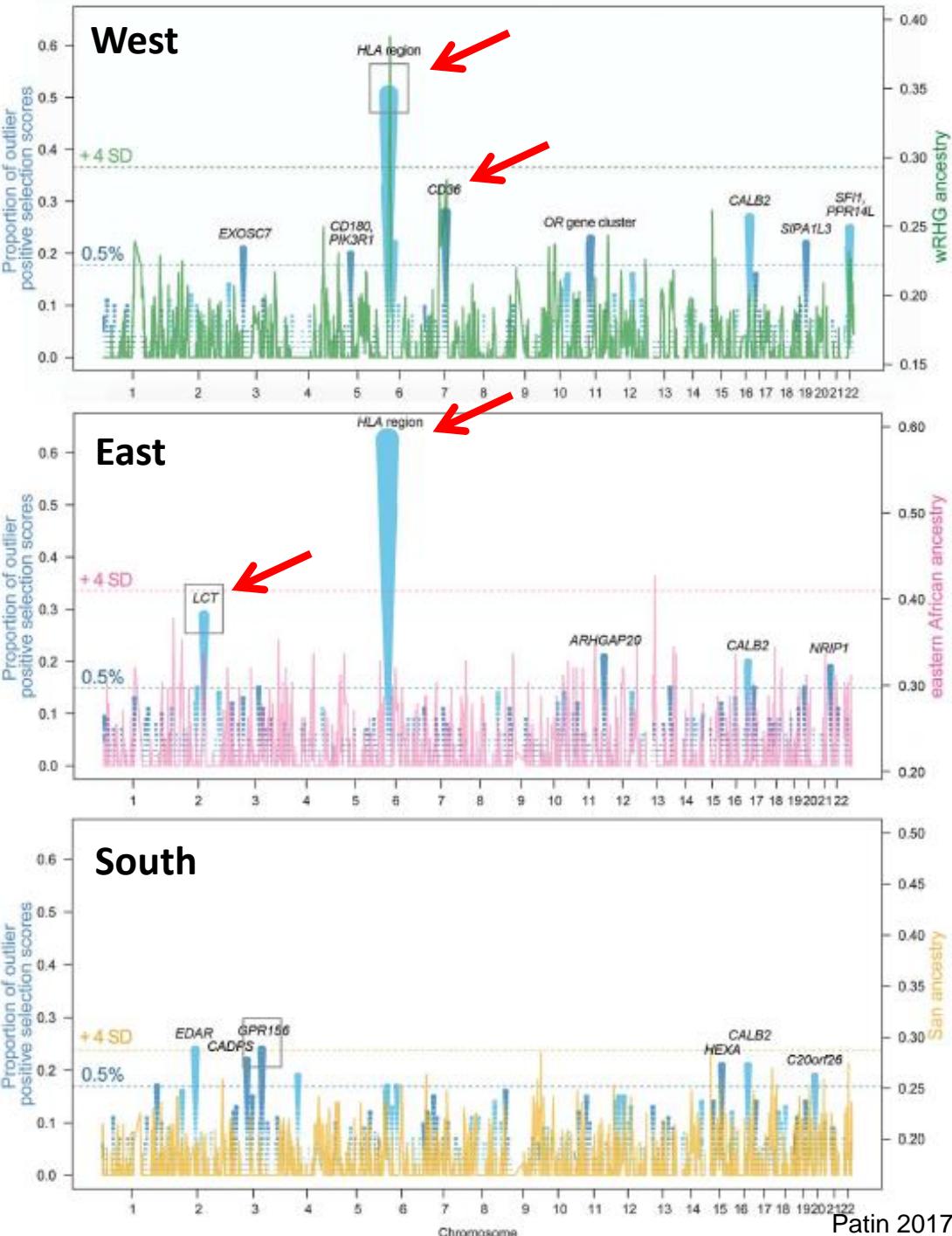
- HLA [W,E] -> Sistema imune.
- CD36 [W] -> Susceptibilidade à malária.
- LCT [E] -> Codifica lactase.



Adaptações ‘Bantu’?

- HLA [W,E] -> Sistema imune.
- CD36 [W] -> Susceptibilidade à malária.
- LCT [E] -> Codifica lactase.

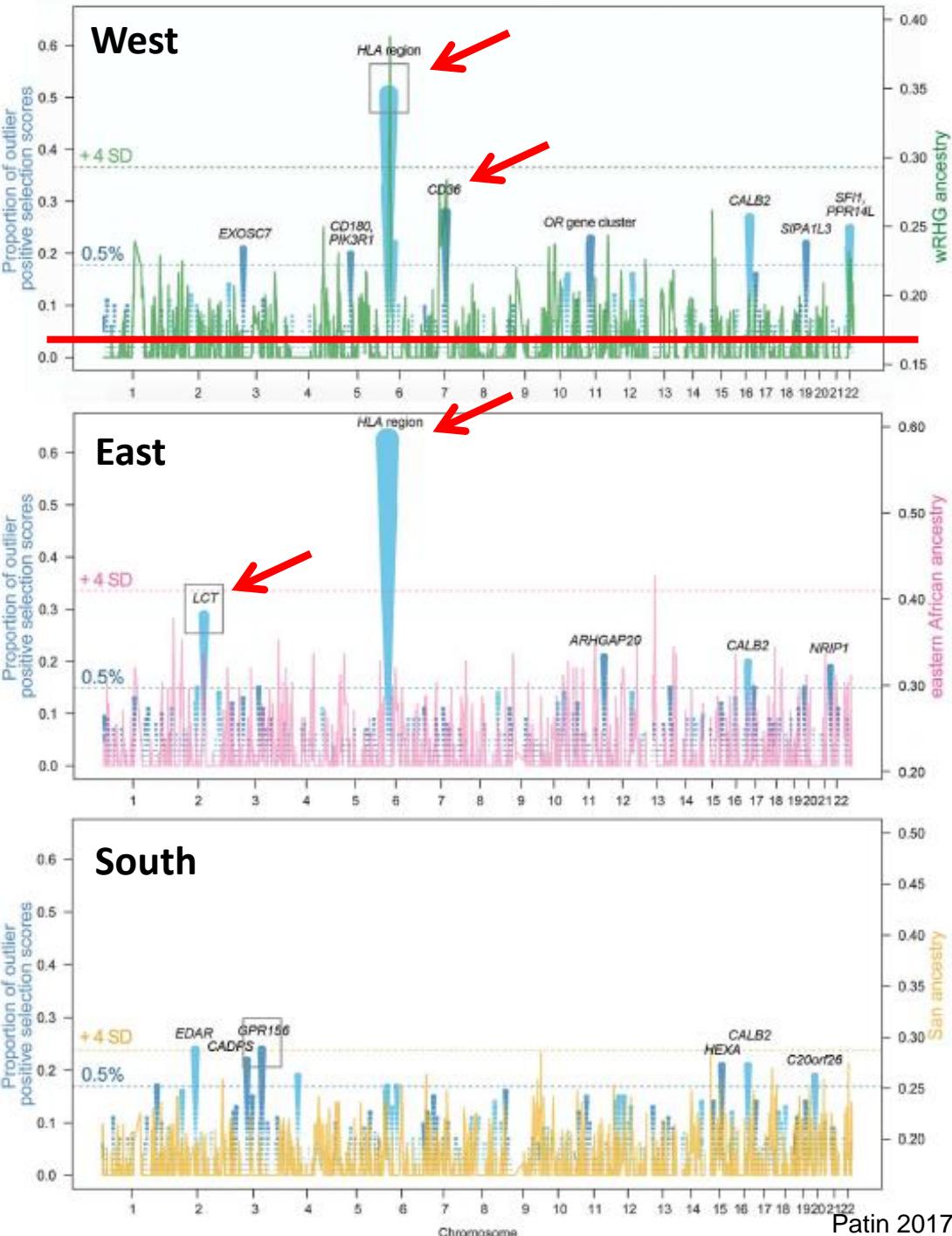
Ancestralidade Pigmeu média entre Bantu do Oeste = ~16%



Adaptações ‘Bantu’?

- HLA [W,E] -> Sistema imune.
- CD36 [W] -> Susceptibilidade à malária.
- LCT [E] -> Codifica lactase.

Ancestralidade Pigmeu média entre Bantu do Oeste = ~16%

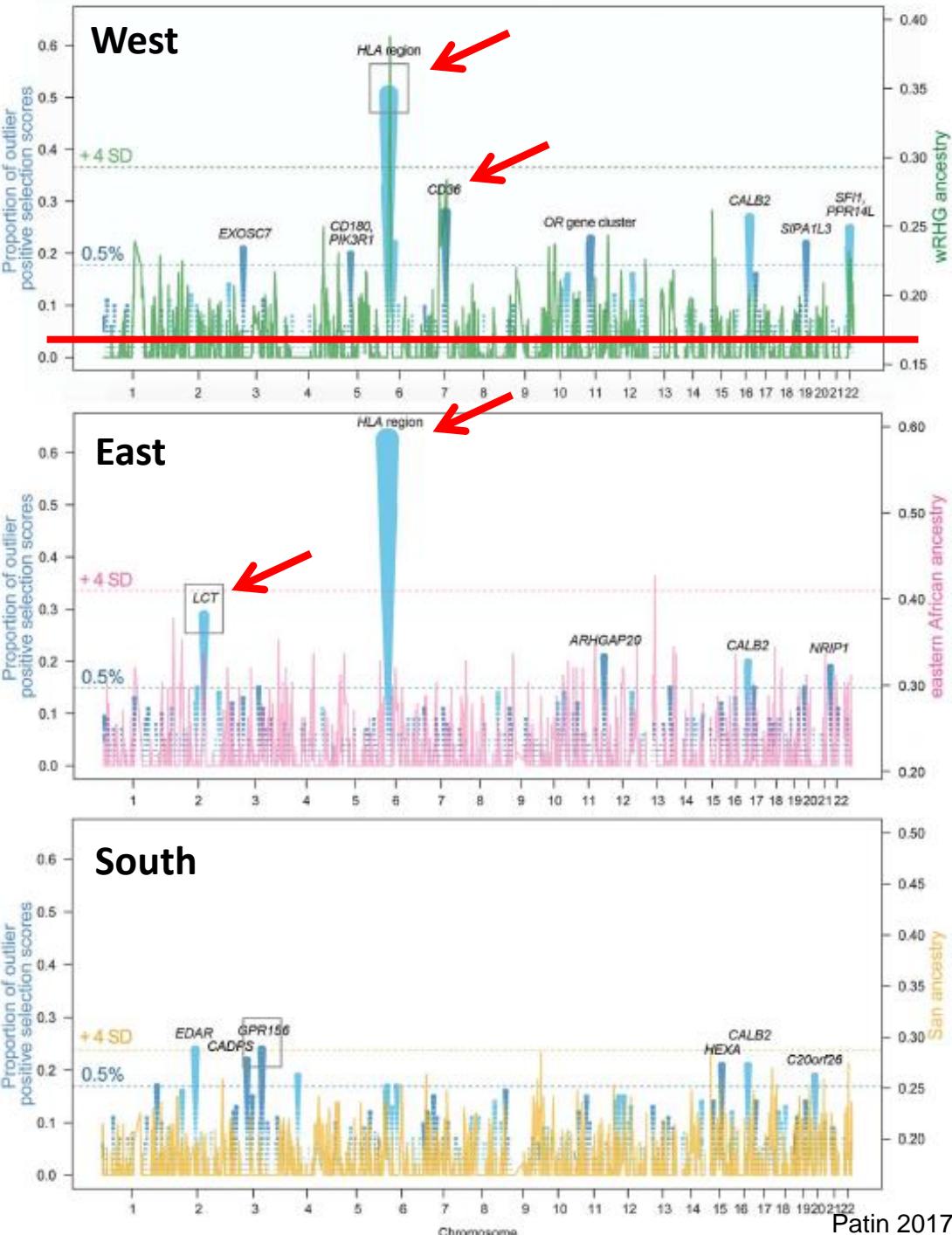


Adaptações ‘Bantu’?

- HLA [W,E] -> Sistema imune.
- CD36 [W] -> Susceptibilidade à malária.
- LCT [E] -> Codifica lactase.

Ancestralidade Pigmeu média entre Bantu do Oeste = ~16%

Ancestralidade Pigmeu na região HLA dos Bantu do Oeste = ~38%



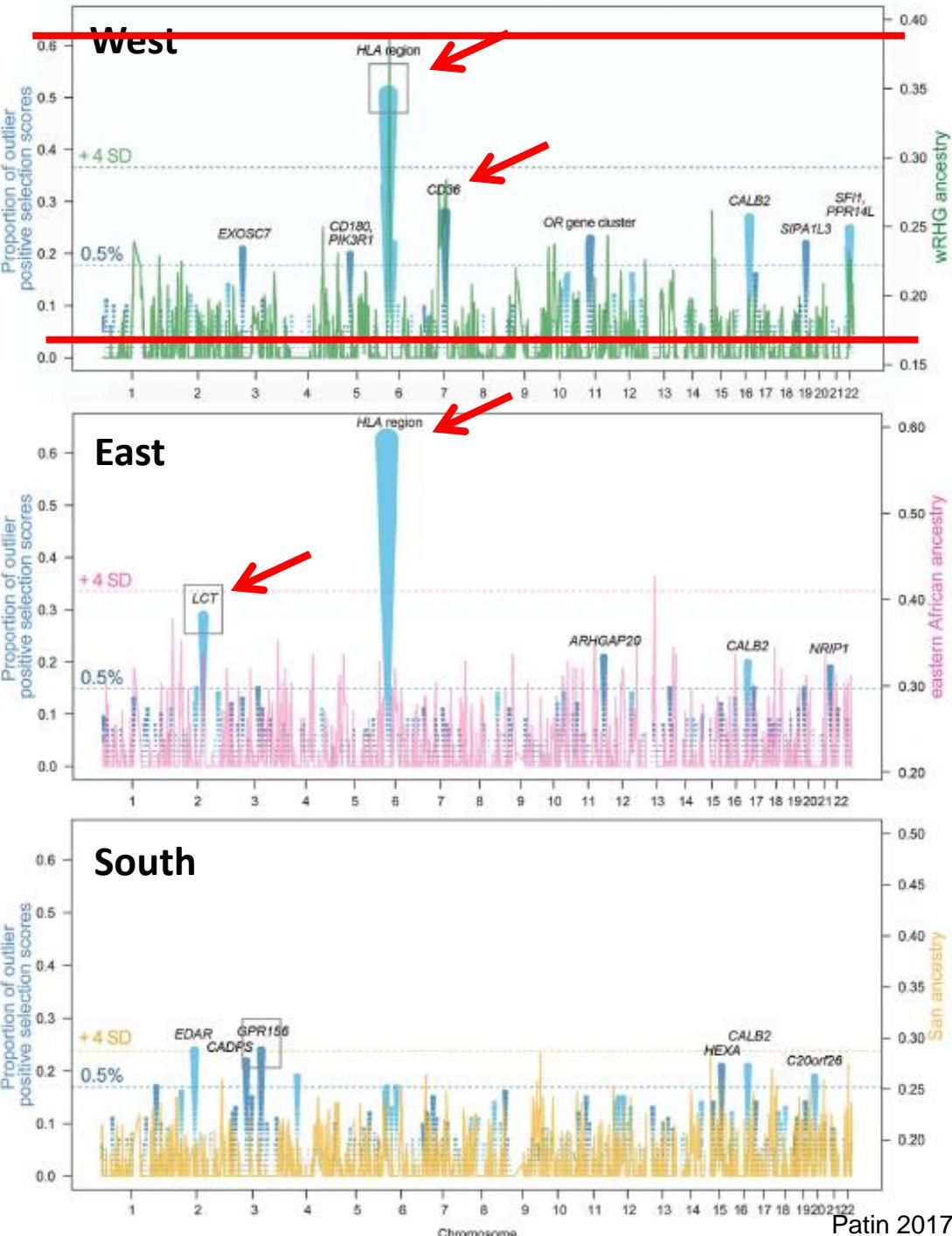
Adaptações ‘Bantu’?

- HLA [W,E] -> Sistema imune.
- CD36 [W] -> Susceptibilidade à malária.
- LCT [E] -> Codifica lactase.

Ancestralidade Pigmeu média entre Bantu do Oeste = ~16%

Ancestralidade Pigmeu na região HLA dos Bantu do Oeste = ~38%

O mesmo é válido para LCT entre Bantu do Leste



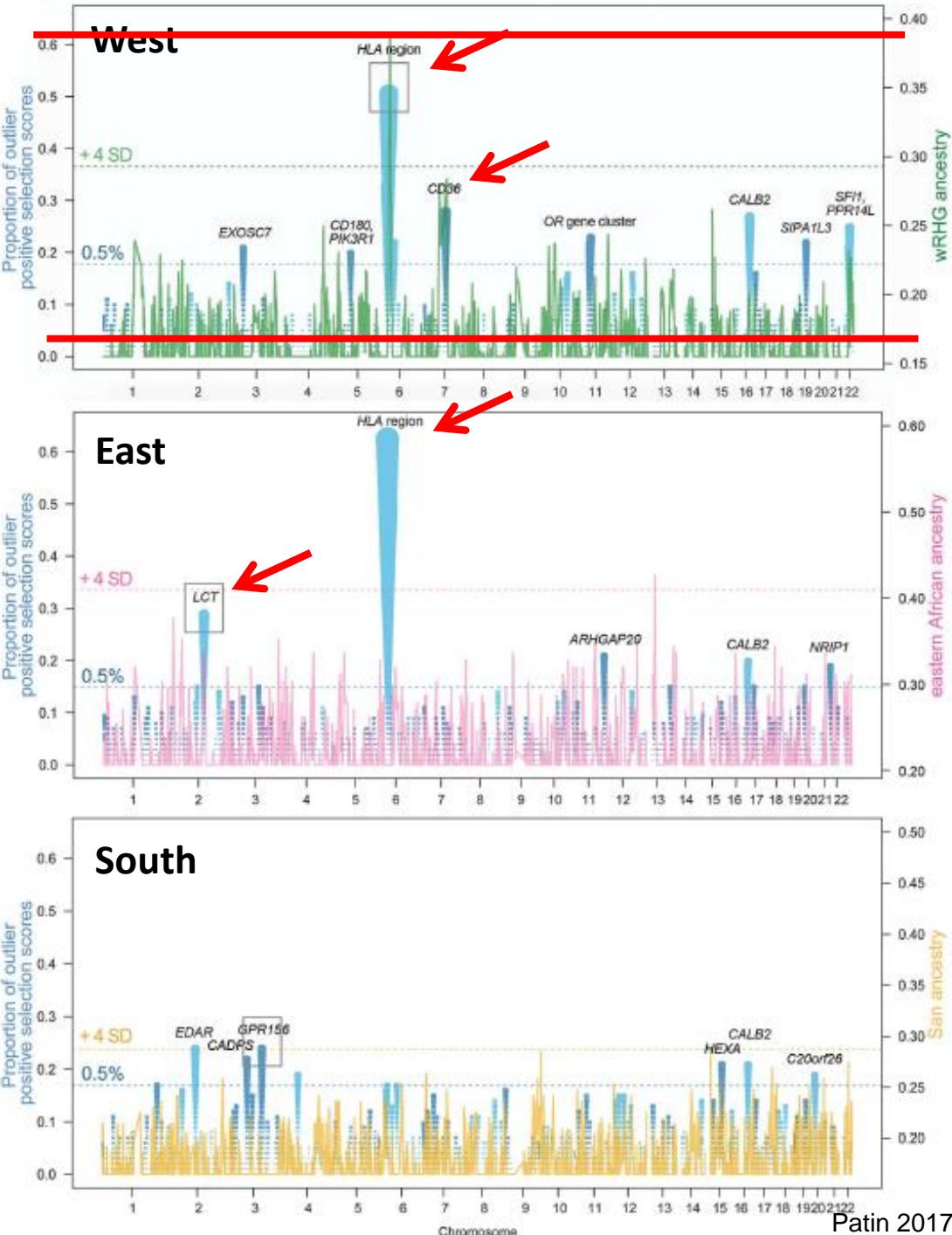
Adaptações ‘Bantu’?

- HLA [W,E] -> Sistema imune.
- CD36 [W] -> Susceptibilidade à malária.
- LCT [E] -> Codifica lactase.

Ancestralidade Pigmeu média entre Bantu do Oeste = ~16%

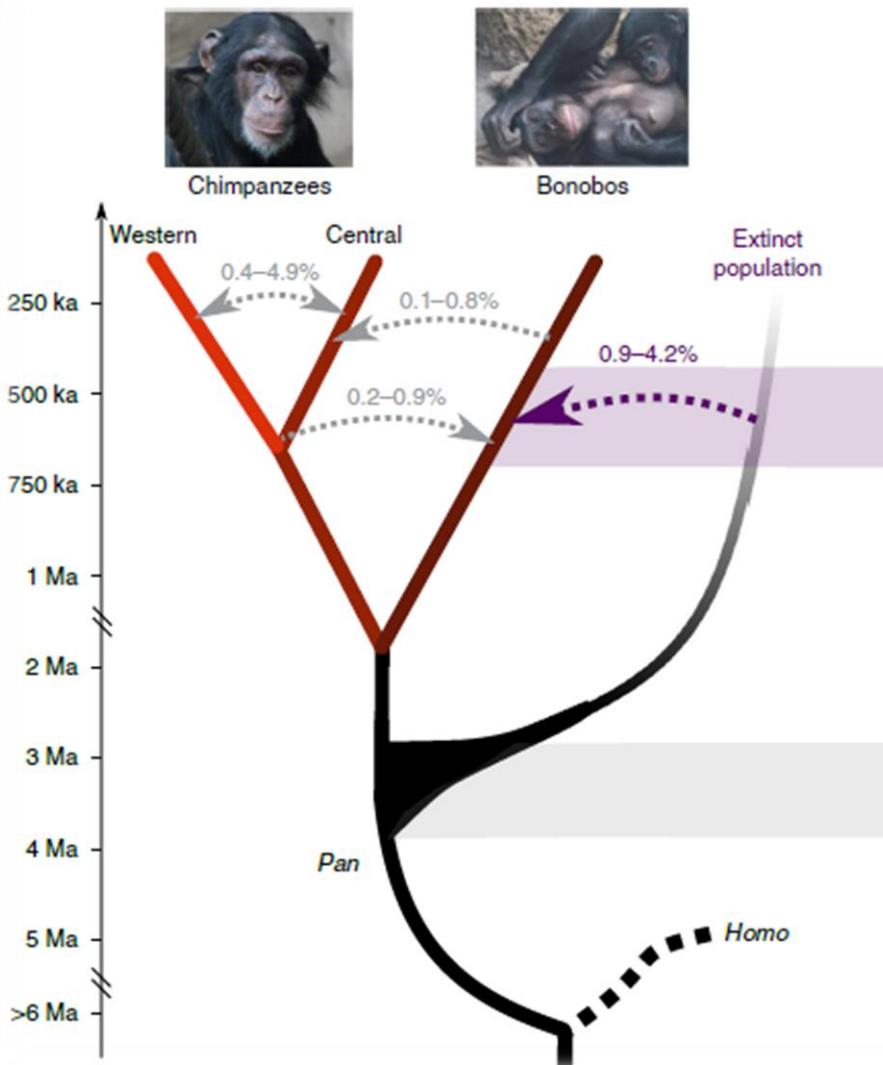
Ancestralidade Pigmeu na região HLA dos Bantu do Oeste = ~38%

O mesmo é válido para LCT entre Bantu do Leste



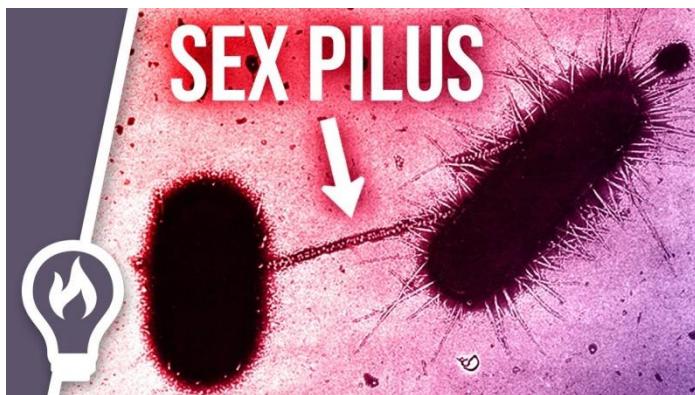
Adaptação por
‘emprestimo’ horizontal
Adaptive introgression

Extended or standard (human) evolution?

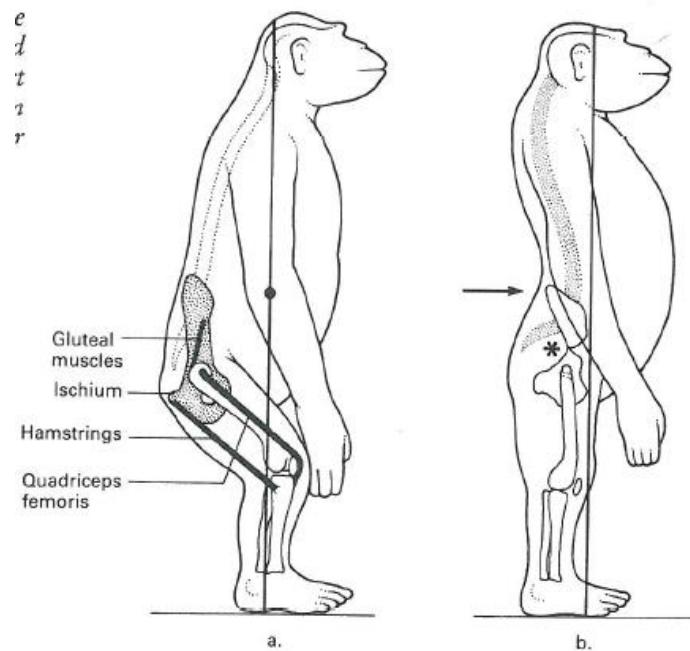


Extended or standard (human) evolution?

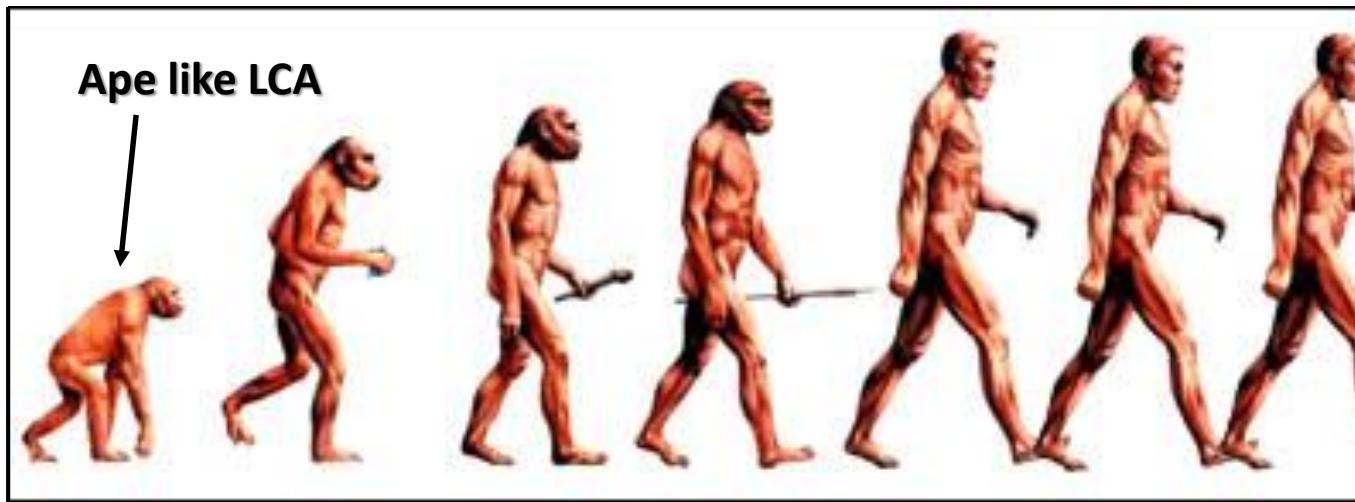
“THEREFORE, WE IDENTIFY A NOVEL MECHANISM, BEYOND SELECTION ON NEW MUTATIONS OR ON STANDING VARIATION, THROUGH WHICH POPULATIONS CAN ADAPT TO LOCAL ENVIRONMENTS” (Jeong 2014)



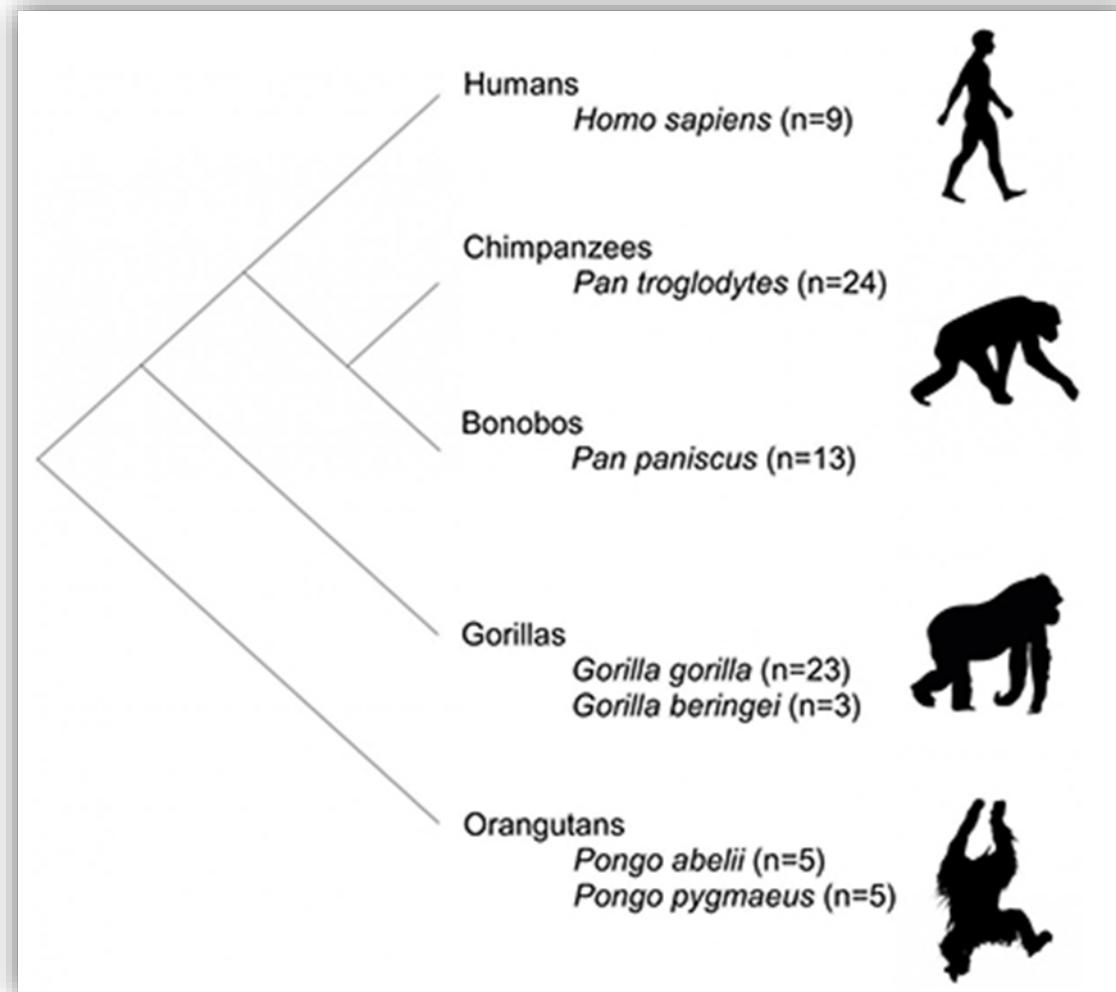
3 - ANCESTRAL COMUM E ILS?



Ancestral comum e ILS?



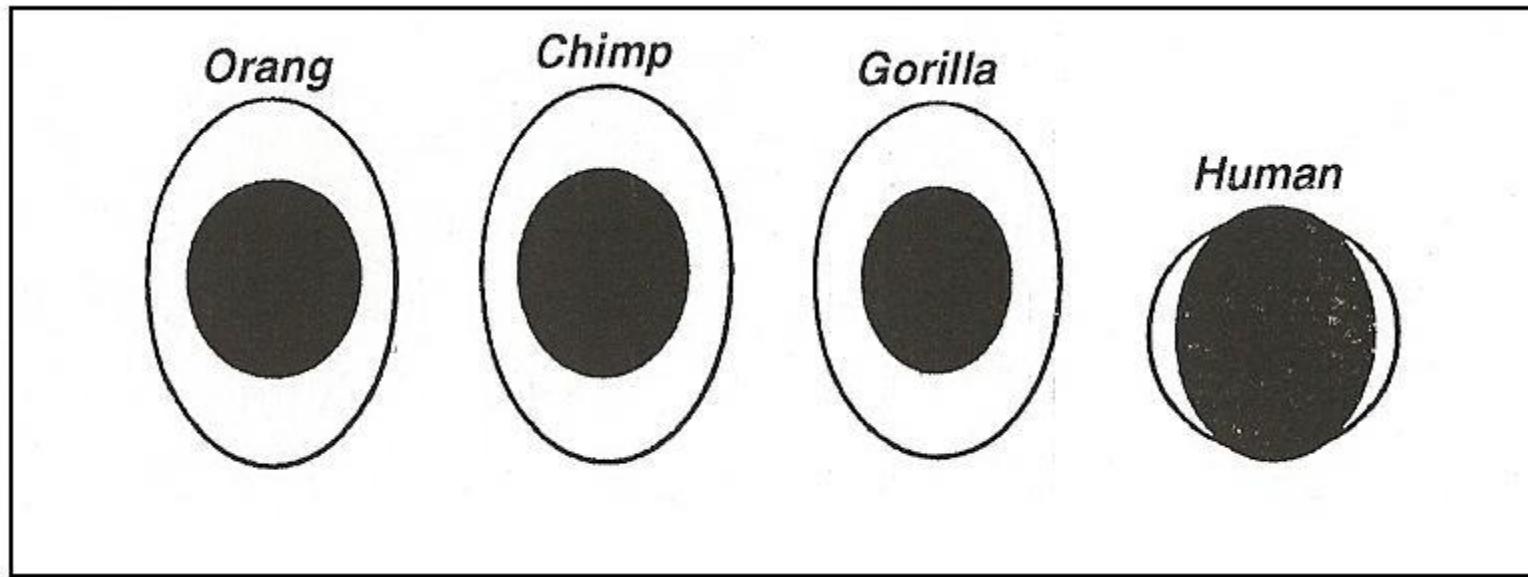
Ancestral comum e ILS?



Ancestral comum e ILS?

The pelvic girdle – sexual dimorphism

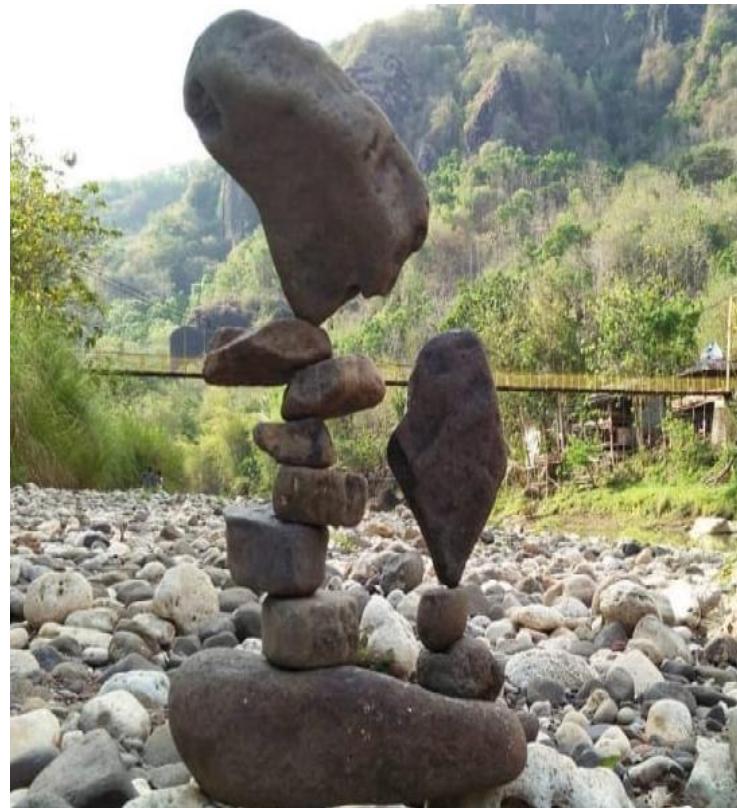
- Great apes are an exception in the sense they have **small cranium** compared to their **true pelvis**.
- Absence of sexual dimorphism in the ape pelvis.



Source: Web

Ancestral comum e ILS?

Bipedal gate



Ancestral comum e ILS?

Humero-femoral index

P. paniscus (extant): 99%

A. afarensis (A.L. 288-1): 85%

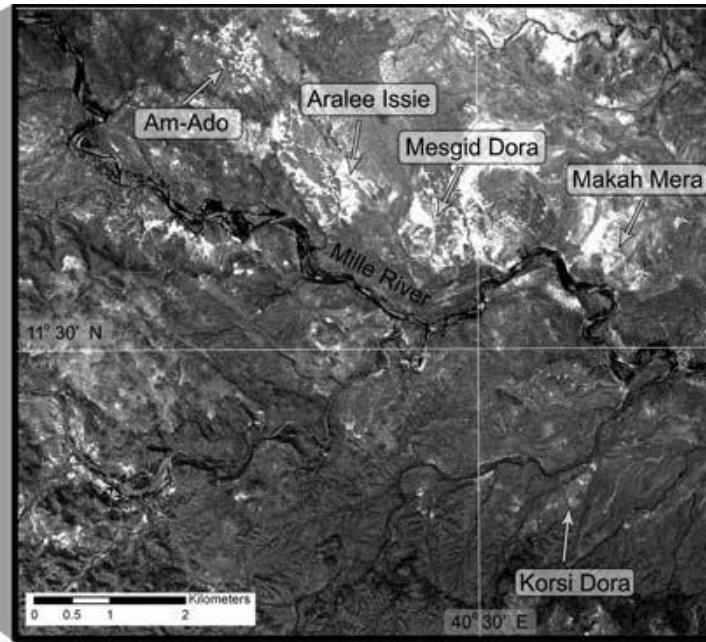
H. sapiens (extant): 75%



Ancestral comum e ILS?

The Woranso-Mille skeleton (*A. afarensis* 3.58 Mya)

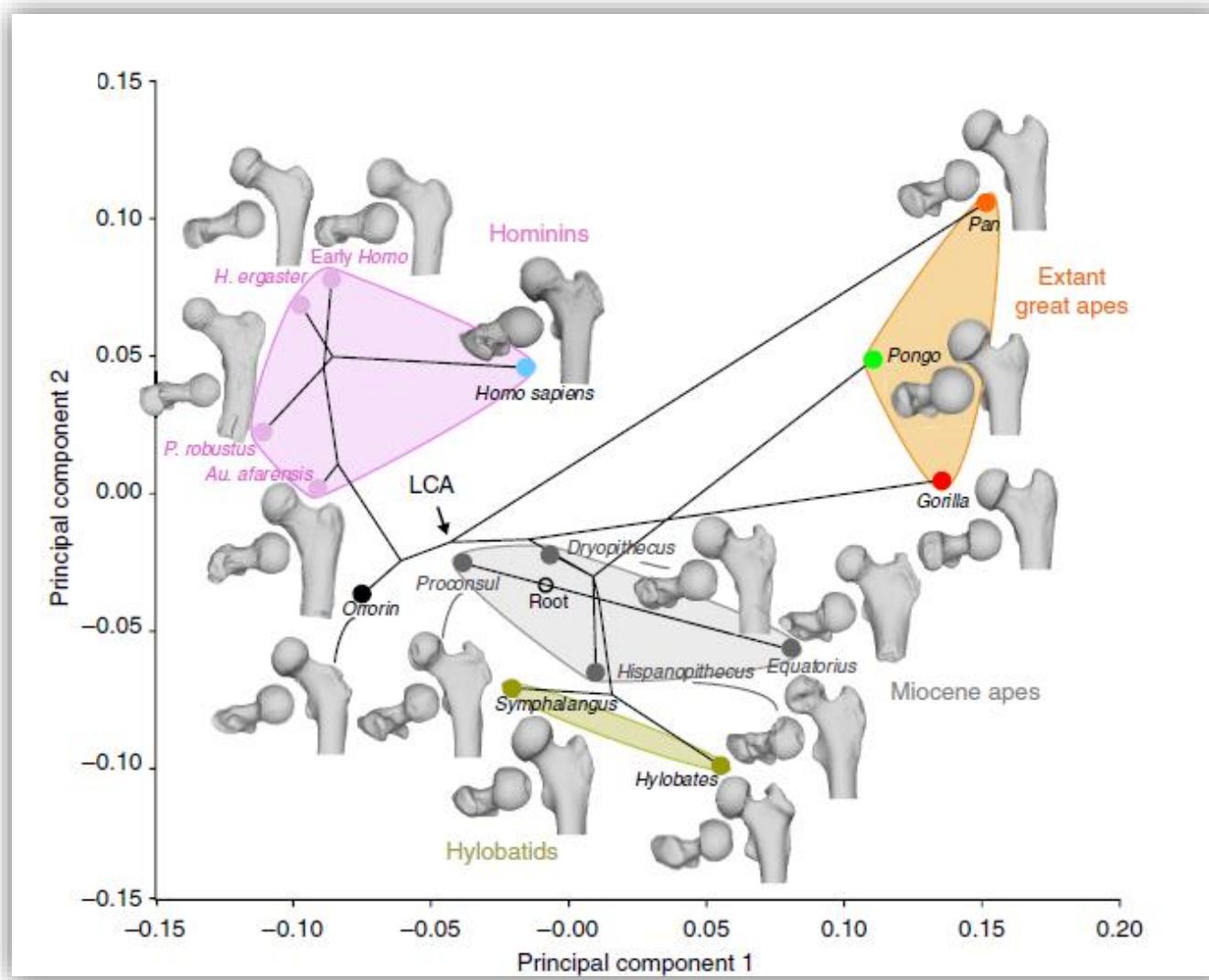
- Discovered in 2005
- This is a large body individual (contrasts to A.L. 288-1)
- Note: it is older than A.L. 288-1
- Accession ID: KSD-VP-1/1



Ancestral comum e ILS?

The evolution of the hominin anterior femur – summary

- Humans are derived but apea are much more – and convergent!!!



Ancestral comum e ILS?

The *Ardipithecus ramidus* foot (4.4 Mya)

- Presence of non-propulsive **abducent hallux**.
- **Lacks** the highly derived tarsometatarsal laxity typical of great apes.
 - Plantar rigidity is actually the primitive condition (leaping demands it).
- Presence of ***os peroneum***
 - Plantar rigidity is actually the primitive condition (leaping demands it).

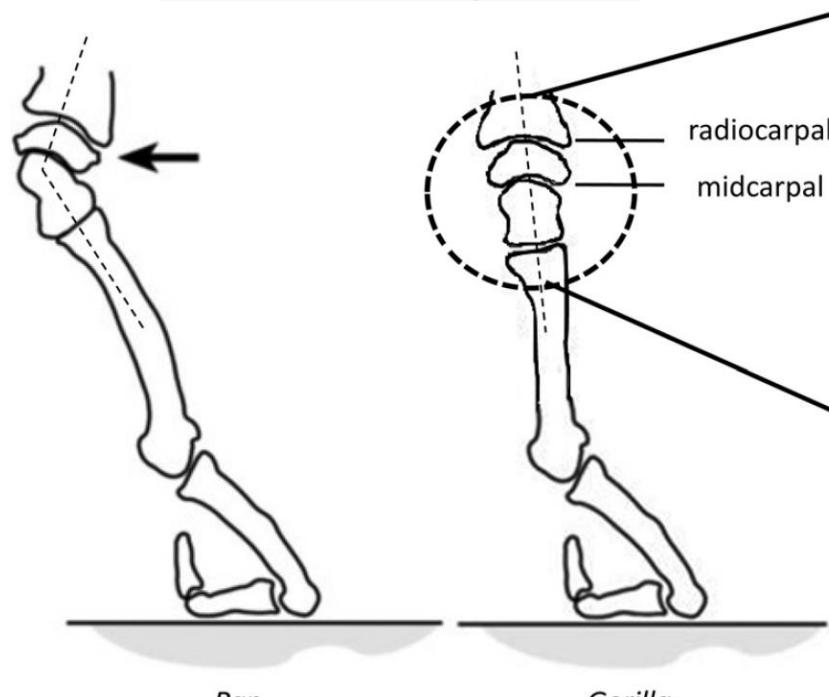
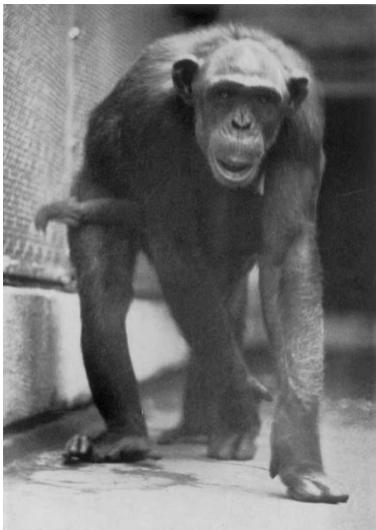


Ancestral comum e ILS?

Knuckle-walking

- Gorillas show increased wrist mobility
- Gorillas have more hyperextended elbow joint (fully pronated arm).
- Sub-equal length of rays 2 through 4 (creating larger stable are to disperse axial load)
- Chimpanzees have more variable wrist posture (palm-in versus palm-back)

Different “wrist posture”



Ancestral comum e ILS?

O genome completo do Gorilla

- Incomplete lineage sorting (ILS).
- Em humanos, chimpanzés e gorilla 36% do genoma está em ILS.

ARTICLE

doi:10.1038/nature10842

Insights into hominid evolution from the gorilla genome sequence

Aylwyn Scally¹, Julien Y. Dutheil^{2†}, LaDeana W. Hillier³, Gregory E. Jordan⁴, Ian Goodhead^{1†}, Javier Herrero⁴, Asger Hobolth², Tuuli Lappalainen⁵, Thomas Mailund², Tomas Marques-Bonet^{3,6,7}, Shane McCarthy¹, Stephen H. Montgomery⁸, Petra C. Schwille⁴, Y. Amy Tang¹, Michelle C. Ward^{3,10}, Yali Xue⁹, Bryndis Yngvadottir⁴, Can Alkan^{9,10}, Lars N. Andersen², Qasim Ayub¹, Edward V. Ball¹², Kathryn Beal⁴, Brenda J. Bradley^{8,13}, Yuan Chen¹, Chris M. Cle'e¹, Stephen Fitzgerald⁴, Tina A. Graves¹⁴, Yong Gu¹, Paul Heath¹, Andreas Heger¹⁵, Emre Karakoc¹⁶, Anja Kolb-Kokociński¹, Gavin K. Laird¹, Gerton Lunter¹⁶, Stephen Meader¹⁵, Matthew Mort¹⁷, James C. Mullikin¹⁷, Kasper Munch², Timothy D. O'Connor⁹, Andrew D. Phillips¹⁸, Javier Prado-Martinez², Anthony S. Rogers¹⁴, Saba Sajadian³, Dominik Schmidt^{9,10}, Katy Shaw¹², Jared T. Simpson¹⁹, Peter D. Stenson¹², Daniel J. Turner^{1†}, Linda Vigilant¹⁸, Albert J. Vilella⁴, Weldon Whitener¹, Baoli Zhu^{19†}, David N. Cooper¹², Pieter de Jong¹⁹, Emmanuel T. Dermizakis¹⁸, Evan E. Eichler^{3,11}, Paul Flicek⁴, Nick Goldman⁴, Nicholas I. Mundy⁸, Zemin Ning¹, Duncan T. Odom^{1,9,10}, Chris P. Ponting¹⁵, Michael A. Quail¹, Oliver A. Ryder²⁰, Stephen M. Searle¹, Wesley C. Warren¹⁴, Richard K. Wilson¹⁴, Mikkel H. Schierup², Jane Rogers^{1†}, Chris Tyler-Smith¹ & Richard Durbin¹

RESEARCH

RESEARCH ARTICLE

GREAT APE GENOMICS

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^{1,4}, Olivia S. Meyerson^{4,5}, Jason G. Underwood^{1,5+}, Bradley J. Nelson¹⁺, Mark J. P. Chaisson^{1,6}, Max L. Dougherty³, Katherine M. Munson¹, Alex R. Hastie¹, Mark Diekhans², Fereydon Hormozdiari⁸, Nicola Lorusso⁹, Kendra Hoekzema¹, Ruolan Qin¹, Karen Clark¹⁰, Archana Raju^{1,2}, AnneMarie E. Welch¹, Melanie Sorensen¹, Carl Baker¹, Robert S. Fulton¹¹, Joel Armstrong², Tina A. Graves-Lindsay¹¹, Ahmet M. Denli¹², Emma R. Hoppet¹, PingIsun Hsieh¹, Christopher M. Hill¹, Andy Wing Chun Pang¹, Joyce Lee⁷, Ernest T. Lam⁷, Susan K. Dutcher¹¹, Fred H. Gage¹², Wesley C. Warren¹¹, Jay Shendure^{1,3}, David Haussler^{2,13}, Valerie A. Schneider¹⁰, Han Cao⁷, Mario Ventura⁹, Richard K. Wilson¹¹, Benedict Paten², Alex Pollen^{4,14}, Evan E. Eichler^{1,2,†}

tential structural and transcript differences observed between the species. Using long-read, long-range sequence and mapping technologies (13–15), we generated new great ape genome assemblies, along with full-length cDNA annotation, without guidance from the human genome. We also generated and analyzed an African genome and an effectively haploid human genome complement to distinguish fixed differences in the human ancestral lineage and to further mitigate human genome reference biases.

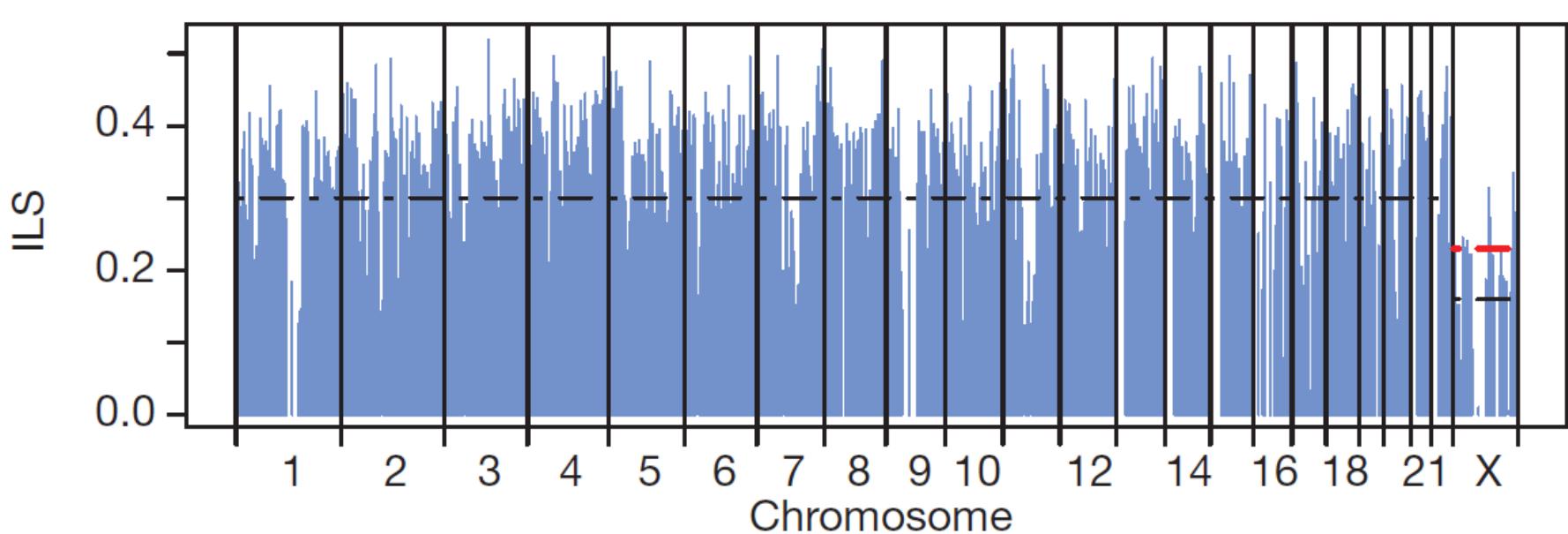
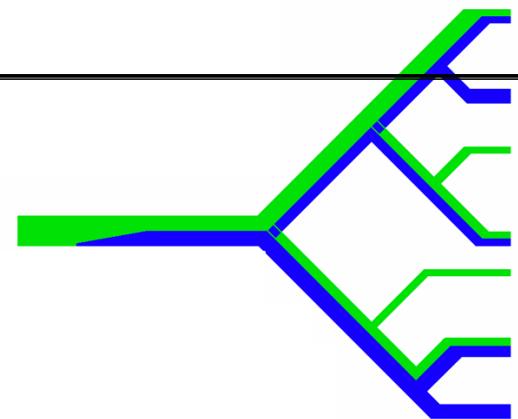
Results
Genome assembly

We sequenced two human, one chimpanzee, and one orangutan genome to high depth (>65-fold coverage) using single-molecule real-time (SMRT; PacBio) sequence data and assembled each ab initio using the same underlying assembly algorithm (Table 1) (16). For each species, we generated assemblies ranging from 2.9 to 3.1 giga-base pairs (Gbp) in size, where most of the euchromatic DNA mapped to <1000 large contigs (Table 1). We

Ancestral comum e ILS?

O genome completo do Gorilla

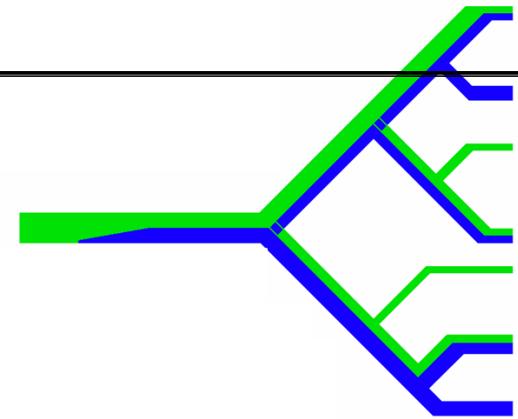
- Incomplete lineage sorting (ILS).
- Em humanos, chimpanzés e gorilla 36% do genoma está em ILS.



Ancestral comum e ILS?

O genome completo do Gorilla

- Incomplete lineage sorting (ILS).
- Em humanos, chimpanzés e gorilla 36% do genoma está em ILS.



IN 36% OF THE GENOME, GORILLA IS CLOSER TO HUMAN OR CHIMPANZEE THAN THE LATTER ARE TO EACH OTHER.

OBRIGADO !

André Strauss

Museu de Arqueologia e Etnologia

Laboratório de Arqueologia e Antropologia Ambiental e
Evolutiva (LAAAE)

strauss@usp.br

