Molecular Portrait of Brazilians

Portrait of Human Genome Diversity

Sérgio Pena
sdpena@gmail.com

Stephanie Keith/Reuters

Counterprotesters Overshadow Boston Rally

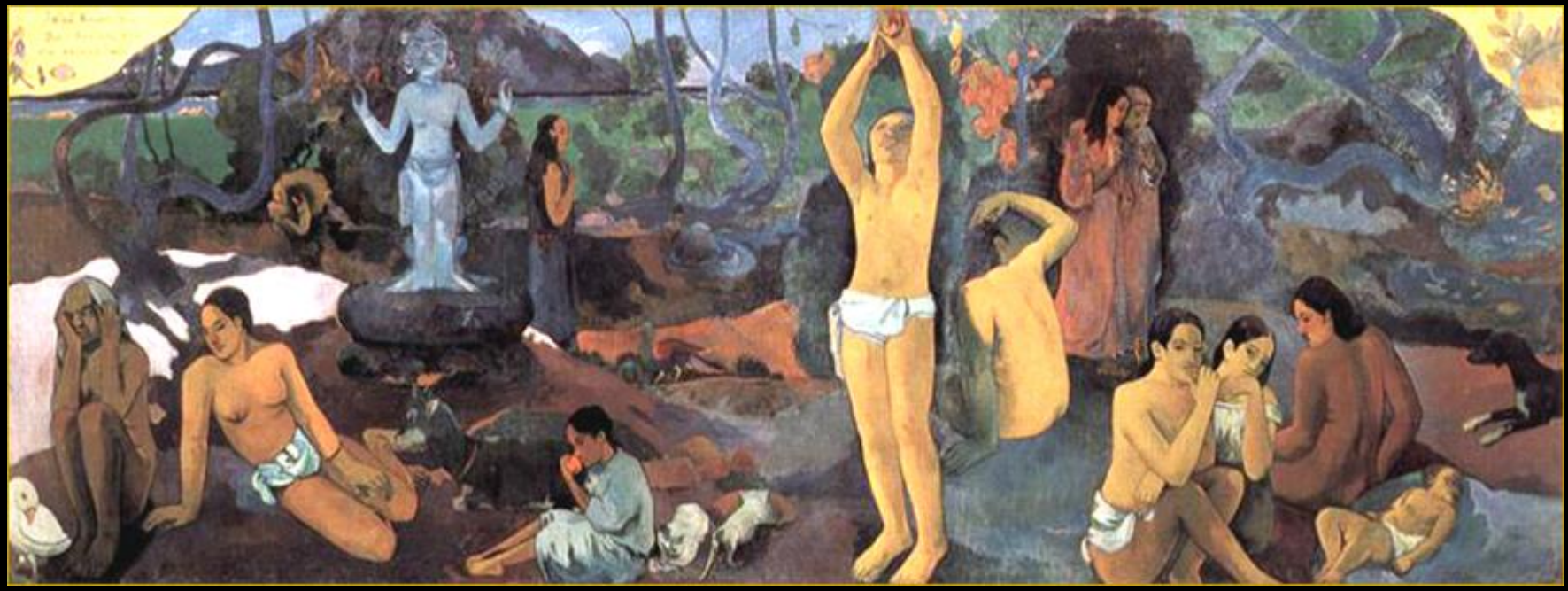
By KATHARINE Q. SEELYE, ALAN BLINDER and JESS BIDGOOD

Thousands of demonstrators poured into the nation's streets and parks on Saturday to denounce white supremacy and Nazism.

I am a member of a fragile species, still new to the Earth, the youngest creatures of any scale, here only a few moments as evolutionary time is measured, a juvenile species, a child of a species. [...]

This is a very big place, and I do not know how it works, nor how I fit in.

Lewis Thomas, *The Fragile Species*



Paul Gauguin, 1897

D'où venons-nous? Qui sommes-nous? Où allons-nous?

The Evolution of Human Diversity

- Humans as members of typological races (pre-Genetics)
- Humans as members of populations (pre-DNA)
- Humans as individual members of genealogies (Genomic Era)

A new paradigm:

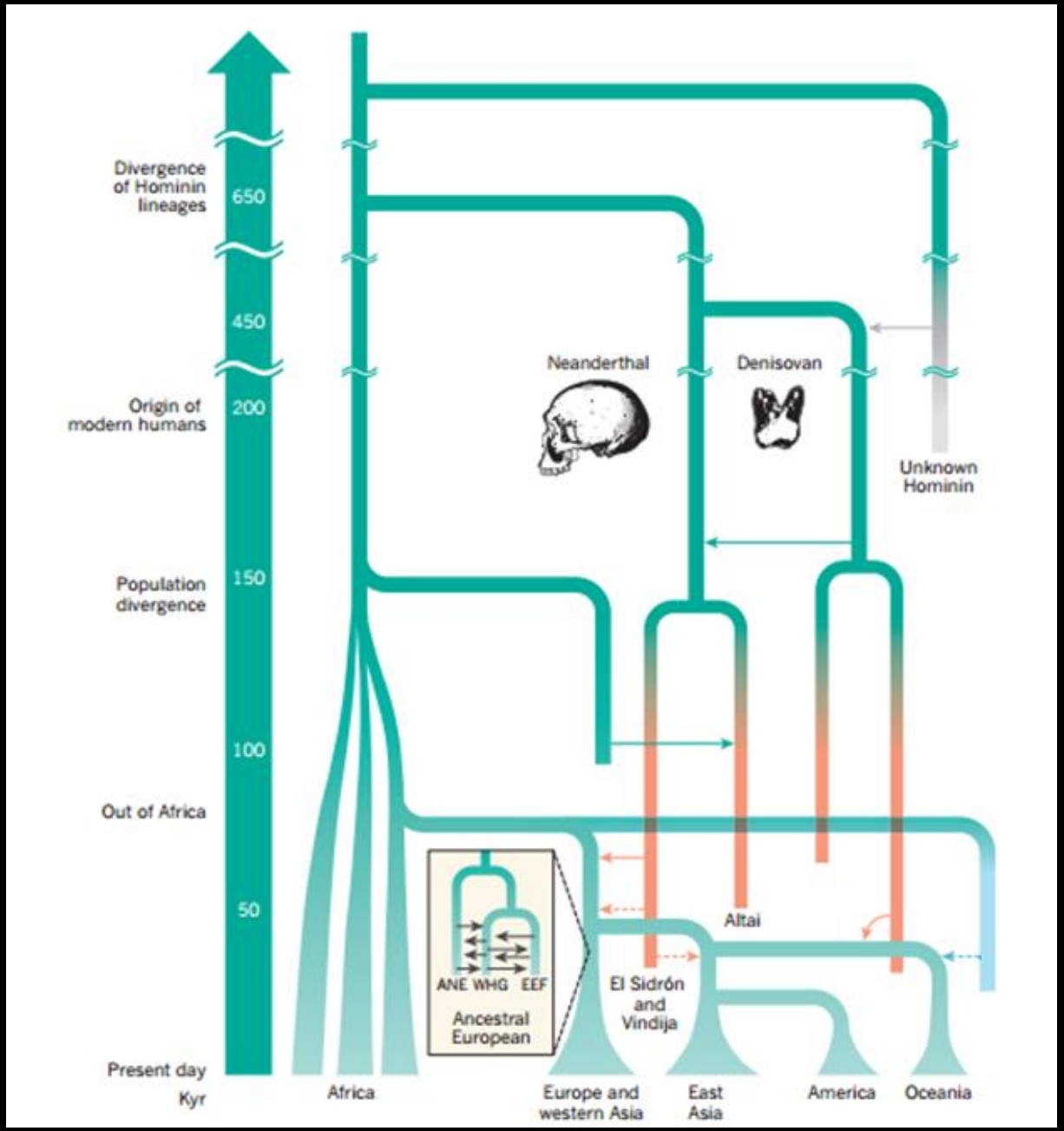
Division of humanity in individuals belonging to genealogies

Three major developments that occured in the Genome Era

- Characterization of the recent unique origin of modern humans in Africa
- Characterization of human genomic individuality at the DNA level
- Characterization of the genealogical structure of humanity

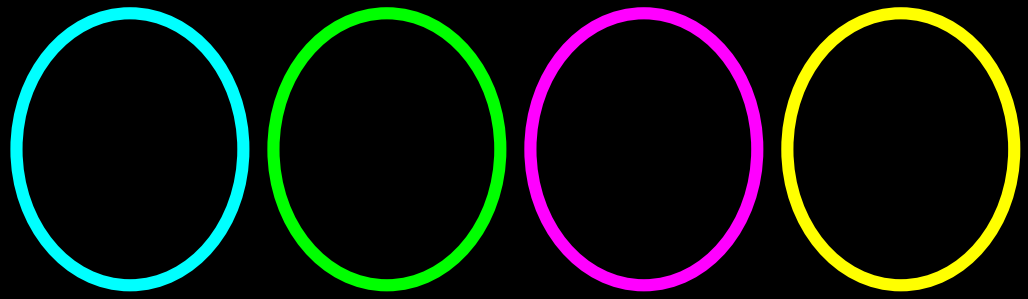

Modern humanity had a single origin in Africa, less than 200,000 years before present

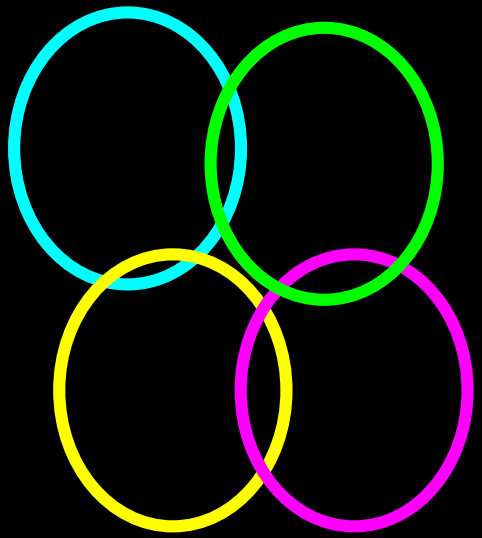
Aproximately 60,000 years ago, modern humanity left Africa and occupied all other continentes

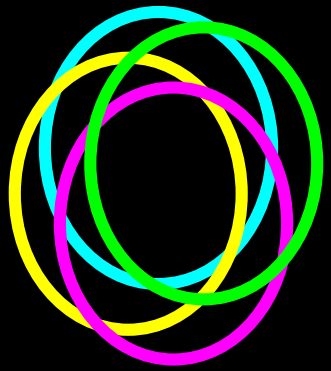

Divergence of Hominin lineages
650
450
Origin of modern humans
200
Population divergence
150
100
Out of Africa
50
Present day
Kyr
Neanderthal
Denisovan
Unknown Hominin
ANE WHG EEF
Ancestral European
Altai
El Sidrón and Vindija
Africa
Europe and western Asia
East Asia
America
Oceania

In this migratory process humanity diversified through the ocurrence of new mutations and adaptations to the diverse continental environments.

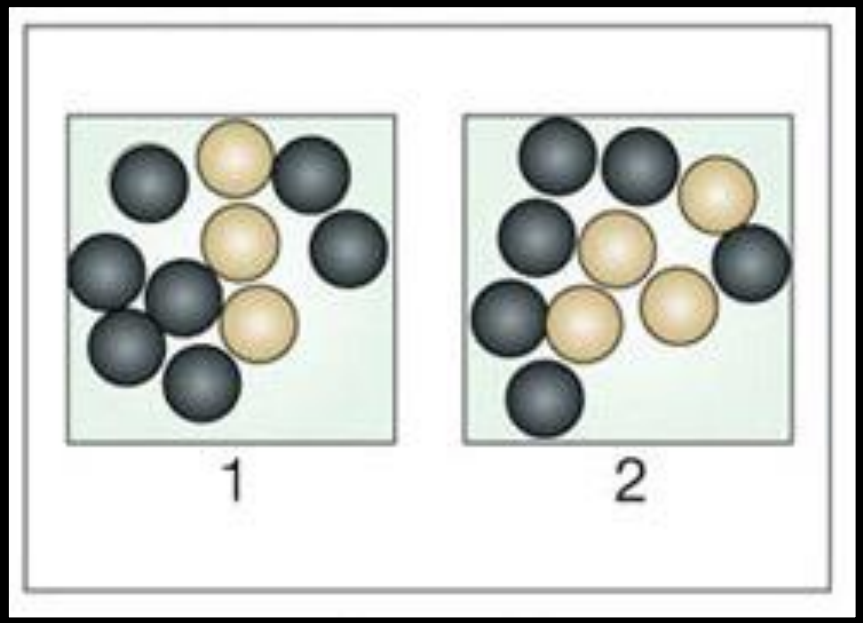
How important was such differenciation?

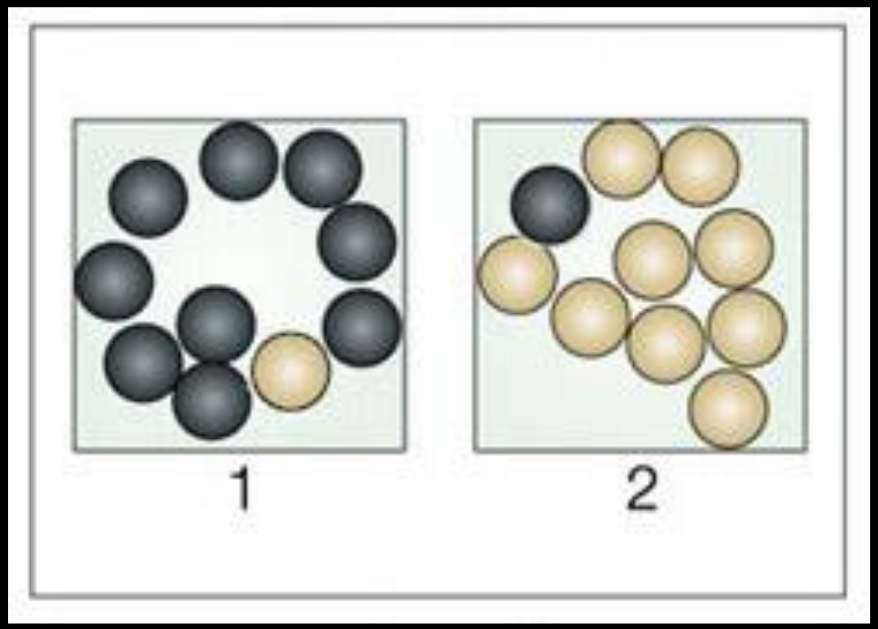




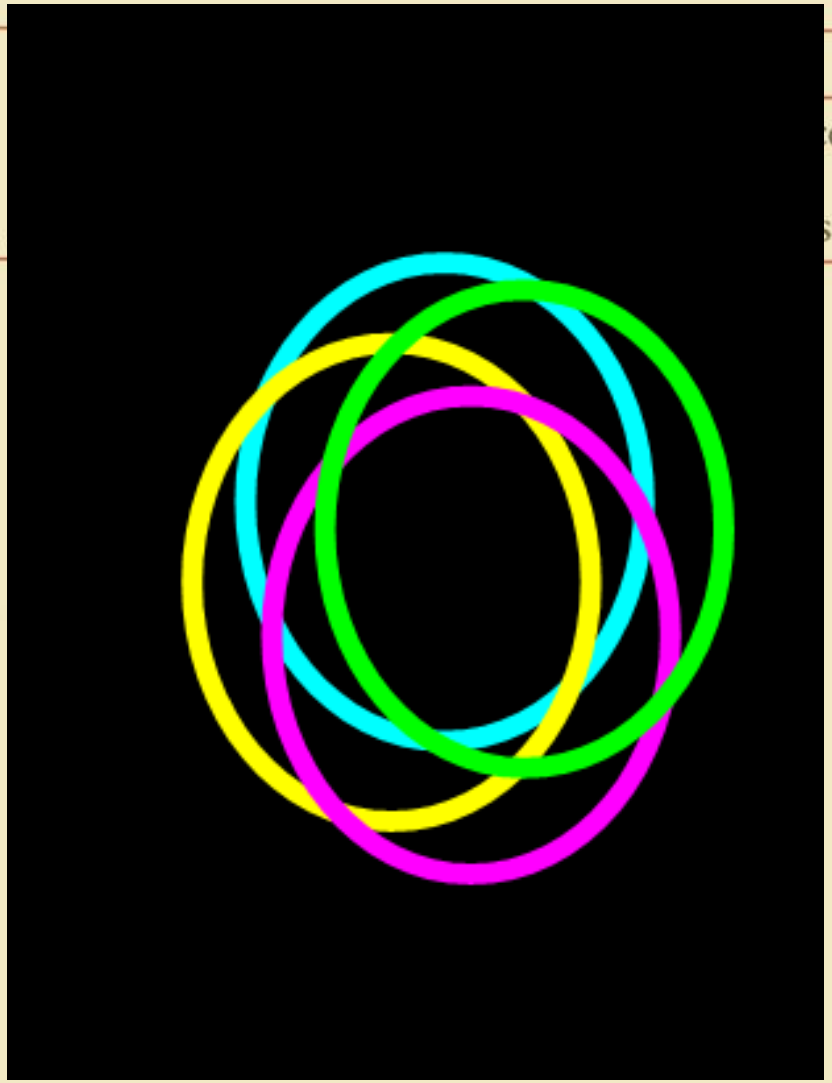


Partition of Variability

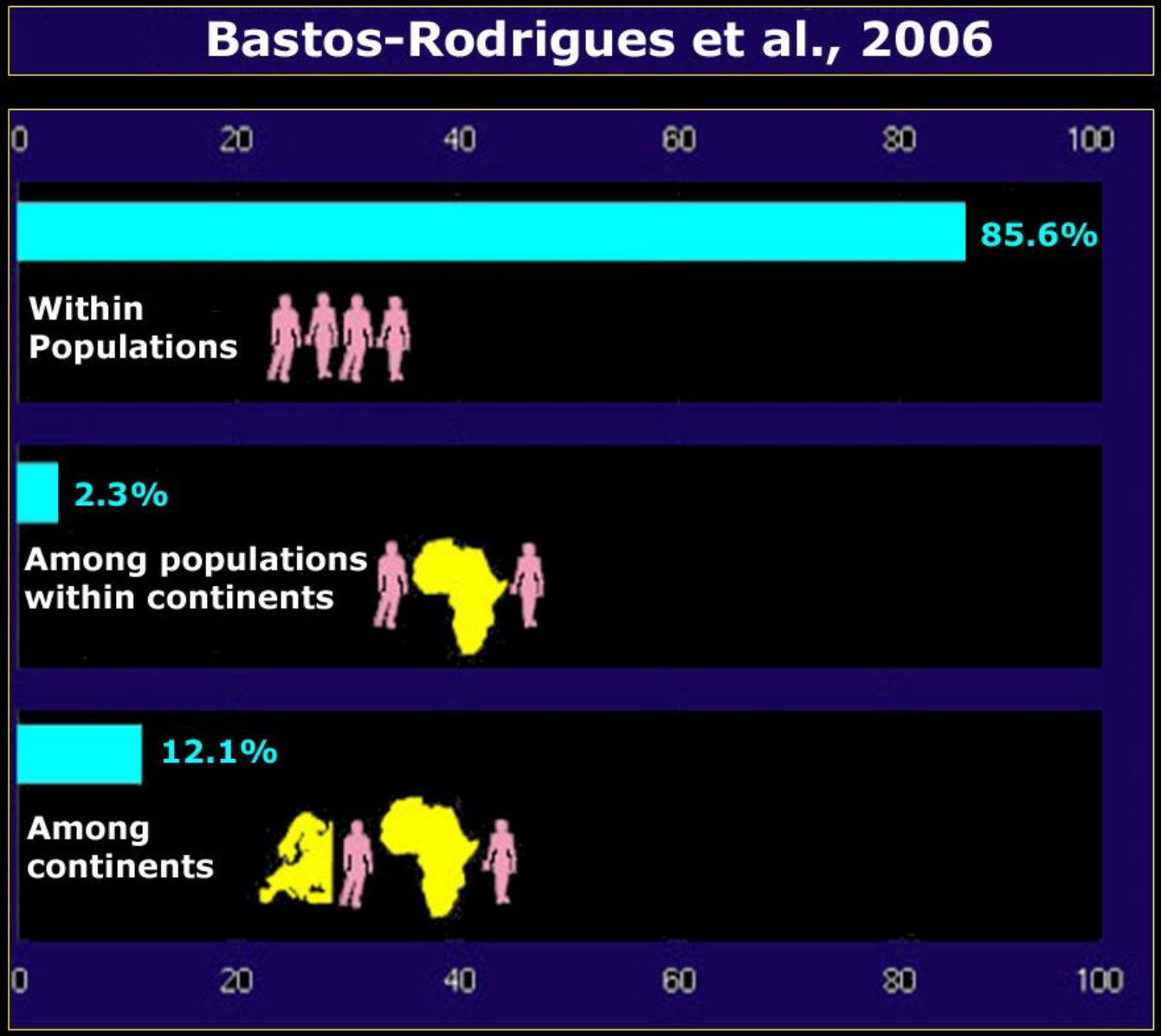




Gene	Total $H_{species}$		es s	Between Races
Hp	.994			.056
Ag	.994			—
Lp	.639			—
Xm	.869			—
Ap	.989			.011
6PGD	.327			.067
PGM	.758			.025
Ak	.184			.131
Kidd	.977			.048
Duffy	.938			.259
Lewis	.994			.002
Kell	.189			.026
Lutheran	.153			.092
P	1.000			.022
MNS	1.746			.048
Rh	1.900			.253
ABO	1.241			.030
Mean		.854	.083	.063



Source: R. C. Lewontin, *Genetic Basis of Evolutionary Change* (Columbia University Press, 1974).



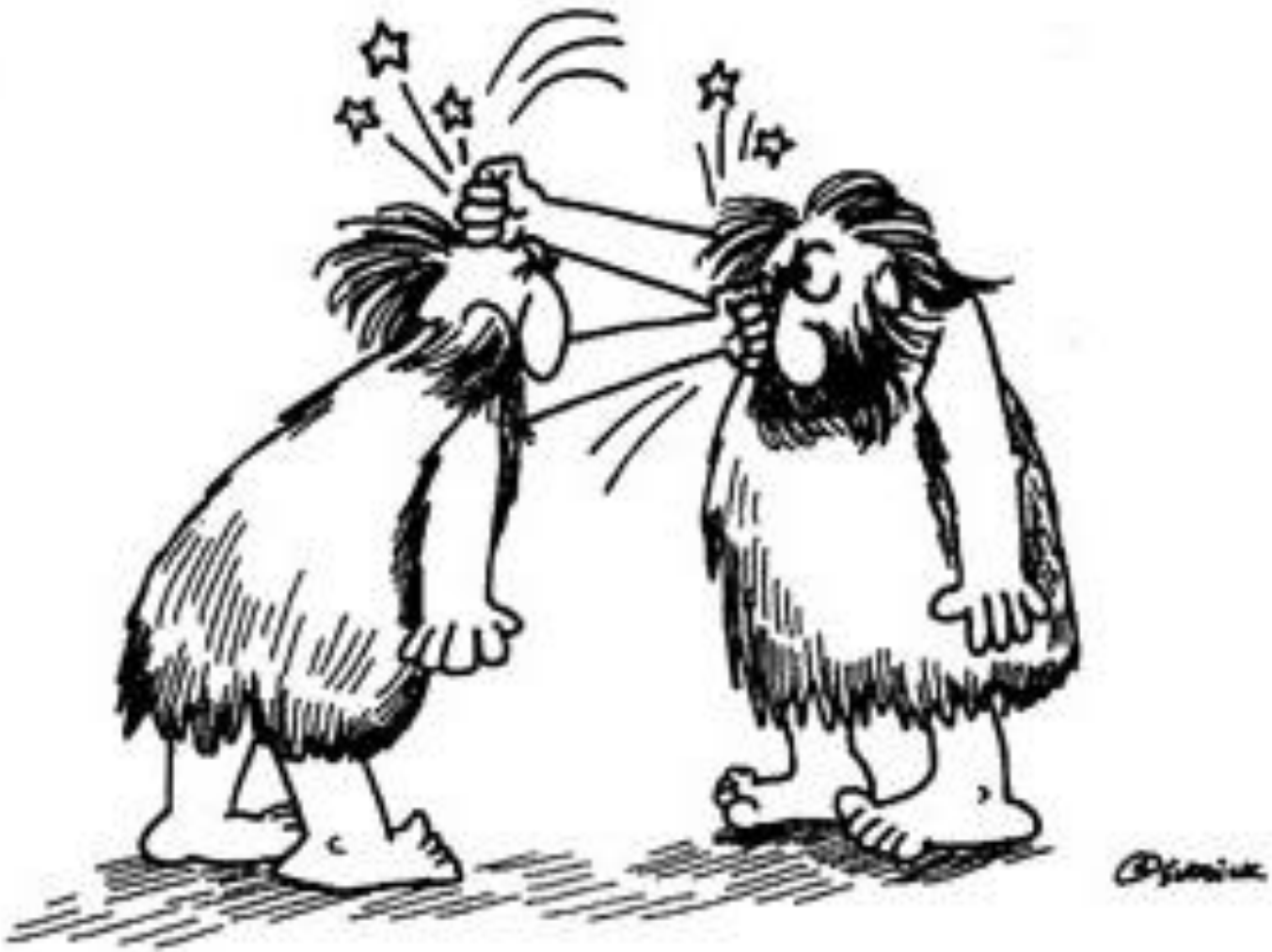
1064 indivíduals from 55 populations – 40 indels

These and many other studies have shown that, from the biological perspective, a significant differentiation of human groups did not occur.

The corollary to this conclusion is that from a scientific standpoint human races do not exist.

The biological inexistence of human races is not related tothe fact that we are all equal, but to the fact that we are all equally diferent

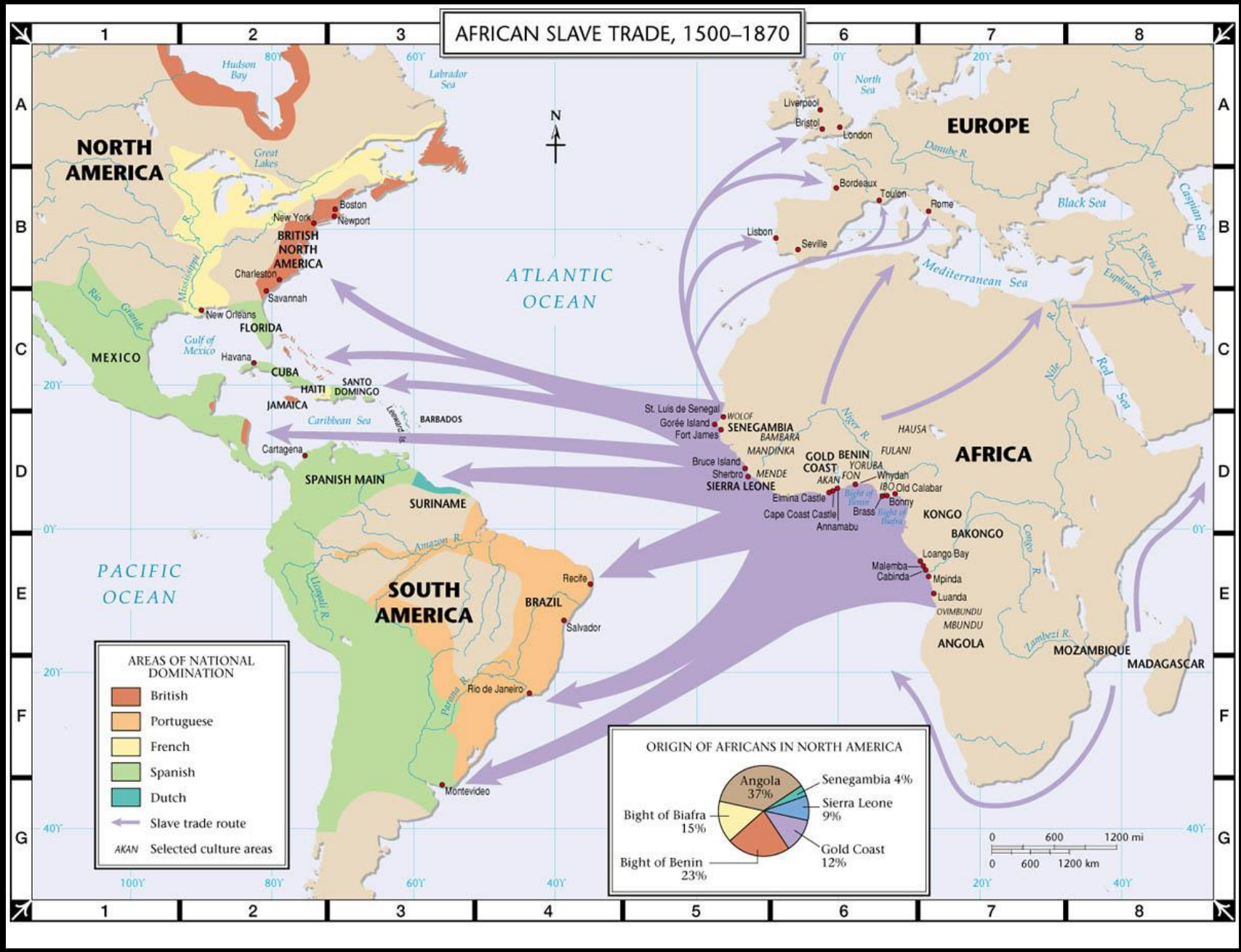

Racialization of
Human Diversity



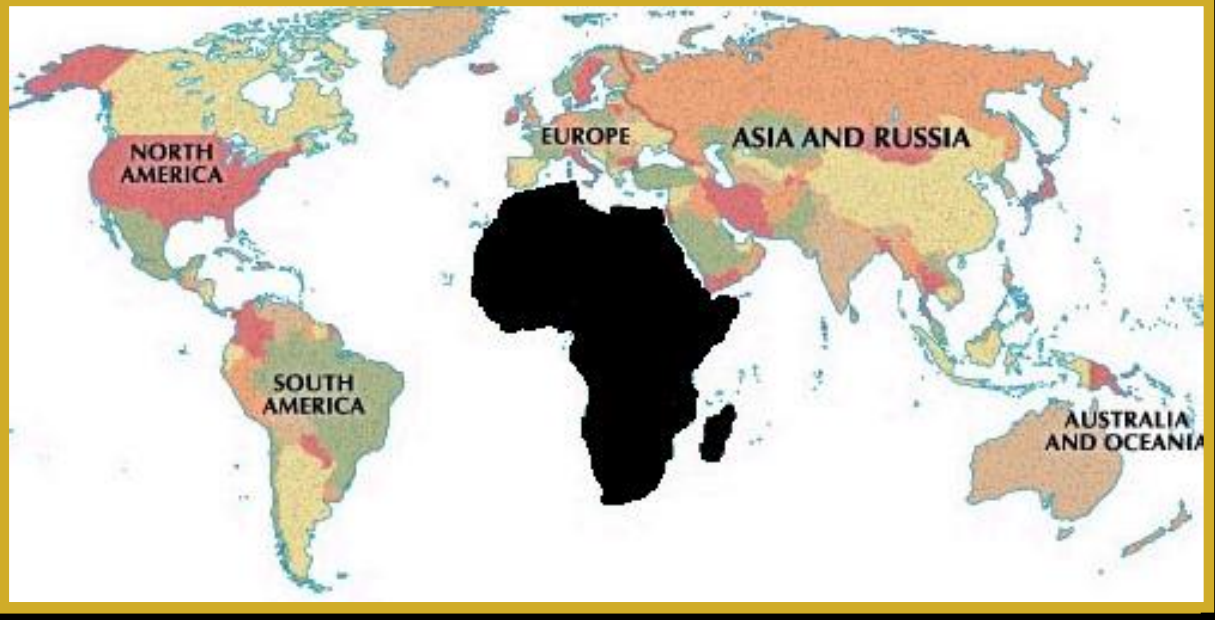
***Homo sapiens*, celebrating their diversity**

16th Century
Transatlantic slave trade

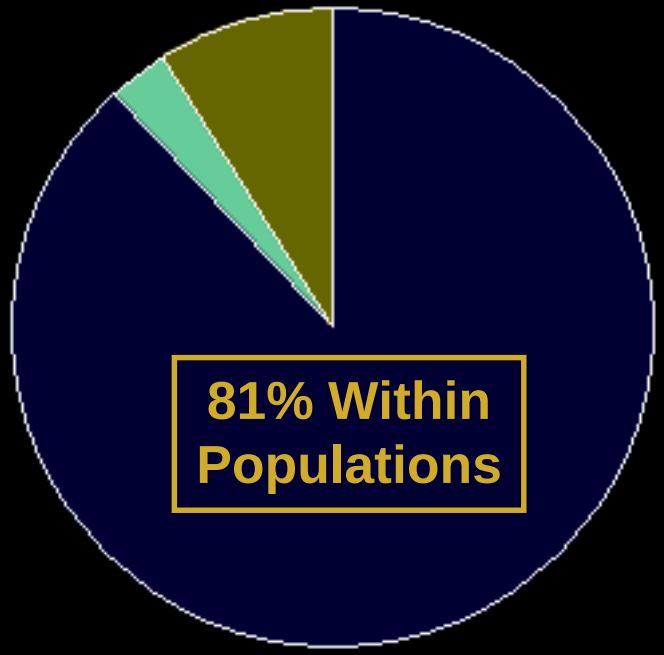
Races were invented!

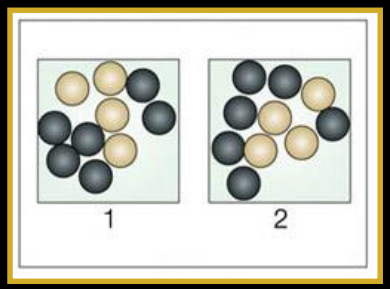

AFRICAN SLAVE TRADE, 1500–1870
NORTH AMERICA
EUROPE
AFRICA
SOUTH AMERICA
ATLANTIC OCEAN
PACIFIC OCEAN
Hudson Bay
Labrador Sea
North Sea
Great Lakes
Mississippi R.
Rio Grande
Gulf of Mexico
Caribbean Sea
Amazon R.
Llanos R.
Paraná R.
Danube R.
Black Sea
Caspian Sea
Mediterranean Sea
Tigris R.
Euphrates R.
Nile R.
Red Sea
Niger R.
Congo R.
Zambezi R.
Leeward Is.
Liverpool
Bristol
London
Bordeaux
Toulon
Rome
Lisbon
Seville
New York
Boston
Newport
Charleston
Savannah
New Orleans
FLORIDA
MEXICO
Havana
CUBA
HAITI
SANTO DOMINGO
JAMAICA
BARBADOS
Cartagena
SPANISH MAIN
SURINAME
BRITISH NORTH AMERICA
St. Luis de Senegal
Gorée Island
Fort James
WOLOF
SENEGAMBIA
BAMBARA
MANDINKA
MENDE
SIERRA LEONE
Bruce Island
Sherbro
GOLD COAST
AKAN
BENIN
FON
YORUBA
FULANI
HAUSA
Whydah
IBO
Old Calabar
Bonny
Brass
Elmina Castle
Cape Coast Castle
Annamabu
Bight of Benin
Bight of Biafra
KONGO
BAKONGO
Loango Bay
Malemba
Cabinda
Mpinda
Luanda
OVIMBUNDU
MBUNDU
ANGOLA
MOZAMBIQUE
MADAGASCAR
Recife
BRAZIL
Salvador
Rio de Janeiro
Montevideo
AREAS OF NATIONAL DOMINATION
British
Portuguese
French
Spanish
Dutch
Slave trade route
AKAN Selected culture areas
ORIGIN OF AFRICANS IN NORTH AMERICA
Angola 37%
Senegambia 4%
Sierra Leone 9%
Gold Coast 12%
Bight of Benin 23%
Bight of Biafra 15%
0 600 1200 mi
0 600 1200 km

Genesis 9:20-25 tells us, "Noah, a man of the soil, proceeded to plant a vineyard. When he drank some of its wine, he became drunk and lay uncovered inside his tent. Ham, the father of Canaan, saw his father's nakedness and told his two brothers outside. But Shem and Japheth took a garment and laid it across their shoulders; then they walked in backward and covered their father's nakedness. Their faces were turned the other way so that they would not see their father's nakedness. When Noah awoke from his wine and found out what his youngest son had done to him, he said, ‘Cursed be Canaan! The lowest of slaves will he be to his brothers.’"

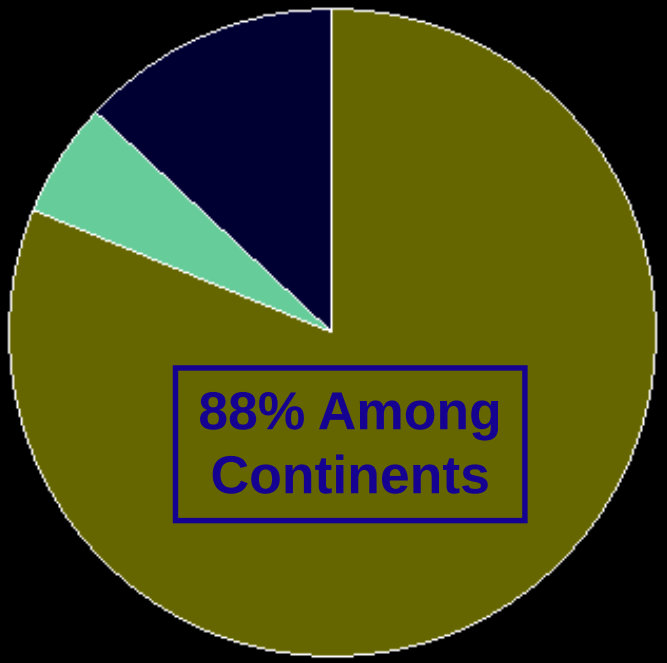

NORTH AMERICA
EUROPE
ASIA AND RUSSIA
SOUTH AMERICA
AUSTRALIA AND OCEANIA

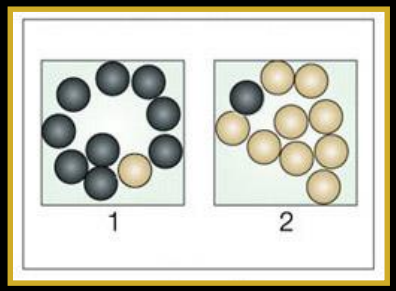
Craniometry

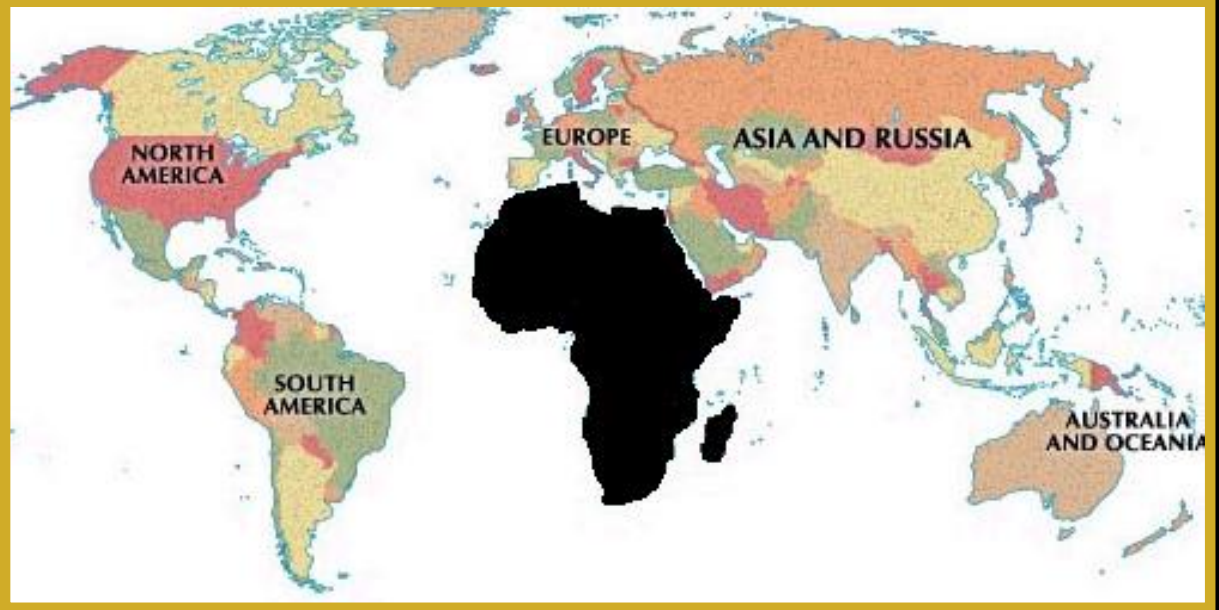




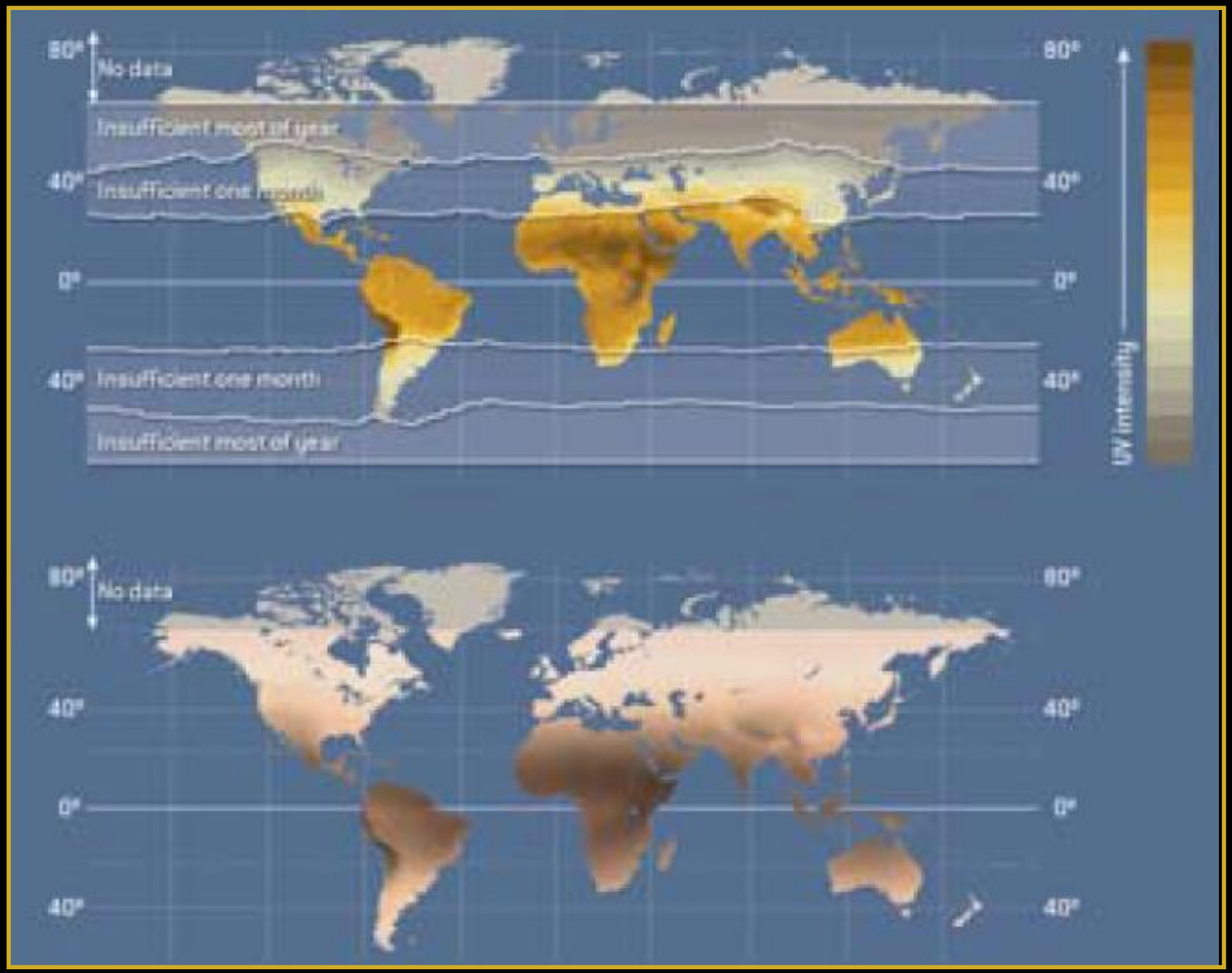
Skin color







These continental variation of skin pigmentation and morphological characteristics represent evolutionary adaptations to the local geographical environment.



Jablonski & Chaplin, 2002


MEDITERRANEAN SEA
SAHARA
RED SEA
Lake Chad
Niger R.
MOSSI
ORIGINAL BANTU HOMELAND
BENIN
NOK
Nile R.
Congo R.
Equator
ATLANTIC OCEAN
KONGO
Lake Victoria
INDIAN OCEAN
Zambezi R.
MUTAPA
ZIMBABWE
NATAL
BANTU MIGRATIONS
Original Bantu homeland
Bantu states, c. 14th century
East Bantu migrations
West Bantu migrations
0
500
1000
MILES

LETTER

Nature, 2014

doi:10.1038/nature12960

Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European

Iñigo Olalde[1]*, Morten E. Allentoft[2]*, Federico Sánchez-Quinto[1], Gabriel Santpere[1], Charleston W. K. Chiang[3], Michael DeGiorgio[4,5], Javier Prado-Martinez[1], Juan Antonio Rodríguez[1], Simon Rasmussen[6], Javier Quilez[1], Oscar Ramírez[1], Urko M. Marigorta[1], Marcos Fernández-Callejo[1], María Encina Prada[7], Julio Manuel Vidal Encinas[8], Rasmus Nielsen[9], Mihai G. Netea[10], John Novembre[11], Richard A. Sturm[12], Pardis Sabeti[13,14], Tomàs Marquès-Bonet[1,15], Arcadi Navarro[1,15,16,17], Eske Willerslev[2] & Carles Lalueza-Fox[1]

Table 1 | Mesolithic genome allelic state at 10 nonsynonymous variants recently selected in Europeans

Allelic state	Gene	Name	SNP	Amino-acid change	Function
La Braña 1 carries the derived allele	*PTX4*	Pentraxin 4	rs2745098	Arg281Lys	May be involved in innate immunity
	UHRF1BP1	UHRF1 binding protein 1	rs11755393	Gln454Arg	Risk locus for systemic lupus erythematosus
	GPATCH1	G patch domain containing 1	rs10421769	Leu520Ser	Receptor for OmpA expressed by *E. coli*
	WWOX	WW domain-containing oxidoreductase	rs12918952	Ala179Thr	Acts as a tumour suppressor and has a role in apoptosis
	CCDC14	Coiled-coil domain-containing protein 14	rs17310144	Thr365Pro	Unknown
La Braña 1 carries both the ancestral and the derived allele	*SETX*	Senataxin	rs1056899	Val2587Ile	Involved in spinocerebellar ataxia and amyotrophic lateral sclerosis
	TDRD12	Tudor domain containing 12	rs11881633	Glu413Lys	Unknown
La Braña 1 retains the ancestral allele	*C12orf29*	Chromosome 12 open reading frame 29	rs9262	Val238Leu	Unknown
	SLC45A2	Solute carrier family 45, member 2	rs16891982	Leu374Phe	Associated with skin pigmentation
	SLC24A5	Solute carrier family 24, member 5	rs1426654	Ala111Thr	Associated with skin pigmentation

The human genome has approximately 20 thousand genes.

Probably less than 20 of these genes are related with the determination of skin color.

The color of the skin is not genetically associated with any intellectual, physical and emotional ability. Thus, arguments used by racists do not have any scientific value.

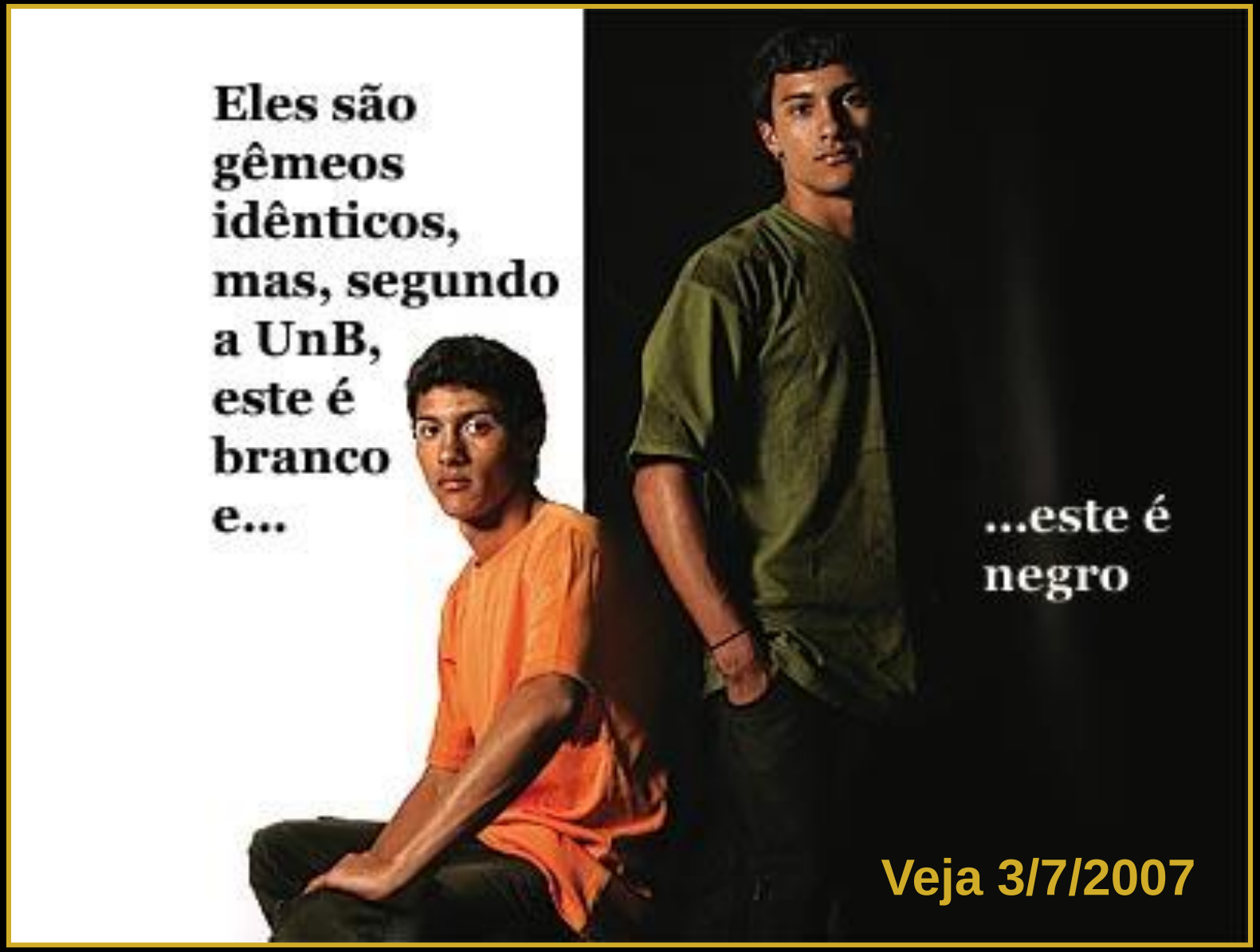
The small number of genes associated with skin color makes it possible for close relatives, even brothers and sisters, to differ significantly in skin pigmentation, although they may have identical levels of African ancestry

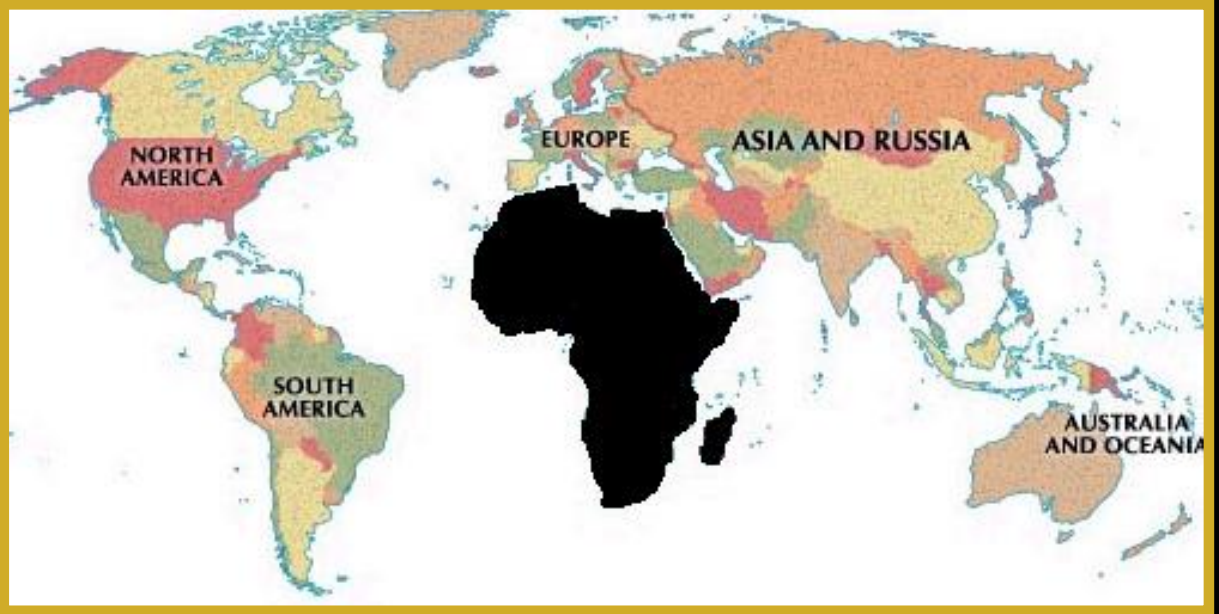
As irmãs Clara e Luíza, de cinco anos

Hoje EM DIA

Brasil, 27 de Outubro de 2006

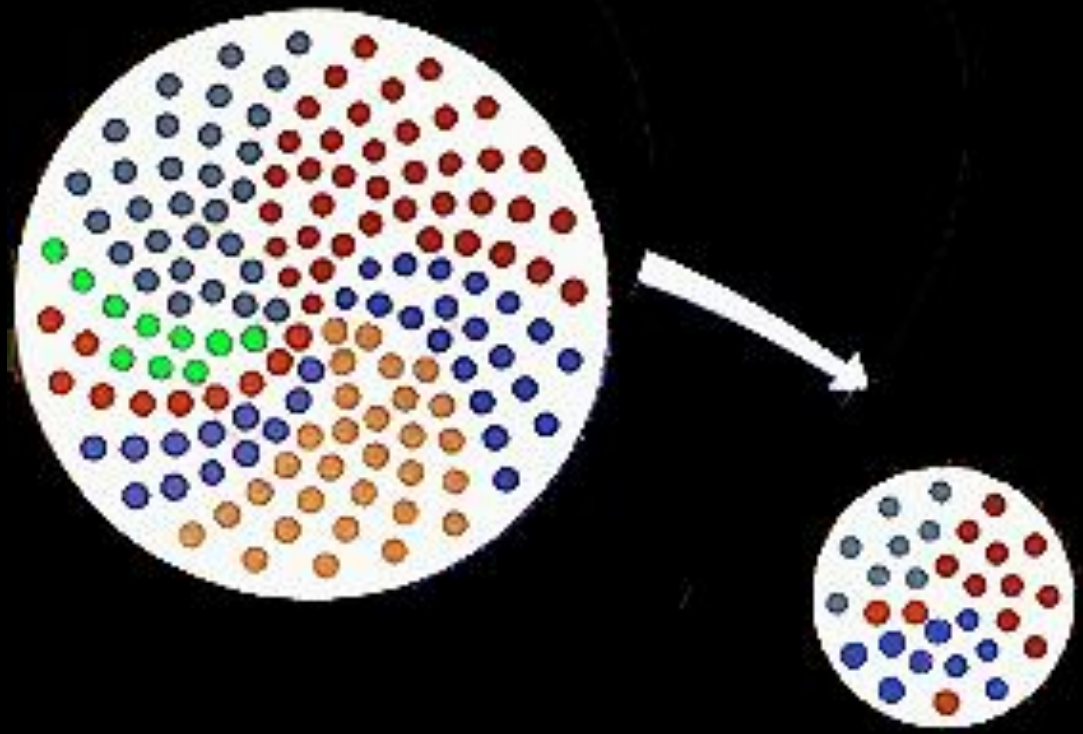
Besides, skin pigmentation has complex polygenic genetic inheritance, is susceptible to important influences of the environment and its classification depends on subjective evaluation.


Eles são gêmeos idênticos, mas, segundo a UnB, este é branco e...
...este é negro
Veja 3/7/2007

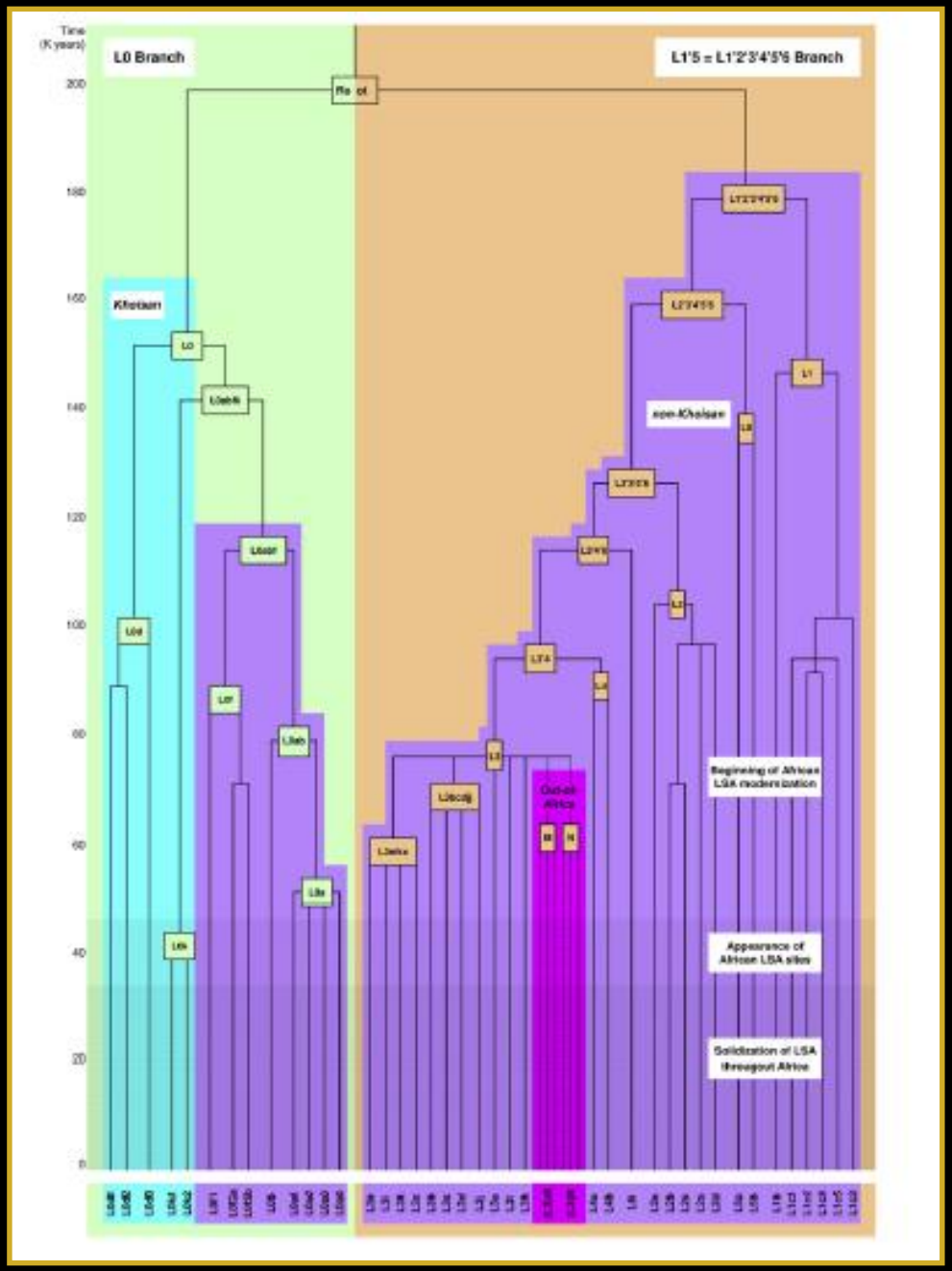


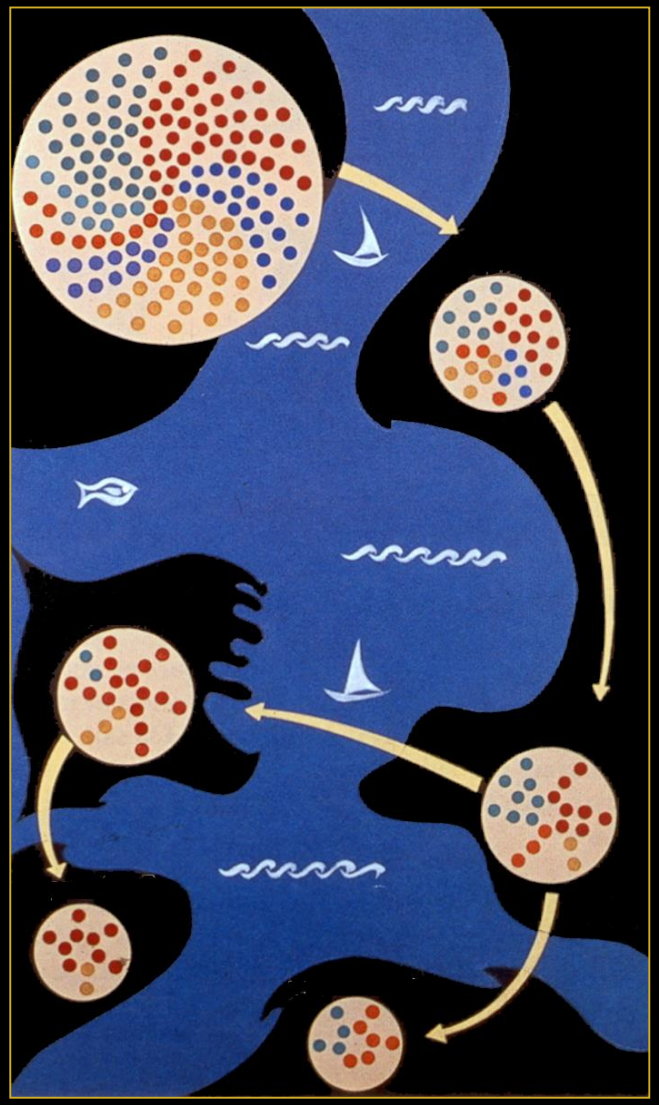
All racial question is literally skin deep

Aproximately 60,000 years ago, modern humanity left Africa and occupied all other continentes



Founder effect


Time (K years)
L0 Branch
L1'5 = L1'2'3'4'5'6 Branch
200
180
160
140
120
100
80
60
40
20
0
Khoisan
non-Khoisan
Beginning of African LSA modernization
Appearance of African LSA sites
Solidification of LSA throughout Africa



Serial founder effects

Three major developments that occured in the Genome Era

- Characterization of the recent unique origin of modern humans in Africa
- **Characterization of human genomic individuality at the DNA level**
- Characterization of the genealogical structure of humanity

Genome Report:

Sérgio Pena

Viewing Genome: 128: Sérgio Pena

Genome Details:

Edit Details

ID: **PG890**

Display Name: **Sérgio Pena**

Gender: **Male**

Sequencing provider: **Illumina**
Sequencing date: **2013**
Sequencing type:
Sequencing technique:

Tissue source of genomic material: **Blood**
DNA sample ID:

Genome reference version: **HomoSapiens_GRCh37**
dbSNP version: **dbSNP build 146**
Enlis annotation version: **9**

Call Coverage Summary:

Full genome call percent:	**89.281%**
Reference genome length:	3,095,693,981
Number of bases called:	2,763,866,304
Number of bases not called:	331,827,677
Gene call percent:	**96.982%**
Reference gene length:	1,641,887,253
Number of bases called:	1,592,335,280
Number of bases not called:	49,551,973
Exon call percent:	**96.787%**
Reference exon length:	105,240,049
Number of bases called:	101,858,786
Number of bases not called:	3,381,263
Protein-coding call percent:	**97.647%**
Reference protein-coding length:	40,483,648
Number of bases called:	39,530,922
Number of bases not called:	952,726

Genome Report:

Sérgio Pena

Viewing Genome: 128: Sérgio Pena

Variation Summary:

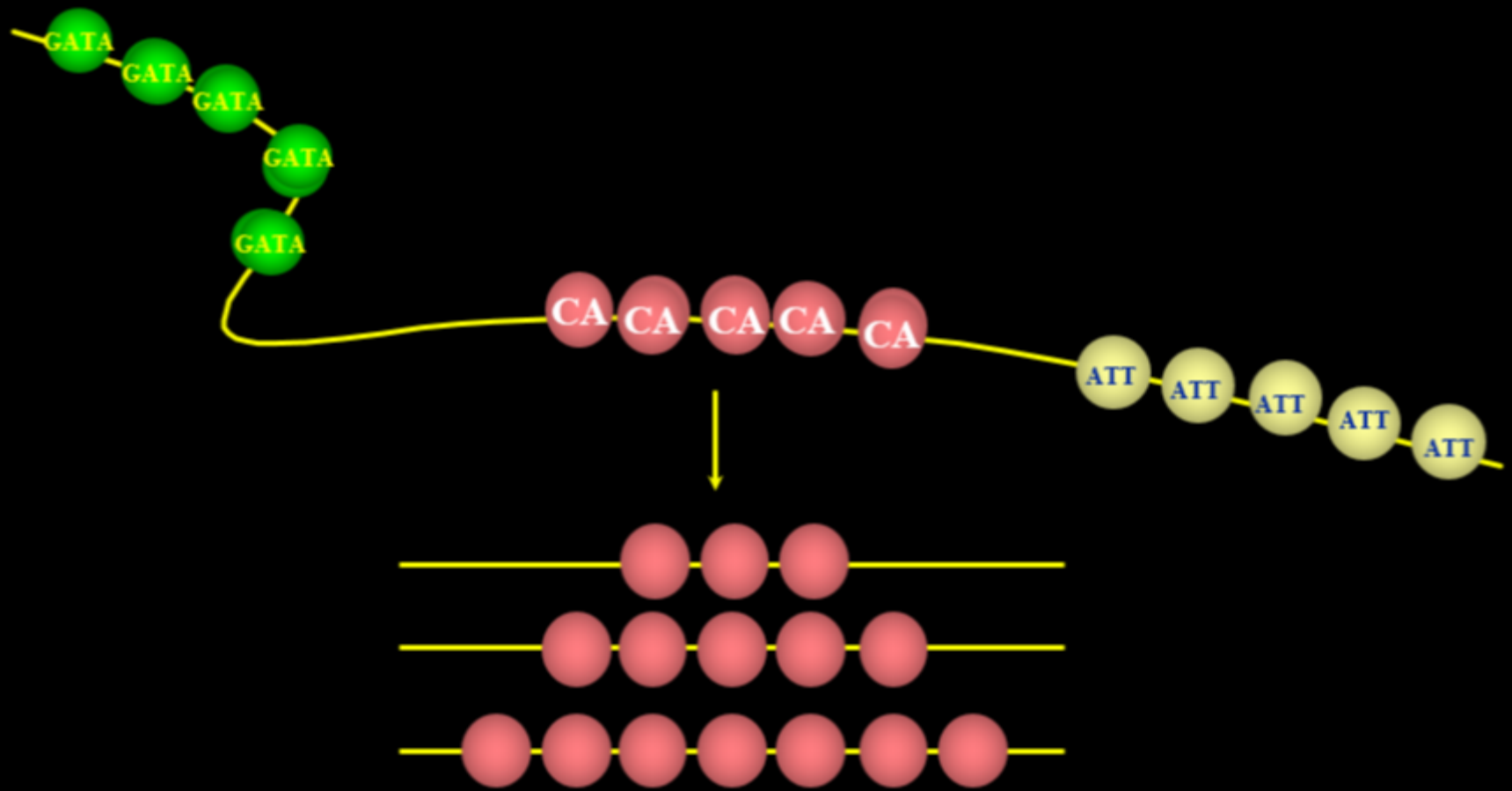
Variation Counts:

Total number of variations:	4,631,989
Heterozygous:	2,147,595
Homozygous (x2):	1,242,197
Total rare variations (GAF <1%):	211,191
Protein-coding variations:	15,148
Rare protein-coding variations (GAF <1%):	666
Gene-associated variations:	2,302,264
Rare gene-associated variations (GAF <1%):	97,712
SNV:	4,631,989
MNV:	0
Insertion:	0
Deletion:	0

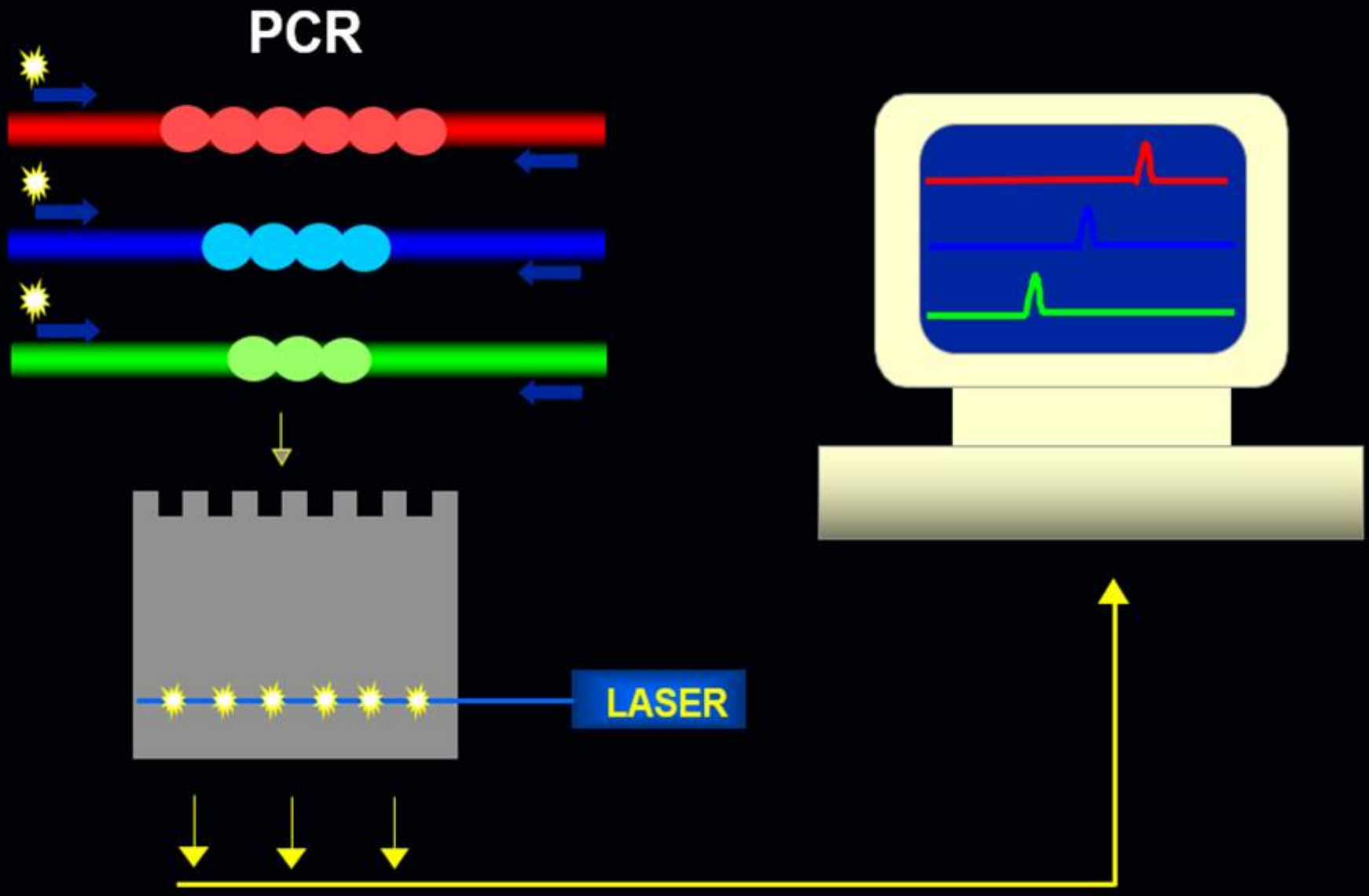
Variations by Gene Impact:

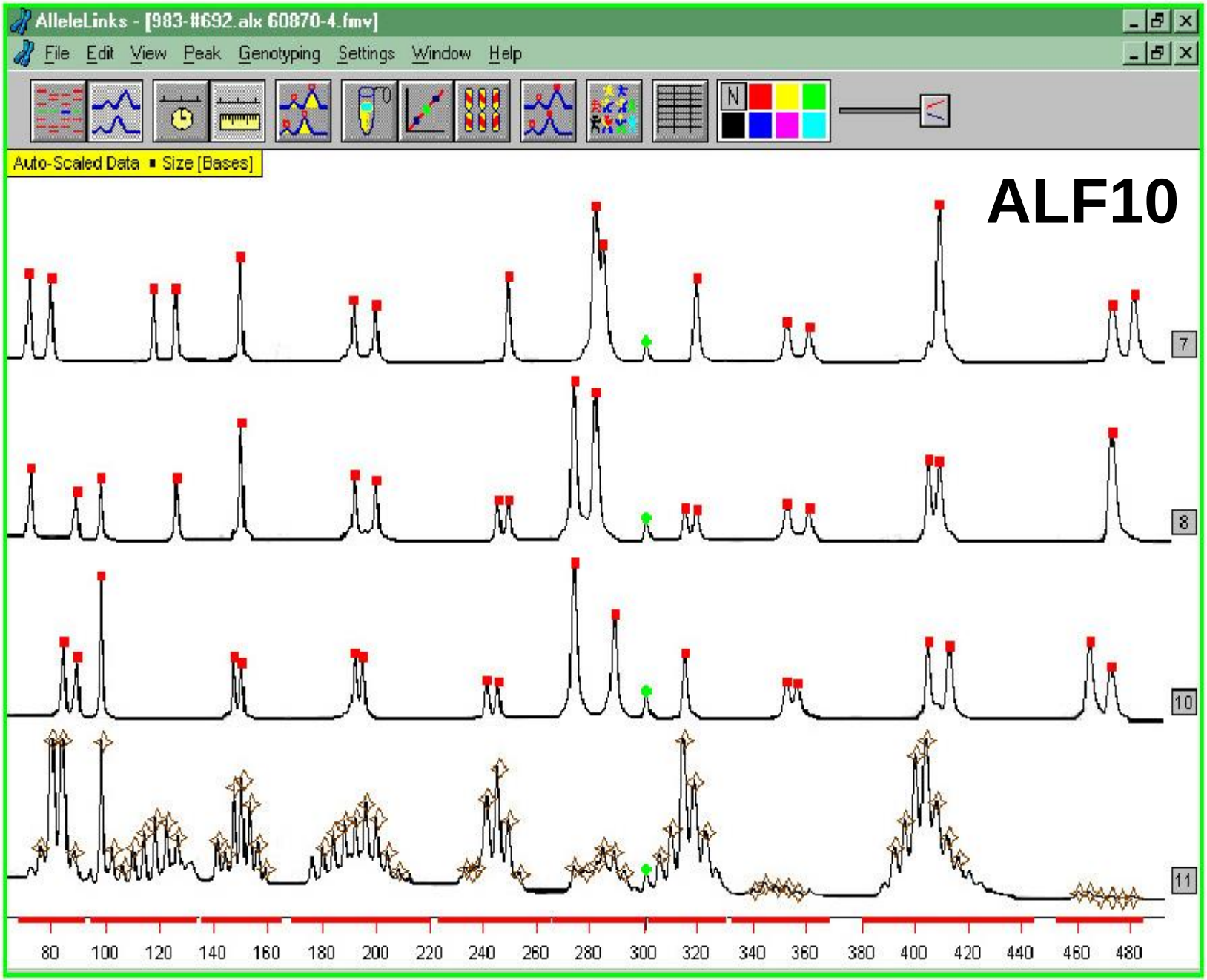
Missense:	14,574
Nonsense:	129
Nonstop:	41
Misstart:	44
Frameshift:	0
Inframe ins/del:	0
Coding synonymous:	15,682
Splice site:	4,817
mRNA untranslated:	100,760
Intron:	2,212,832

Microsatellites



Detection of microsatellite polymorphisms




AlleleLinks - [983-#692.alx 60870-4.fmv]
File Edit View Peak Genotyping Settings Window Help
Auto-Scaled Data ▪ Size [Bases]
ALF10
7
8
10
11
80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420 440 460 480

Probability of Identity of Multiplex ALF10

Loco	PIG
D1S1612	0.04
D2S1353	0.05
D3S2387	0.02
D4S2431	0.04
D5S2501	0.10
D10S1237	0.04
D15S657	0.07
D16S2622	0.20
D18S1270	0.05
IFNAR	0.06
TOTAL	**3×10^{-13}**

Multiplex PCR Systems

GENE LABORATÓRIO

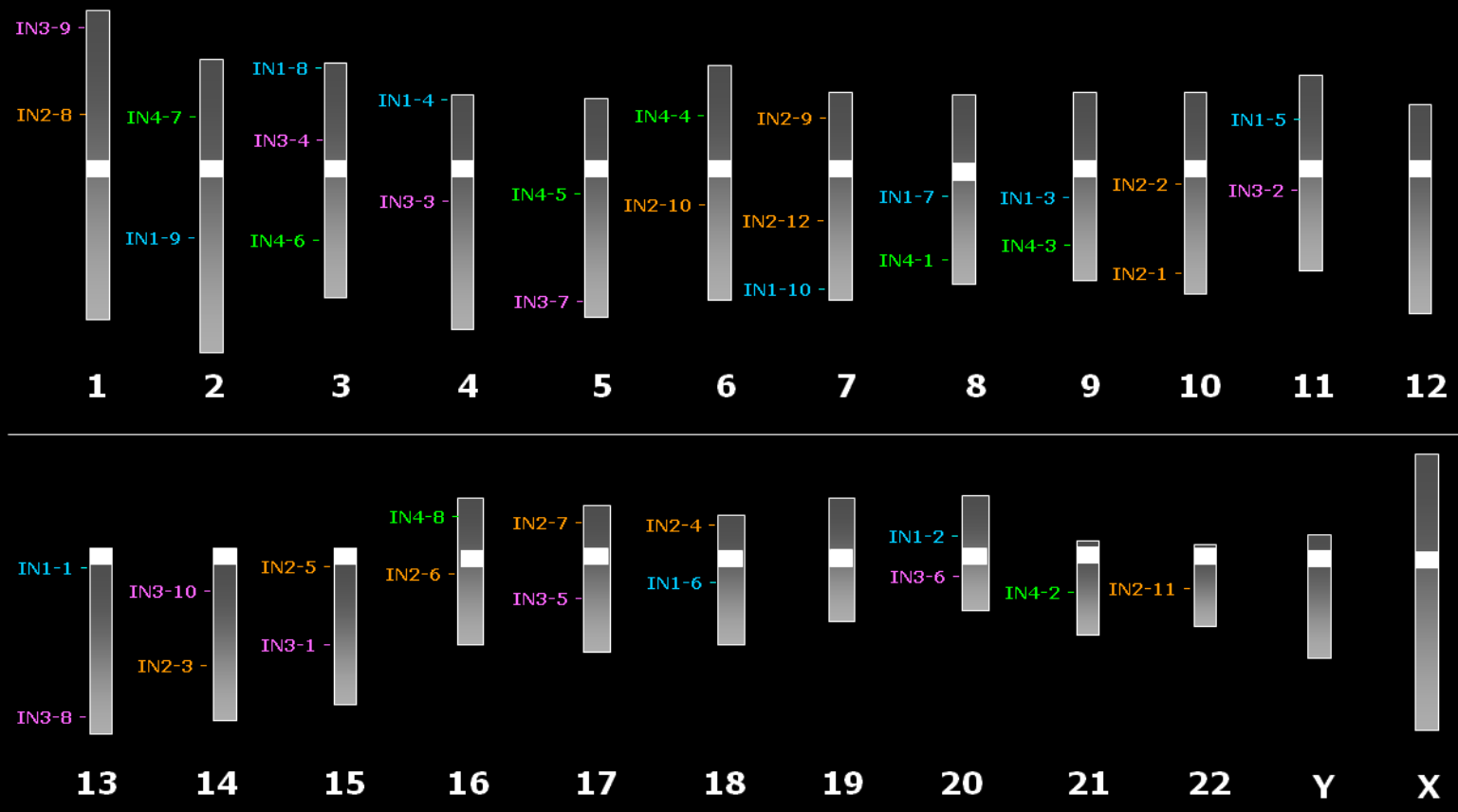
ALF2	5
ALF3	5
ALF5	3
ALF6	6
ALF7	6
ALF8	6
ALF9	5
ALF10	10
	46

Insertion-Deletion Polymorphisms (Indels)

MULTIPLEXES INDELS

localização cromossômica

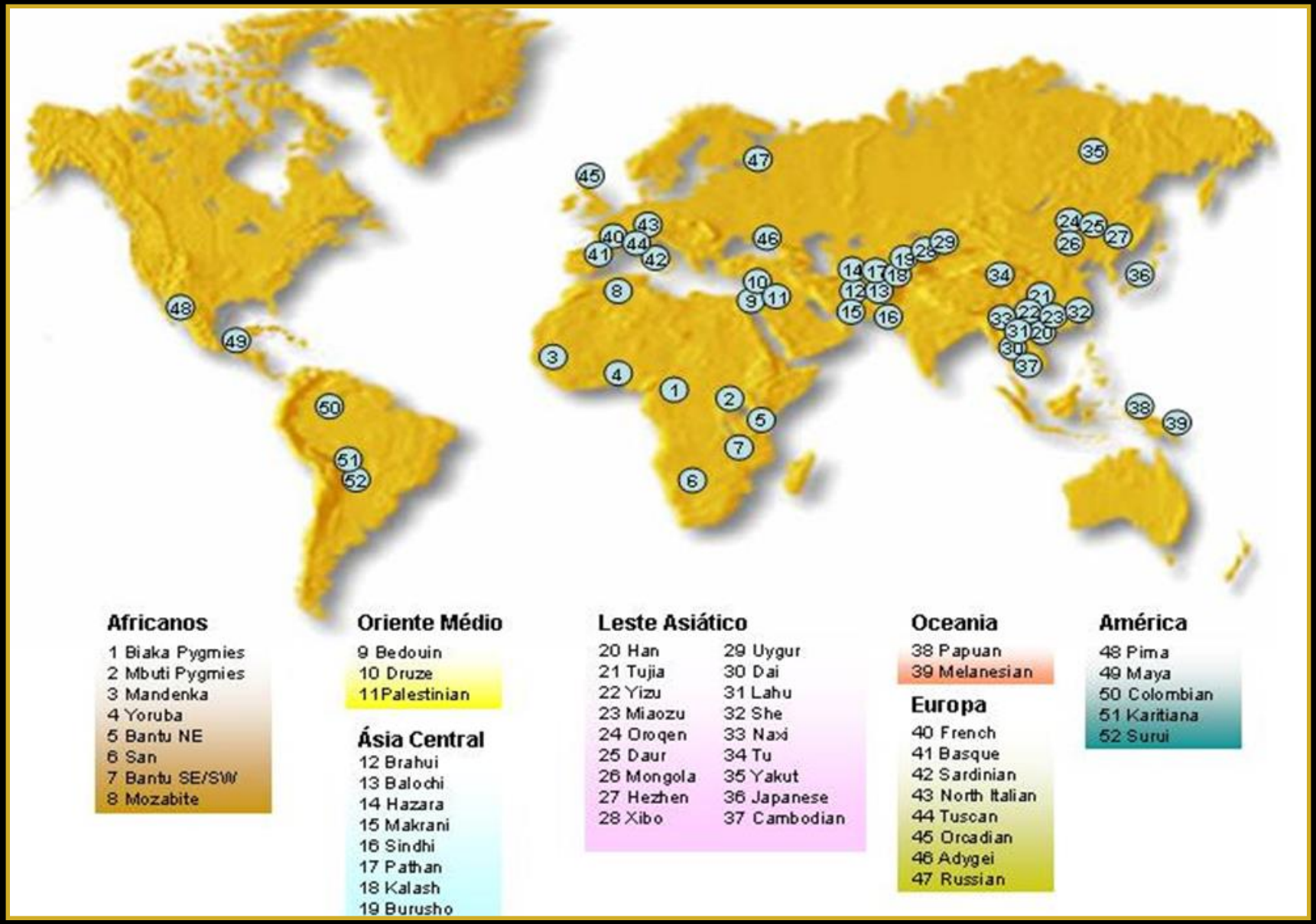
SET1 SET2 SET3 SET4

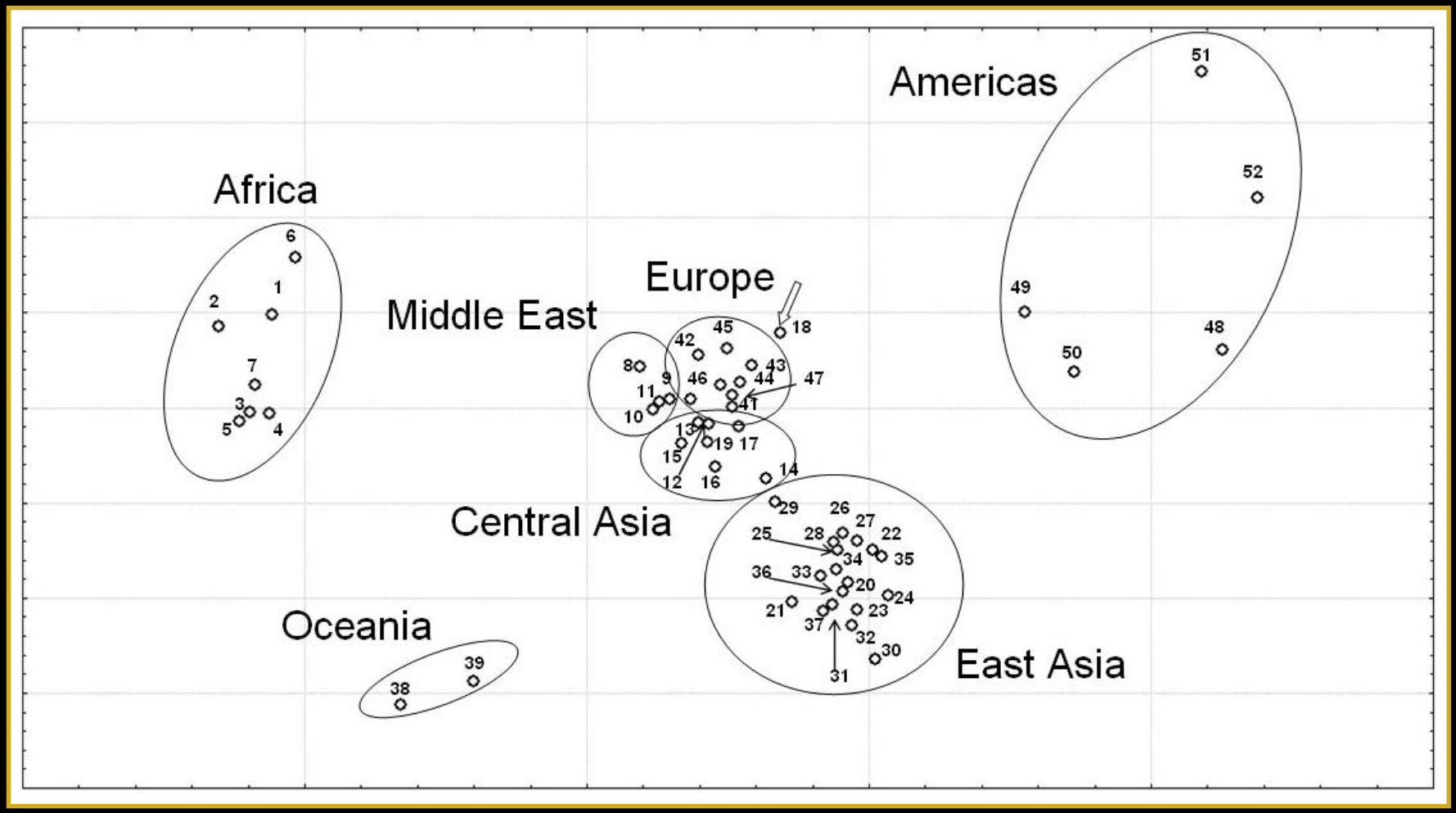


Probability of Genetic Identity
40 Indels
Brazilian population

5.07^{-17}

(0.00000000000000051)


Africanos
1 Biaka Pygmies
2 Mbuti Pygmies
3 Mandenka
4 Yoruba
5 Bantu NE
6 San
7 Bantu SE/SW
8 Mozabite
Oriente Médio
9 Bedouin
10 Druze
11Palestinian
Ásia Central
12 Brahui
13 Balochi
14 Hazara
15 Makrani
16 Sindhi
17 Pathan
18 Kalash
19 Burusho
Leste Asiático
20 Han
21 Tujia
22 Yizu
23 Miaozu
24 Oroqen
25 Daur
26 Mongola
27 Hezhen
28 Xibo
29 Uygur
30 Dai
31 Lahu
32 She
33 Naxi
34 Tu
35 Yakut
36 Japanese
37 Cambodian
Oceania
38 Papuan
39 Melanesian
Europa
40 French
41 Basque
42 Sardinian
43 North Italian
44 Tuscan
45 Orcadian
46 Adygei
47 Russian
América
48 Pima
49 Maya
50 Colombian
51 Karitiana
52 Surui


Americas
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Middle East
Central Asia
Oceania
East Asia
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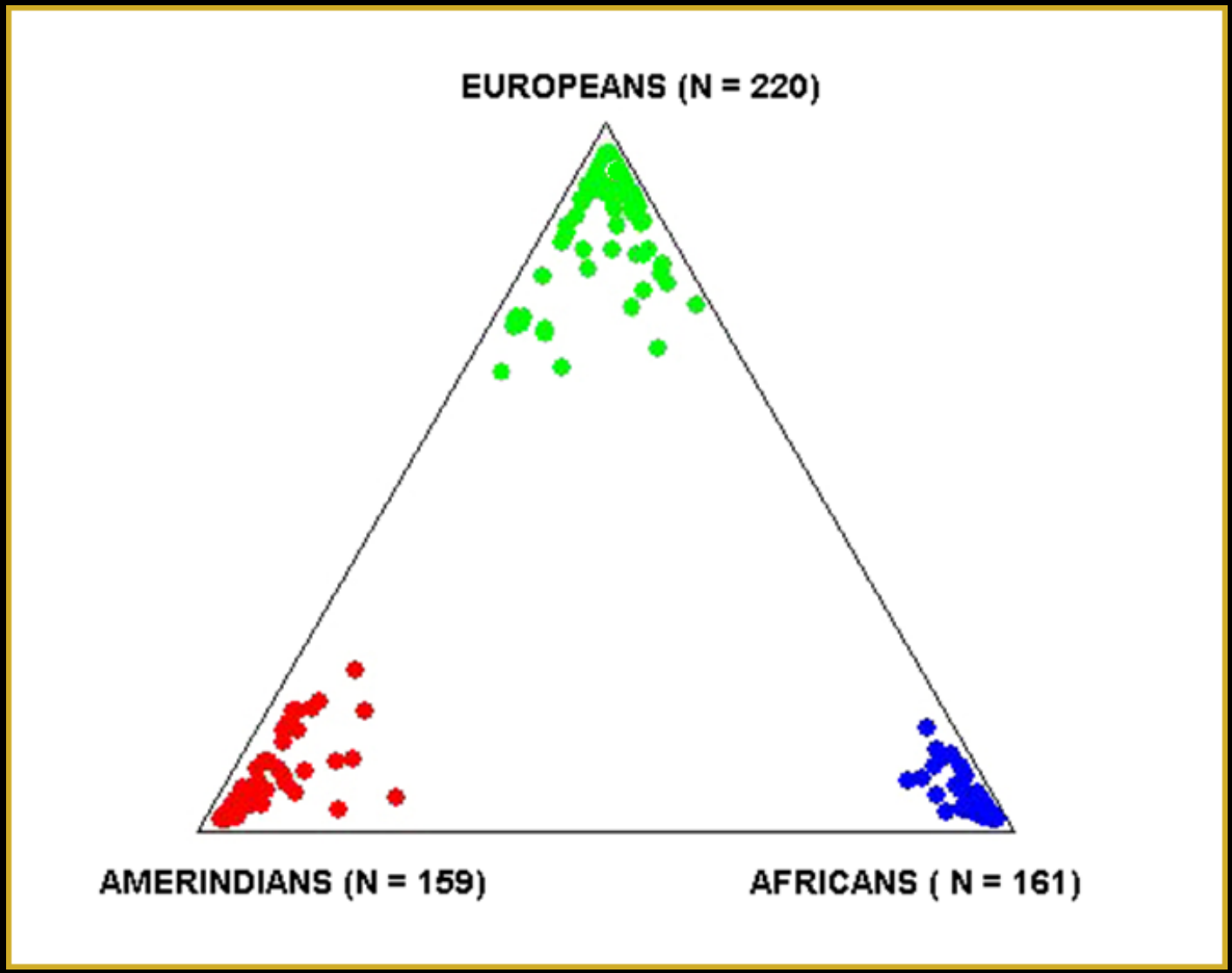
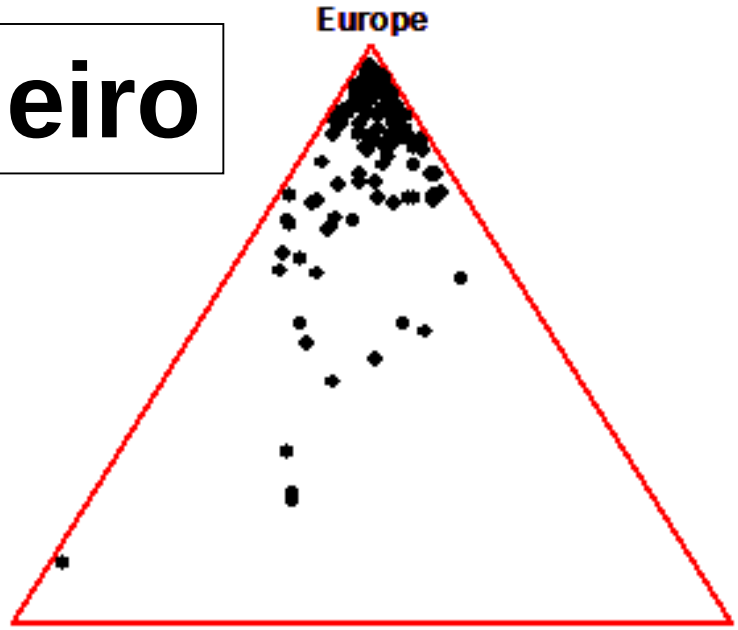
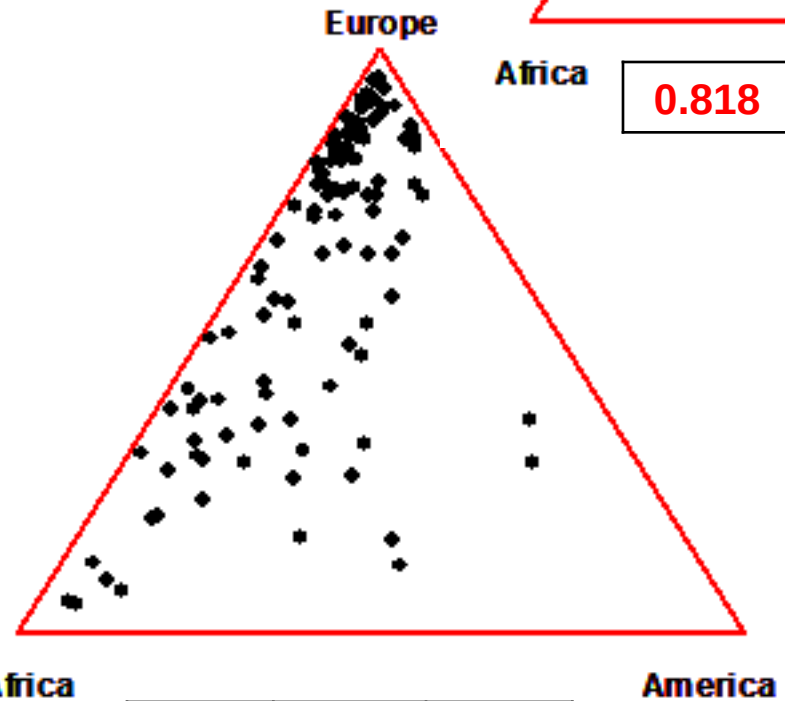

EUROPEANS (N = 220)
AMERINDIANS (N = 159)
AFRICANS (N = 161)

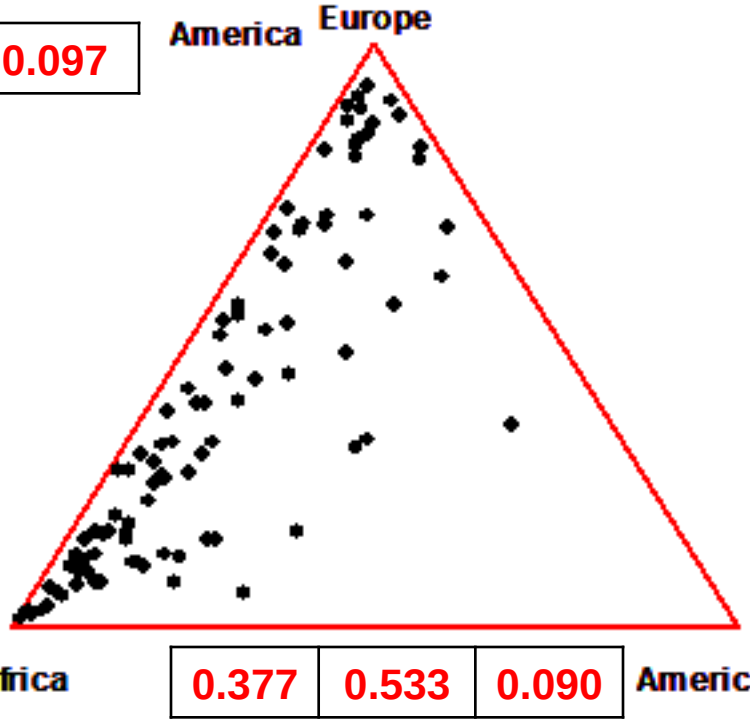
Rio de Janeiro



0.818	0.085	0.097

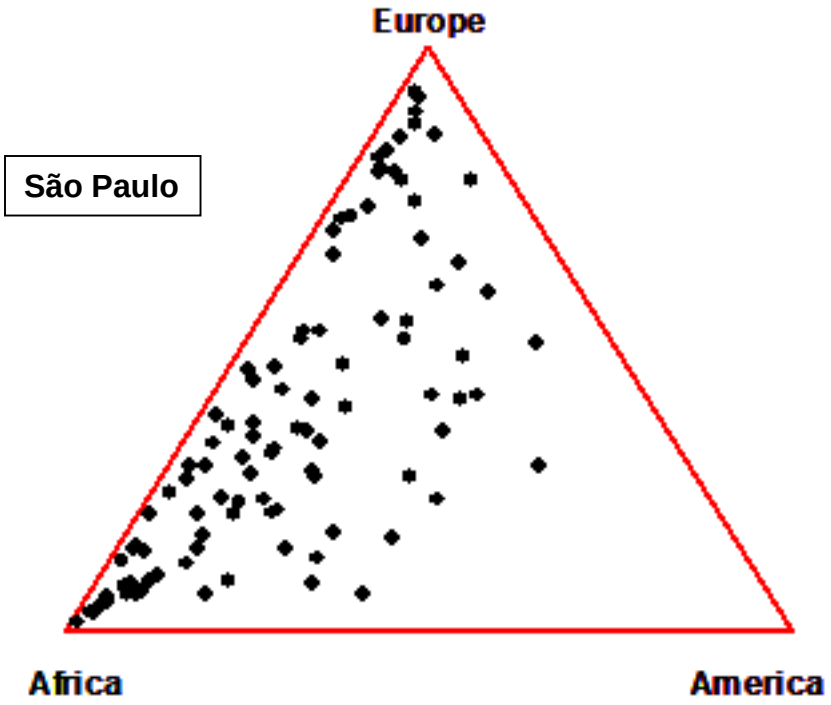


0.622	0.277	0.101



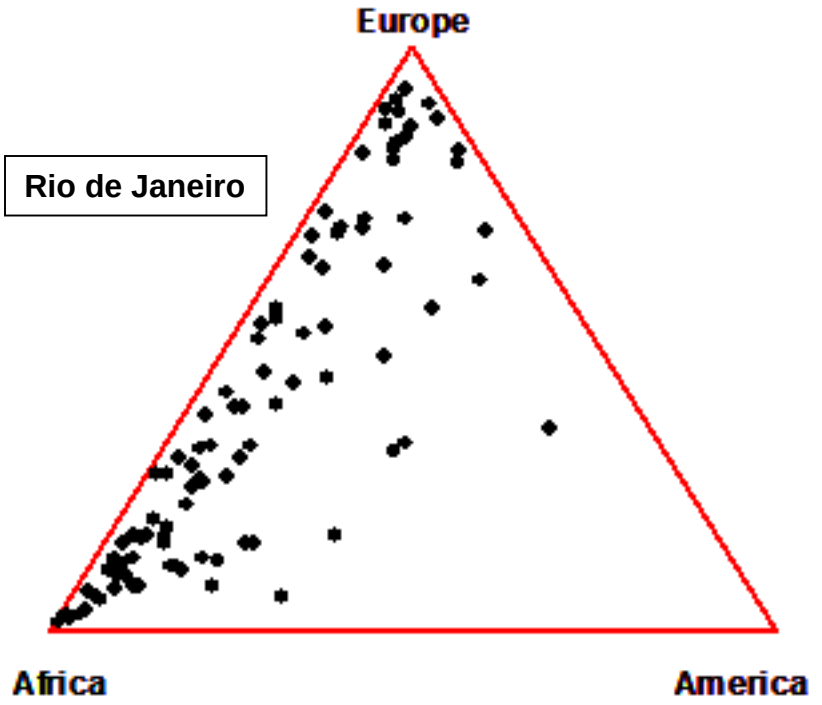
0.377	0.533	0.090

São Paulo



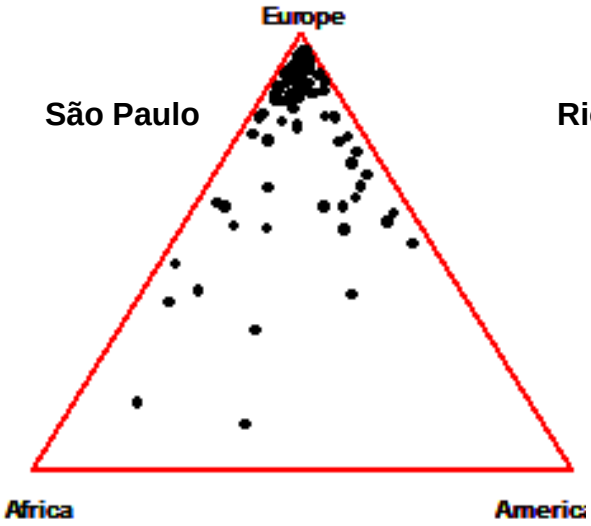
0.373	0.497	0.129

Rio de Janeiro



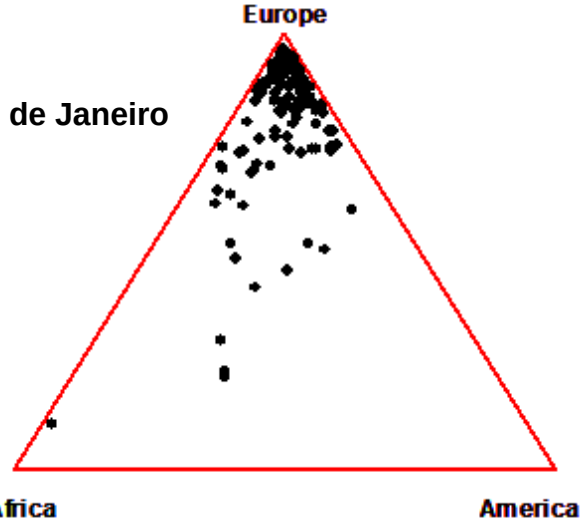
0.377	0.533	0.090

São Paulo



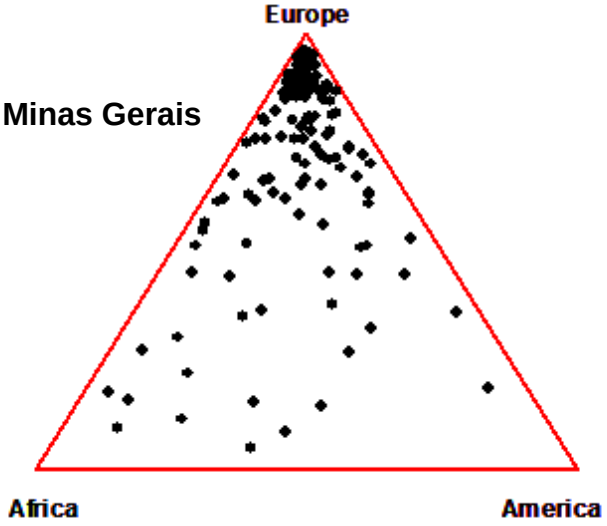
0.784	0.102	0.114

Rio de Janeiro



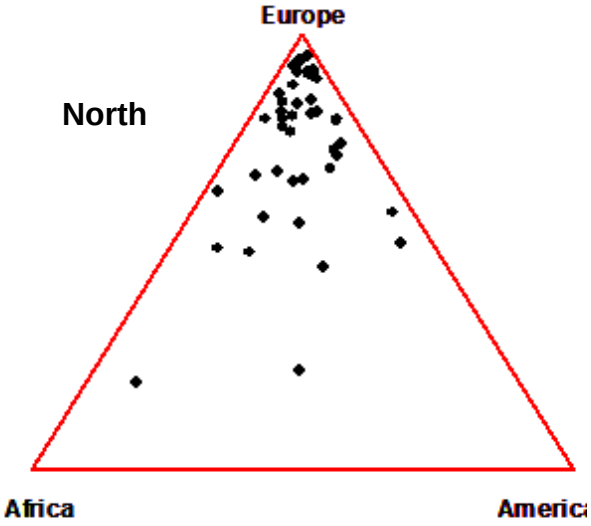
0.818	0.085	0.097

Minas Gerais



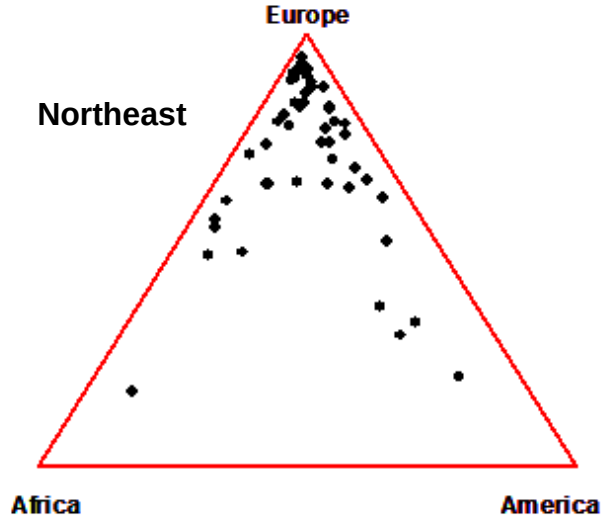
0.713	0.127	0.159

North



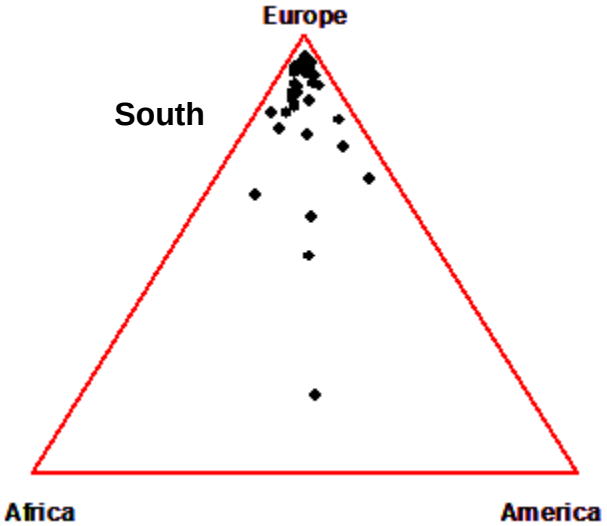
0.748	0.117	0.134

Northeast



0.711	0.147	0.142

South



0.824	0.089	0.087

Three major developments that occured in the Genome Era

- Characterization of the recent unique origin of modern humans in Africa
- Characterization of human genomic individuality at the DNA level
- Characterization of the genealogical structure of humanity

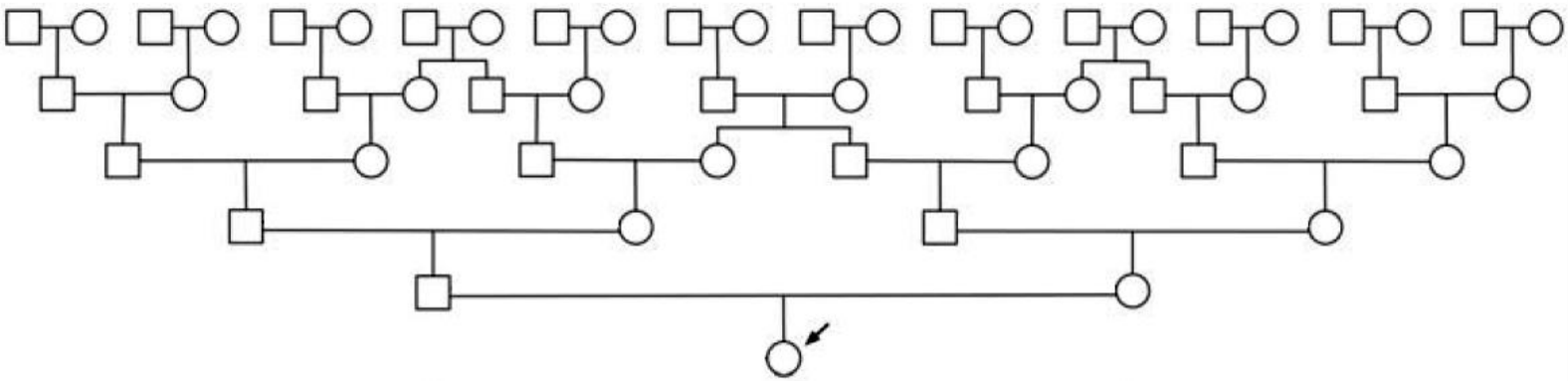
NATURE | VOL 431 | 30 SEPTEMBER 2004 | www.nature.com/nature

letters to nature

Modelling the recent common ancestry of all living humans

Douglas L. T. Rohde[1], Steve Olson[2] & Joseph T. Chang[3]

[1]*Department of Brain and Cognitive Sciences, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139, USA*
[2]*7609 Sebago Road, Bethesda, Maryland 20817, USA*
[3]*Department of Statistics, Yale University, New Haven, Connecticut 06520, USA*



40 2^{12}
30 2^{9}
20 2^{6}
.....
.....
5 32
4 16
3 8
2 4
1 2

Time of the Common Ancestor of a Group of N People

$T_n = \log_2 N$

$\log_2(7{,}000{,}000{,}000) = 32.7$ generations

32.7 X 30 = 981 years before present

Population ~ 67,000,000

$\log_2(67{,}000{,}000) = 26$ generations

26 X 30 = 780 years before present

Charlemagne (742-814) = 1,217 ybp

Time of the Identical Ancestor point of all of N People

$$U_n = 1.77 \log_2 N$$

$$1.77 \log_2(7.000.000.000) = 57.9 \text{ generations}$$

57.9 X 30 = 1,737 years before present

Population ~ 67,000,000

$1.77 \log_2(67,000,000) = 46$ generations

46 X 30 = 1,380 years before present

Charlemagne (742-814) = 1,239 ybp

Clovis I (466-511) = 1,528 ybp

letters to nature

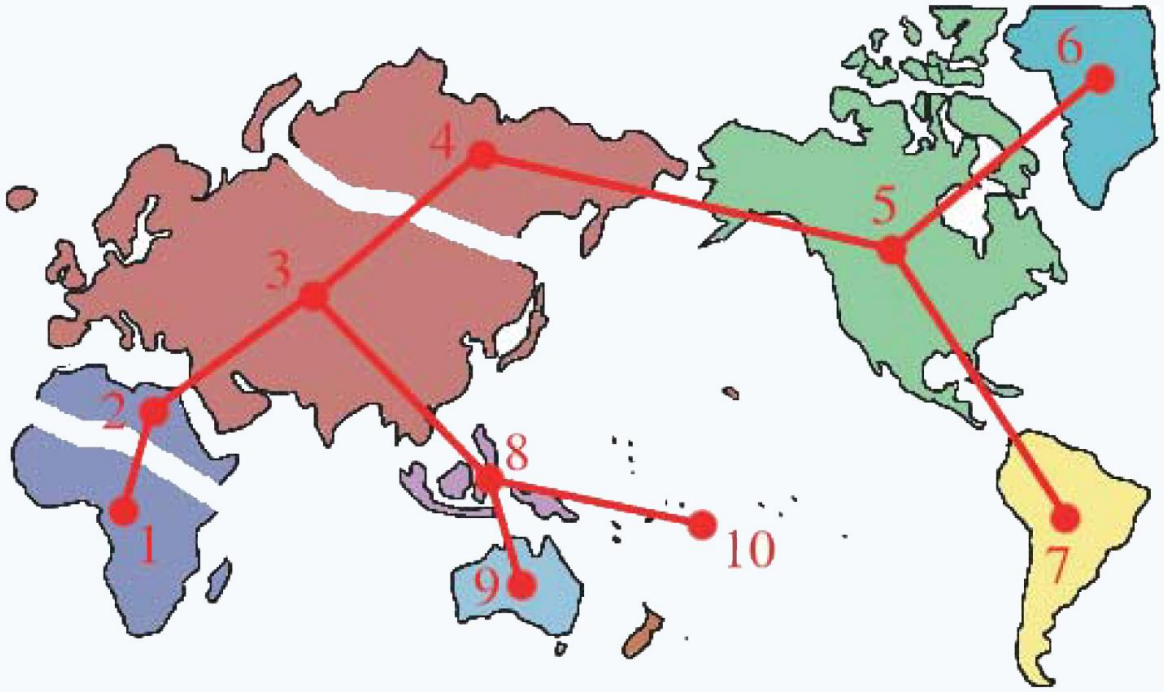


Figure 1 World map viewed as a ten-node graph. This graph has radius 3 and diameter 5.

T_n = 76 generations (~2,300 ybp; ~ 300 BC)
Alexander the Great (356-323 BC)

U_n = 169 generations (~5,000 ybp; ~ 3,000 BC)

TYAN Gathering = Family Gathering

MUSEUM NATIONAL D'HISTOIRE NATURELLE

MUSEE DE L'HOMME

TOUS PARENTS TOUS DIFFERENTS

André LANGANEY

A new paradigm

Division of humanity in individuals belonging to genealogies

“All relatives, all equallydiferent”

Thus, the only scientifically acceptable way to segment humankind is in seven billion individuals, each one possessing an unique genome and a singular life story.

This paradigma is in complete agrément with the idea that human rights apply to individuals, and not to groups.

“At the heart of the Constitution's guarantee of equal protection lies the simple command that the Government must treat citizens "as individuals, not 'as simply components of a racial, religious, sexual or national class”

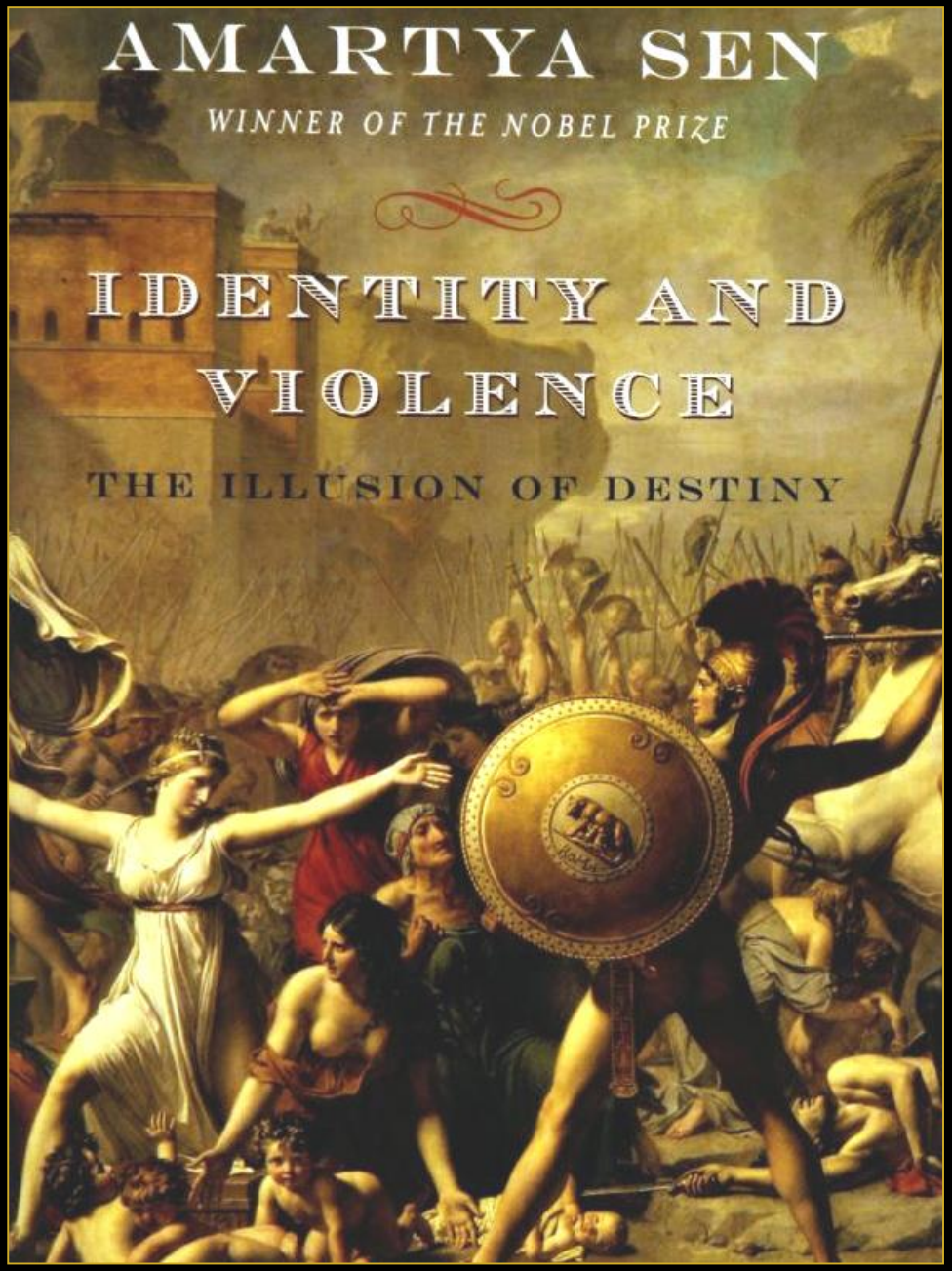
Justice Sandra Day O’Connor

Madness is rare in individuals - but in groups, parties, nations, and ages it is the rule.

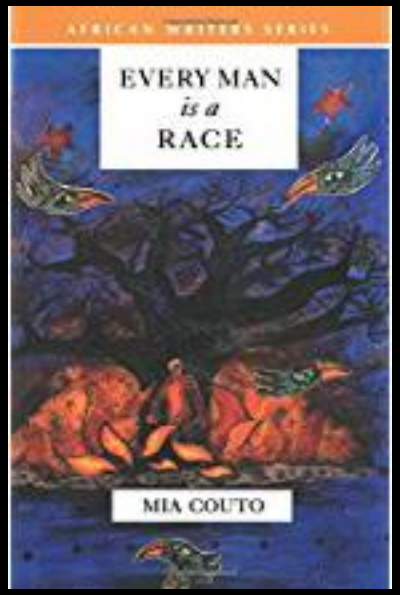
Friedrich Nietzsche
Beyond Good and Evil

- **This paradigma makes sense under the light of evolutionary history**

- **In this perspective group concepts, such as “races” lose meaning and evanesce.**


AMARTYA SEN
WINNER OF THE NOBEL PRIZE
IDENTITY AND VIOLENCE
THE ILLUSION OF DESTINY

The paradigm that emphasizes the singularity of the individual is the only one that does not limit a plural definition of personal identity by the group imposition of single unidimensional major criteria



João Passarinheiro

Deposition of the bird salesman to the police

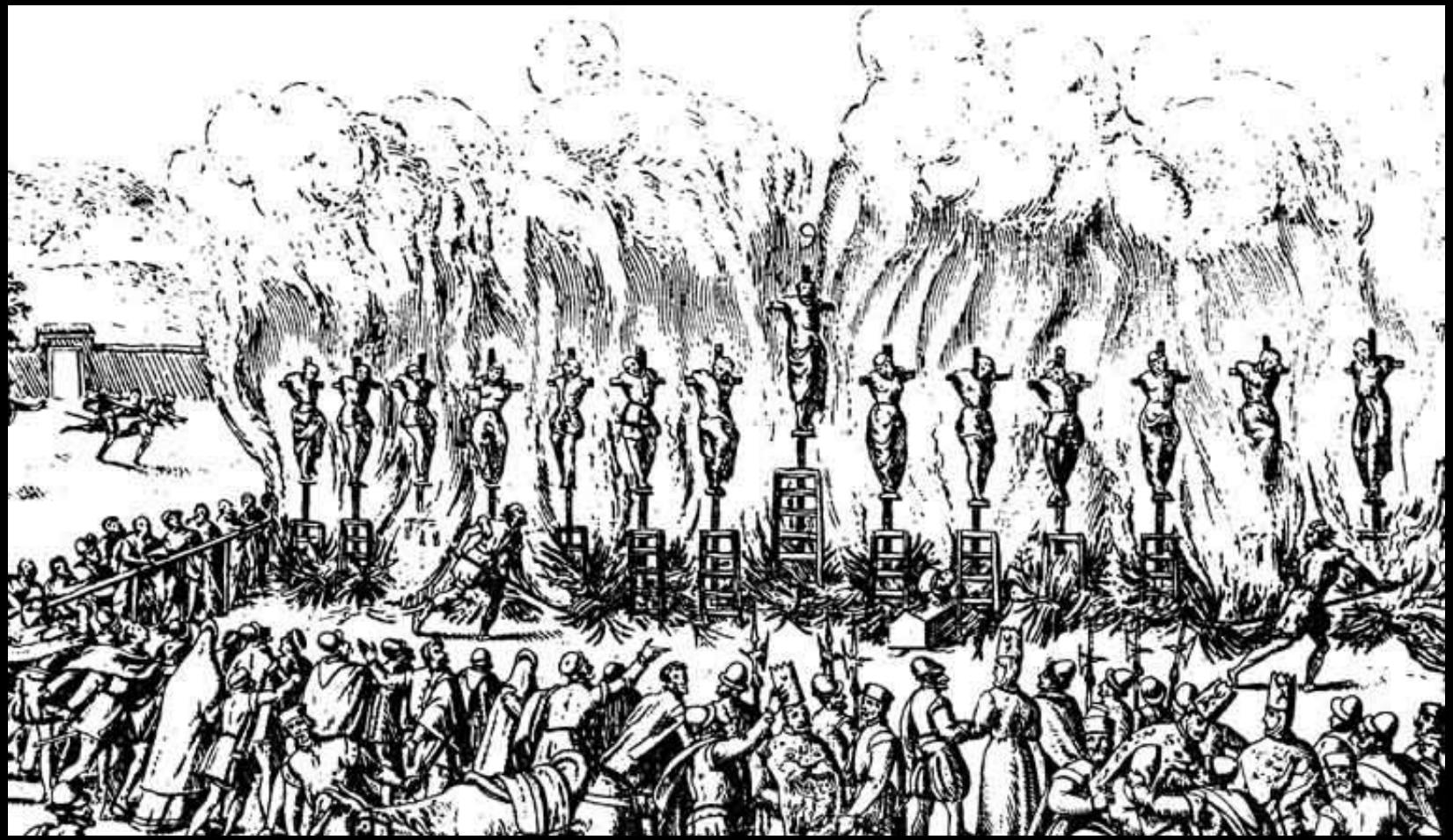
Asked about his race, he answered:

- I am my own race, João Passarinheiro.

When asked to explain, he added:

- My race is myself. Each person is an individual humanity. Each one is a race, mister policeman...

Witch-Craze - Europe 16th and 17th Centuries



Witch-Craze - Europe 16th and 17th Centuries

MALLEVS MALEFICARVM,

MALEFICAS ET EARVM

hæresim frameâ conterens,

EX VARIIS AVCTORIBVS COMPILATVS,

& in quatuor Tomos iustè distributus,

QVORVM DVO PRIORES VANAS DÆMONVM versutias, præstigiosas eorum delusiones, superstitiosas Strigimagarum caremonias, horrendos etiam cum illis congressus; exactam denique tam pestiferæ sectæ disquisitionem, & punitionem complectuntur. Tertius praxim Exorcistarum ad Dæmonum, & Strigimagarum maleficia de Christi fidelibus pellenda; Quartus verò Artem Deletriciam, Benedictionalem, & Exorcismalem continent.

TOMVS PRIMVS.

Indices Auctorum, capitum, rerúmque non desunt.

Editio nouissima, infinitis penè mendis expurgata; cuique accessit Fuga Dæmonum & Complementum artis exorcisticæ.

Vir siue mulier, in quibus Pythonicus, vel diuinationis fuerit spiritus, morte moriatur
Leuitici cap. 10.

LVGDVNI,
Sumptibus CLAVDII BOVRGEAT, sub signo Mercurij Galli.

M. DC. LXIX.
CVM PRIVILEGIO REGIS.

Hugh Trevor-Roper

The decline in prosecution of witches was caused in great part by the scientific revolution of the 17th Century, which made impossible the continuity of the belief in witchcraft.

Royal Society – founded in 1660

Science as “candle in the dark”
Carl Sagan

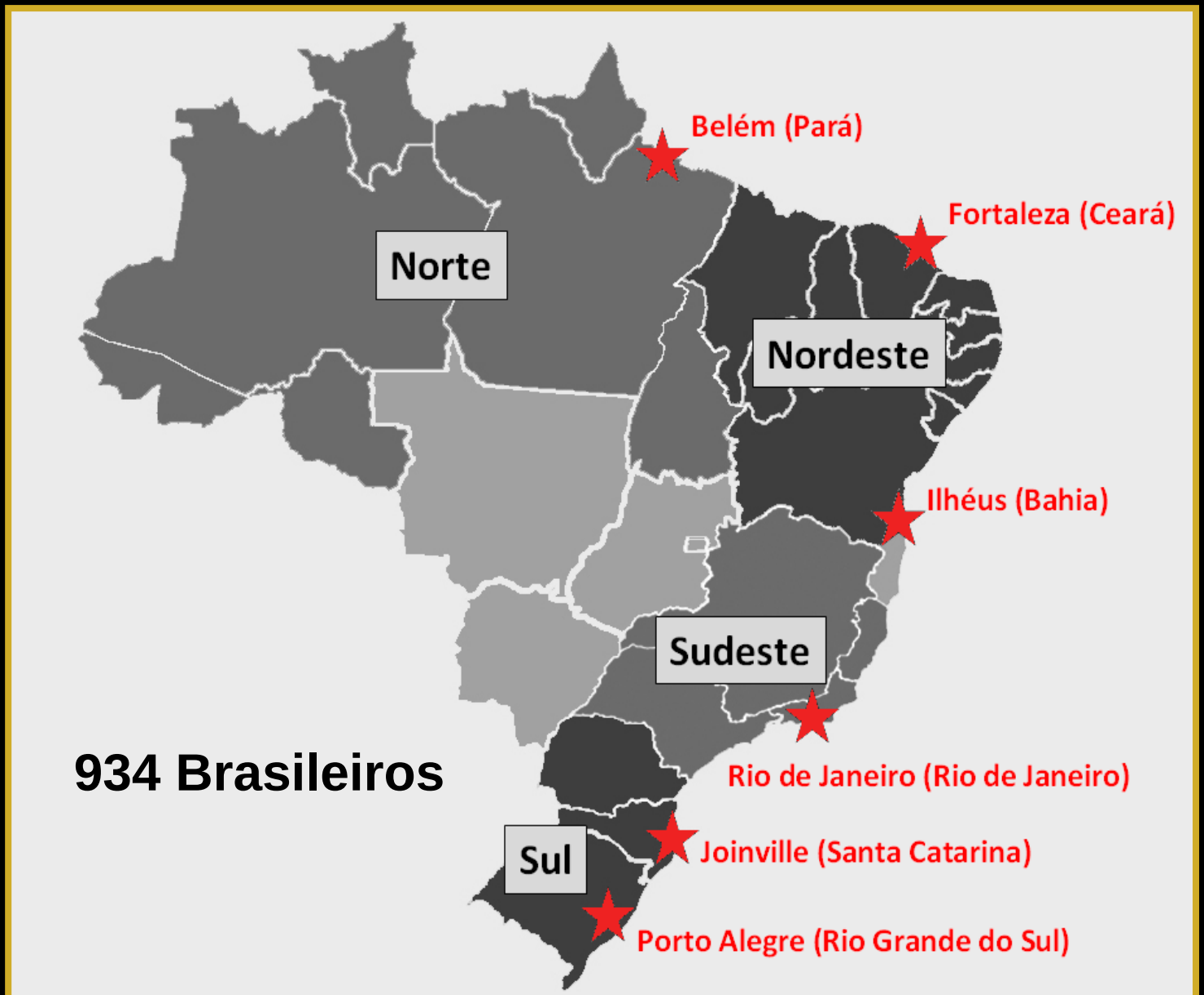
We should create a raceless society, in which the uniqueness of the individual is valued and celebrated.

“There are those that look at things the way they are, and ask why? I dream of things that never were, and ask why not?”

Robert Kennedy

The end

Thus, the only possible basis to deal with genetic variation in Brazilians is on a person-by-person basis, as 185 million different individuals, unique in their genomes and in their life histories


Belém (Pará)
Fortaleza (Ceará)
Norte
Nordeste
Ilhéus (Bahia)
Sudeste
934 Brasileiros
Rio de Janeiro (Rio de Janeiro)
Sul
Joinville (Santa Catarina)
Porto Alegre (Rio Grande do Sul)

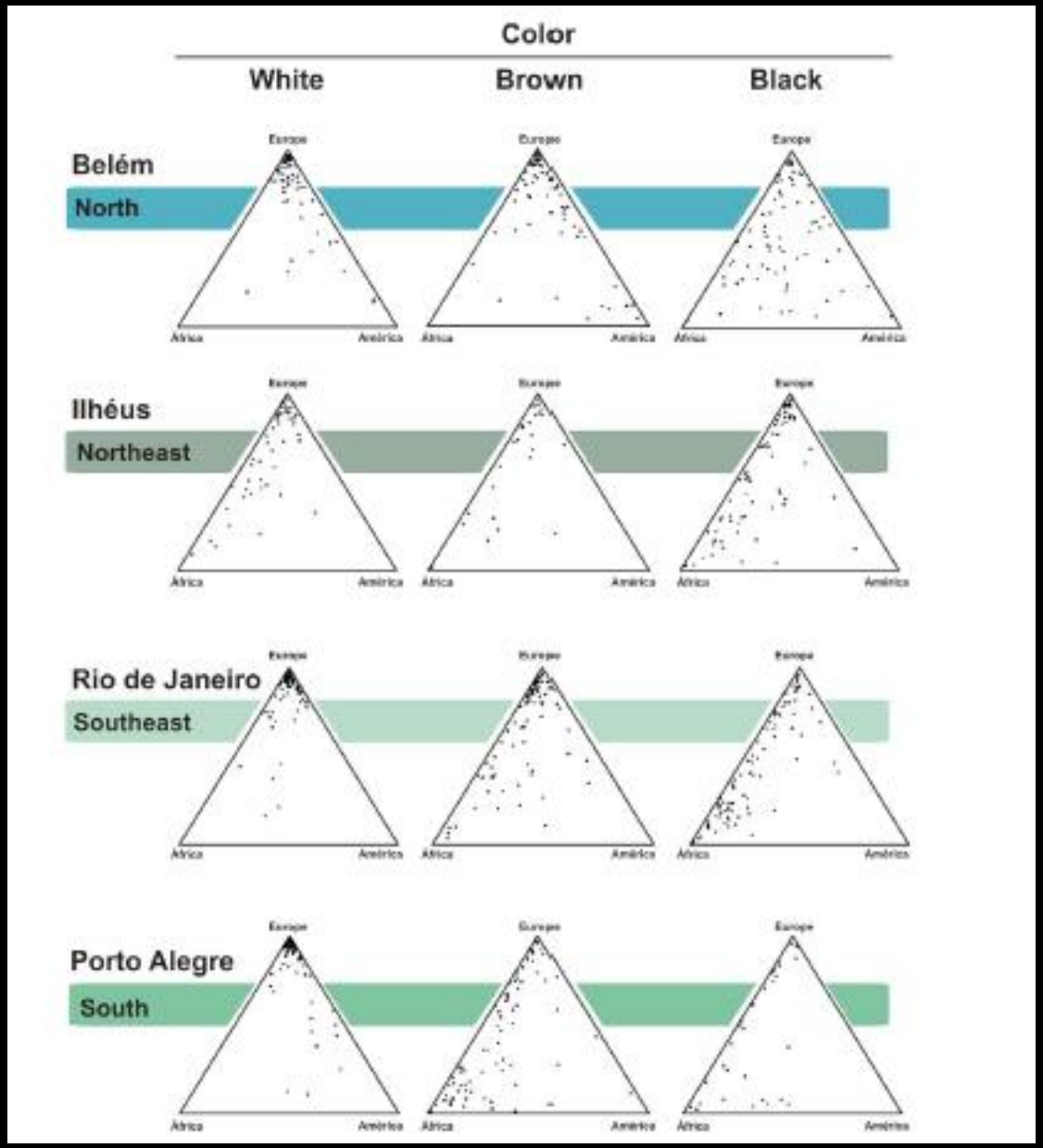
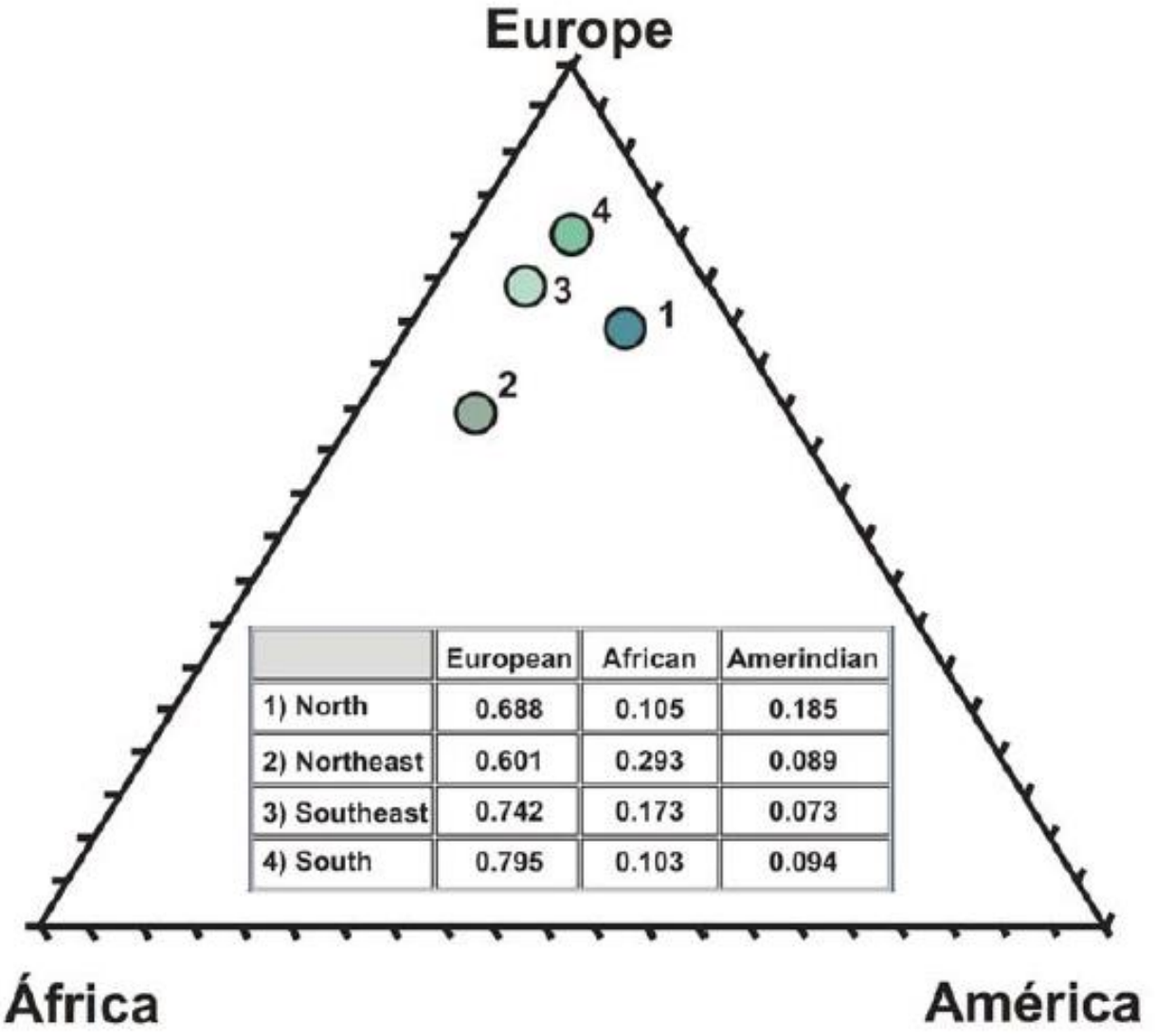

Color
White
Brown
Black
Belém
North
Ilhéus
Northeast
Rio de Janeiro
Southeast
Porto Alegre
South
Europe
África
América

Table 2. Mean and standard error for the estimated Amerindian, European and African ancestries of 934 Brazilian individuals from four regions of the country, self-categorized as having White, Brown and Black color.

Region	Ancestral Roots	Color category						Color-independent "Total Ancestry"
		White		Brown		Black		
		Mean	s.e.	Mean	s.e.	Mean	s.e.	
North	European	0.782	0.026	0.686	0.034	0.524	0.031	0.697
(Pará)	African	0.077	0.011	0.106	0.016	0.275	0.023	0.109
	Amerindian	0.141	0.022	0.209	0.030	0.201	0.026	0.194
Northeast	European	0.668	0.037	0.603	0.060	0.539	0.034	0.606
(Bahia)	African	0.244	0.033	0.308	0.057	0.359	0.014	0.303
	Amerindian	0.088	0.012	0.089	0.020	0.101	0.031	0.091
Northeast	European	0.758	0.032	0.728	0.029	N.S.	N.S.	
(Ceará)	African	0.133	0.017	0.144	0.021	N.S.	N.S.	
	Amerindian	0.109	0.021	0.128	0.015	N.S.	N.S.	
Southeast	European	0.861	0.016	0.675	0.028	0.427	0.032	0.737
(Rio de Janeiro)	African	0.074	0.011	0.238	0.025	0.495	0.032	0.189
	Amerindian	0.065	0.007	0.087	0.012	0.079	0.009	0.074
South	European	0.855	0.021	0.442	0.037	0.431	0.062	0.777
(Rio Grande do Sul)	African	0.053	0.019	0.444	0.035	0.459	0.052	0.127
	Amerindian	0.093	0.006	0.114	0.016	0.110	0.026	0.096
South	European	N.S.	N.S.	N.S.	N.S.	0.293	0.031	
(Santa Catarina)	African	N.S.	N.S.	N.S.	N.S.	0.596	0.030	
	Amerindian	N.S.	N.S.	N.S.	N.S.	0.111	0.012	

N.S. Not studied.

doi:10.1371/journal.pone.0017063.t002



	European	African	Amerindian
1) North	0.688	0.105	0.185
2) Northeast	0.601	0.293	0.089
3) Southeast	0.742	0.173	0.073
4) South	0.795	0.103	0.094

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PLoS one

The Genomic Ancestry of Individuals from Different Geographical Regions of Brazil Is More Uniform Than Expected

Sérgio D. J. Pena[1]*, Giuliano Di Pietro[2], Mateus Fuchshuber-Moraes[3], Julia Pasqualini Genro[4], Mara H. Hutz[4], Fernanda de Souza Gomes Kehdy[1], Fabiana Kohlrausch[3], Luiz Alexandre Viana Magno[5], Raquel Carvalho Montenegro[6], Manoel Odorico Moraes[6], Maria Elisabete Amaral de Moraes[6], Milene Raiol de Moraes[7], Élida B. Ojopi[8], Jamila A. Perini[3], Clarice Racciopi[1], Ândrea Kely Campos Ribeiro-dos-Santos[7], Fabrício Rios-Santos[2], Marco A. Romano-Silva[5], Vinicius A. Sortica[4], Guilherme Suarez-Kurtz[3]

1 Departamento de Bioquímica e Imunologia, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, 2 Departamento de Ciências da Saúde, Universidade Estadual de Santa Cruz, Ilhéus, Brazil, 3 Coordenação de Pesquisa/Divisão de Farmacologia, Instituto Nacional do Câncer, Rio de Janeiro, Brazil, 4 Departamento de Genética, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil, 5 Instituto Nacional de Ciência e Tecnologia de Medicina Molecular (INCT MM), Laboratório de Neurociência, Faculdade de Medicina, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, 6 Unidade de Farmacologia Clínica, Departamento de Fisiologia e Farmacologia, Faculdade de Medicina da Universidade Federal do Ceará, Fortaleza, Brazil, 7 Laboratório de Genética Humana e Médica, Universidade Federal do Pará, Guamá, Brazil, 8 Laboratório de Neurociências, Instituto de Psiquiatria, Faculdade de Medicina, Universidade de São Paulo, São Paulo, Brazil

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O GLOBO

Ex-chefe da Polícia é indiciado pela PF

• Após depoimento na sede da Polícia Federal, o delegado Allan Turnowski, ex-chefe da Polícia Civil do Rio, foi indiciado sobre, em novo desdobramento da Operação Guilhotina. Turnowski é acusado de vazar informações para um dos 30 policiais presos na ação. O crime pode pena de dois a seis anos de prisão. Página 14 a 16
• Luiz Garcia

— Dr. Allan é uma página Turnowski da nossa história!

Um país mais europeu

Genética de brasileiros revela menor ancestralidade negra e indígena

• O primeiro grande estudo genético sobre a ancestralidade dos brasileiros trouxe um resultado surpreendente e potencialmente polêmico: a população teria, preponderantemente, raízes ancestrais europeias, mesmo nas regiões Norte e Nordeste do país, onde, oficialmente, a presença indígena e negra fosse dominante. Segundo o trabalho coordenado pelo geneticista Sérgio Danilo Pena, da UFMG, a "europeização" do Brasil se deu devido ao fluxo de 6 milhões de imigrantes da Europa a partir do fim do século XIX. Página 36

Oposição abre batalha no STF pelo mínimo de 2012

Ação vai alegar que definição do valor por decreto é inconstitucional

• Texto-base foi aprovado o mínimo de R$ 545 para este ano, e também para o Supremo Tribunal Federal a batalha pelo salário de 2012. Dois partidos da oposição, o PSDB e o PPS, decidiram ir ao STF caso o Senado mantenha o artigo 3º do projeto aprovado na Câmara, que prevê a fixação do mínimo por decreto presidencial até 2015. Para os oposicionistas, o artigo é inconstitucional, pois tira do Congresso o poder de decidir sobre o tema — algo previsto na Constituição. Ontem, três ministros do Supremo consideraram que o artigo pode, de fato, causar problemas ao Planalto. O governo, porém, acredita a tese de inconstitucionalidade e diz que o decreto apenas fixará um valor a partir da fórmula de cálculo aprovada no Congresso. Depois da vitória na Câmara, o governo começa a costurar alianças táticas, entre elas o PSB e seu ministro, Carlos Lupi (Trabalho). Nove dos 27 deputados pedetistas e dois petistas votaram pelos R$ 560. No Senado, o governo espera contar com 58 votos, mas já sabe que o petista Paulo Paim (RS) planeja apresentar emenda pelos R$ 560. Nas ruas e na oposição, o clima entre era de desilusão com o fraco desempenho na Câmara. Página 3 a 10, Merval Pereira e editorial "Vitória da valorização do mínimo"

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DIRETOR DE REDAÇÃO: OTAVIO FRIAS FILHO ANO 90 ★ SEXTA-FEIRA, 18 DE FEVEREIRO DE 2011 ★ Nº 29.906 EDIÇÃO NACIONAL ★ CONCLUÍDA ÀS 20H55 ★ R$ 2,50

EUA ampliam acesso a cirurgia de obesidade

A FDA, agência dos EUA que regula remédios e alimentos, reduziu os limites de obesidade exigidos na cirurgia de banda gástrica, que usa uma espécie de anel para reduzir o estômago.

Pacientes com IMC igual a 30 e doenças associadas à gordura, como diabetes, poderão ser operados. Antes, exigia-se IMC 35. Saúde C6

No Rio, ex-chefe da Polícia Civil é indiciado pela PF

Allan Turnowski, ex-chefe da Polícia Civil do Rio, foi indiciado pela PF por suspeita de divulgar informações sobre ações policiais.

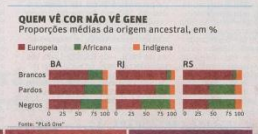
Ele deixou o cargo em meio à Operação Guilhotina, que apura corrupção na polícia. "Não recebi propina nem vazei informação", declarou. Cotidiano C4

BARBARA GANCIA

Governo brasileiro e Berlusconi têm seus pontos comuns Cotidiano C2

Rasan Jamal/Associated Press

Mulheres aguardam notícias de vítimas de confronto entre manifestantes antigoverno e forças de segurança em hospital de Manama, capital do Bahrein



Conflito mata menos 13 na L e cinco no Bal

Opositores do ditador líbio Gaddafi pro fúria' com protestos em 4 cidades; atos

Confrontos entre opositores e grupos pró-governo deixaram entre 13 e 20 mortos entre anteontem e ontem na Líbia. No Bahrein, militares ocuparam a capital depois de as forças repressivas matarem cinco.

Em resposta à onda de protestos nos países do norte da África e do Oriente Médio, a ditadura líbia de Muammar Gaddafi mobilizou até atiradores de elite para conter protestos em quatro cidades do país.

Estupro de repórter americana no Egito causa polêmica Mundo A20

Divulgação

ILUSTRADA

Pinacoteca expõe 170 fotos do russo Aleksandr Ródtchenko E4

Estreia o filme 'Besouro Verde', com Seth Rogen E6

CIÊNCIA

BRANCO *no preto*

DNA de negros e pardos do Brasil tem forte presença europeia C7

Grupo quer hotel seis estrelas em hospital tombado

A venda do conjunto tombado que hospedou o hospital Umberto Primo (ex-Matarazzo) está perto do fim. O grupo internacional Allard quer restaurar a área para fazer um hotel seis estrelas.

Dona do prédio, a Previ, fundo de pensão dos funcionários do Banco do Brasil, confirma "o estágio avançado" da negociação, mas não o investidor. Cotidiano C5

Joel Silva/Folhapress

Vista do Umberto Primo, que também é conhecido como hospital Matarazzo, em São Paulo

Governo já p 2007 apagõe

Desde 2007 um estudo do Ministério de Minas e Energia já apontava que o risco de apagões chegaria a um índice crítico em 2011.

Diz o estudo que a situação melhoraria em 2012, com a entrada em operação de dezenas de subestações e do sistema do rio Madeira.

EDITORIAIS Opinião A2

Leia **"Quem tem a força"**, sobre a aprovação do salário mínimo; e **"Exagero antitabagista"**, acerca de projeto para restringir o fumo em áreas livres.

62 páginas
313.680 exemplares

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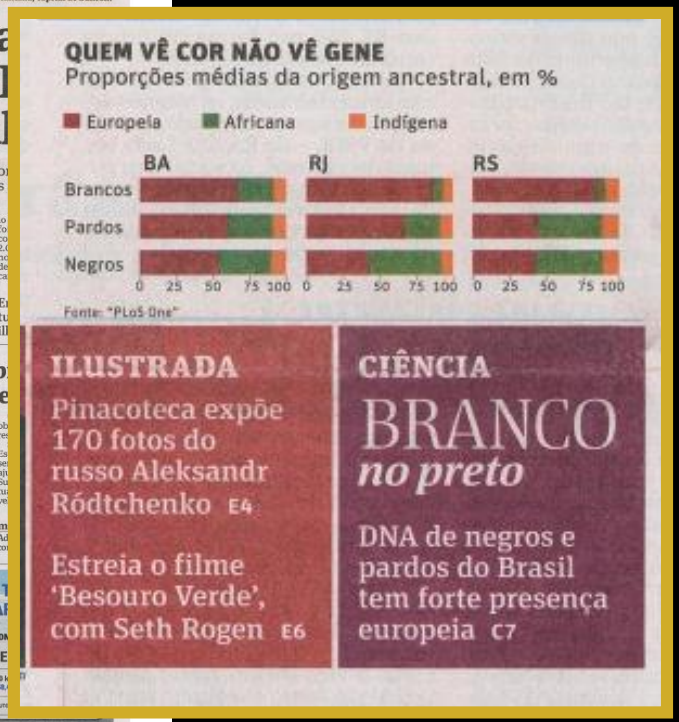
ATMOSFERA Cotidiano C2

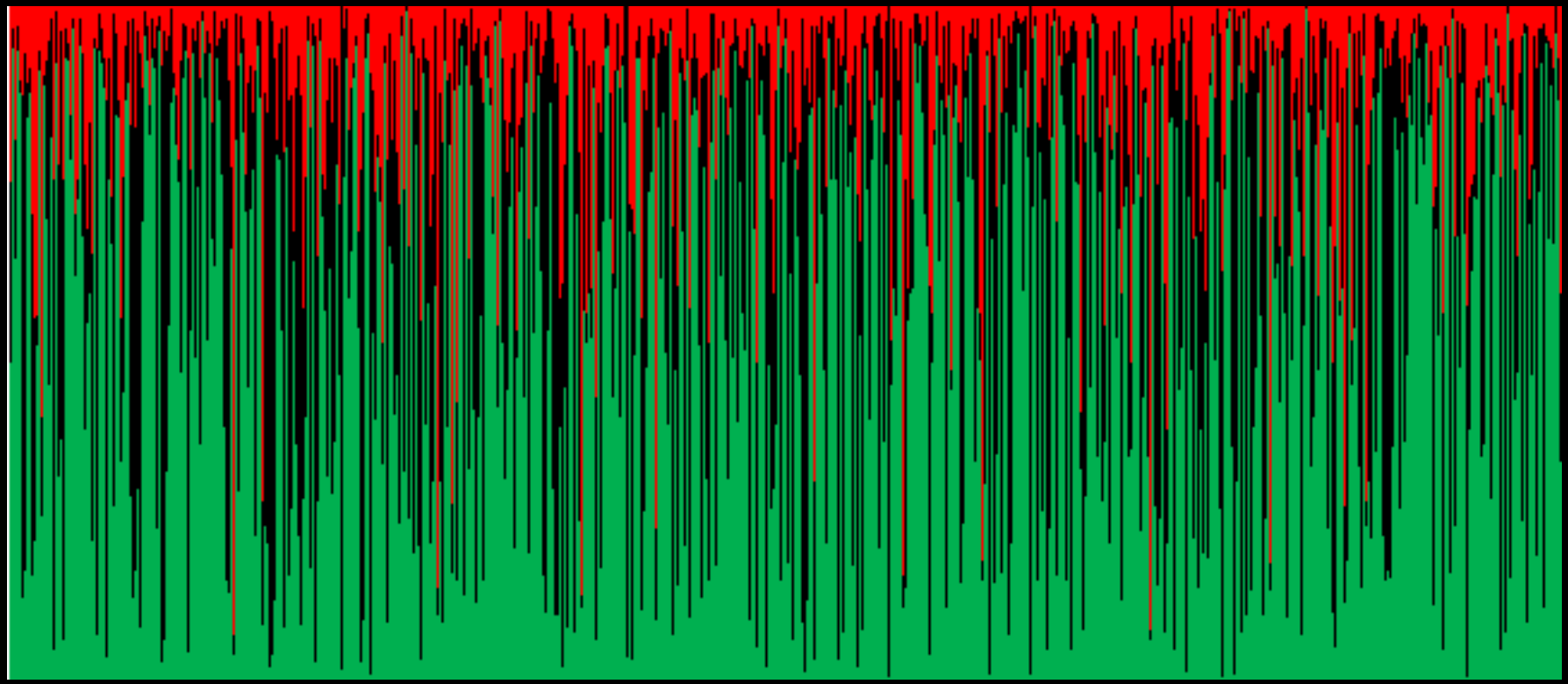
Chuva na maior parte do país

Lua crescente

VEJA NA PÁGINA 5.



Ancestralidade de 934 brasileiros
Ordem aleatória

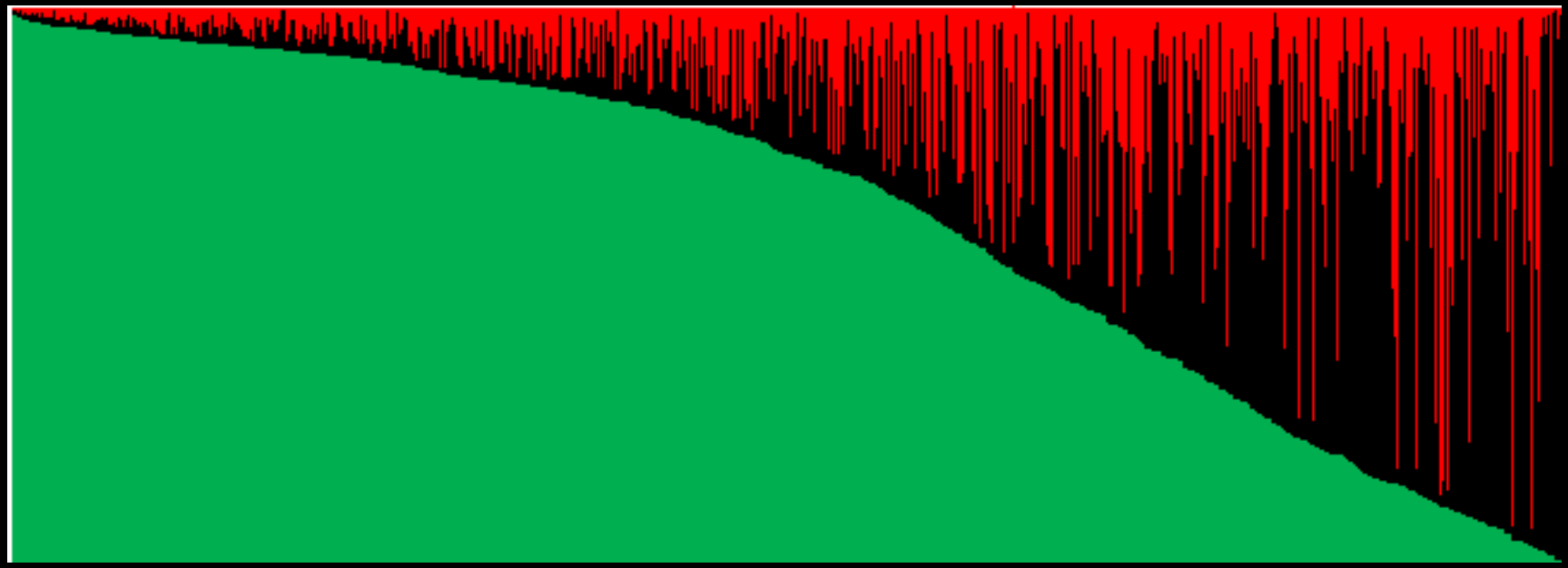


Ancestralidade europeia

Ancestralidade africana

Ancestralidade ameríndia

934 brasileiros
Ordem decrescente de ancestralidade europeia



Ancestralidade europeia

Ancestralidade africana

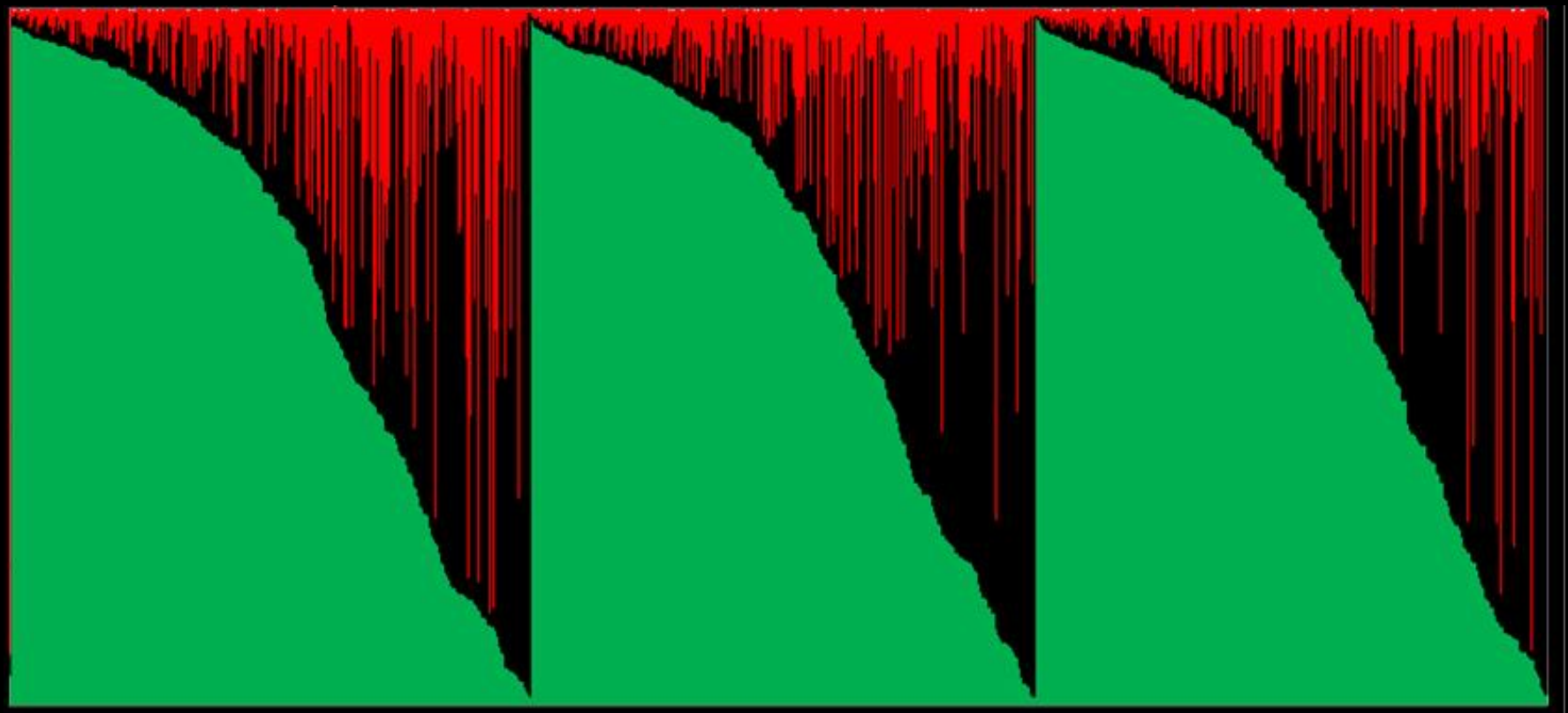
Ancestralidade ameríndia

O IBGE nos seus censos não computa ancestralidade. Ele usa somente auto-classificação impondo um pequeno número de categorias de cor de pele.

As categorias de cor branca. parda e preta são responsáveis por mais de 99% da população brasileira.

934 brasileiros
Ordem decrescente de ancestralidade europeia

Brancos **Pardos** **Pretos**



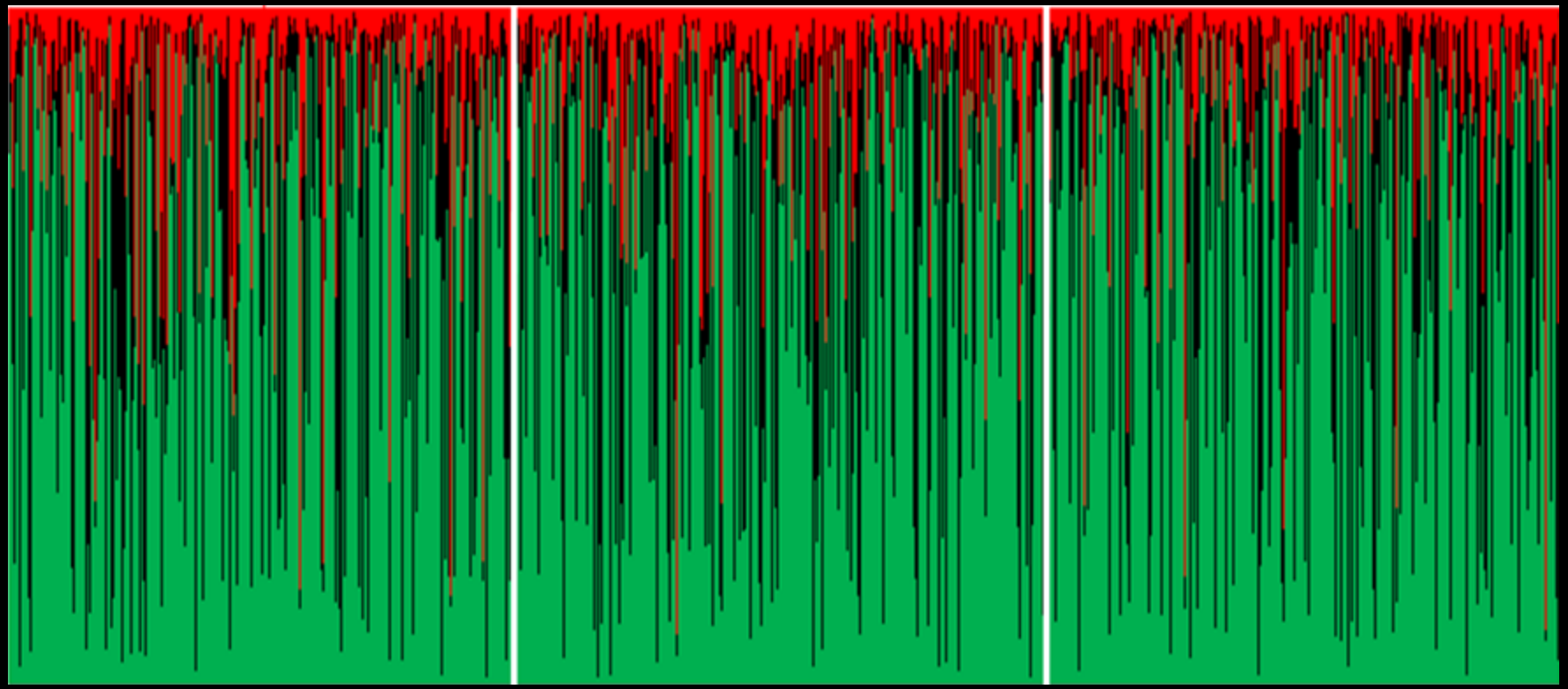
Ancestralidade europeia

Ancestralidade africana

Ancestralidade ameríndia

934 brasileiros
Ordem aleatória

Brancos **Pardos** **Pretos**



Ancestralidade europeia

Ancestralidade africana

Ancestralidade ameríndia

Conclusões

- Cada brasileiro tem uma proporção singular de ancestralidade europeia. ameríndia e africana.
- A relação entre cor de pele e ancestralidade no Brasil é tênue.
- Nas várias regiões do Brasil. cores de pele possuem significados diversos.
- A única divisão biologicamente coerente dos brasileiros é em 190 milhões de pessoas.
- Cientificamente não se justifica a segmentação dos brasileiros em grupos de cor de pele para tratamento diferencial pela lei.

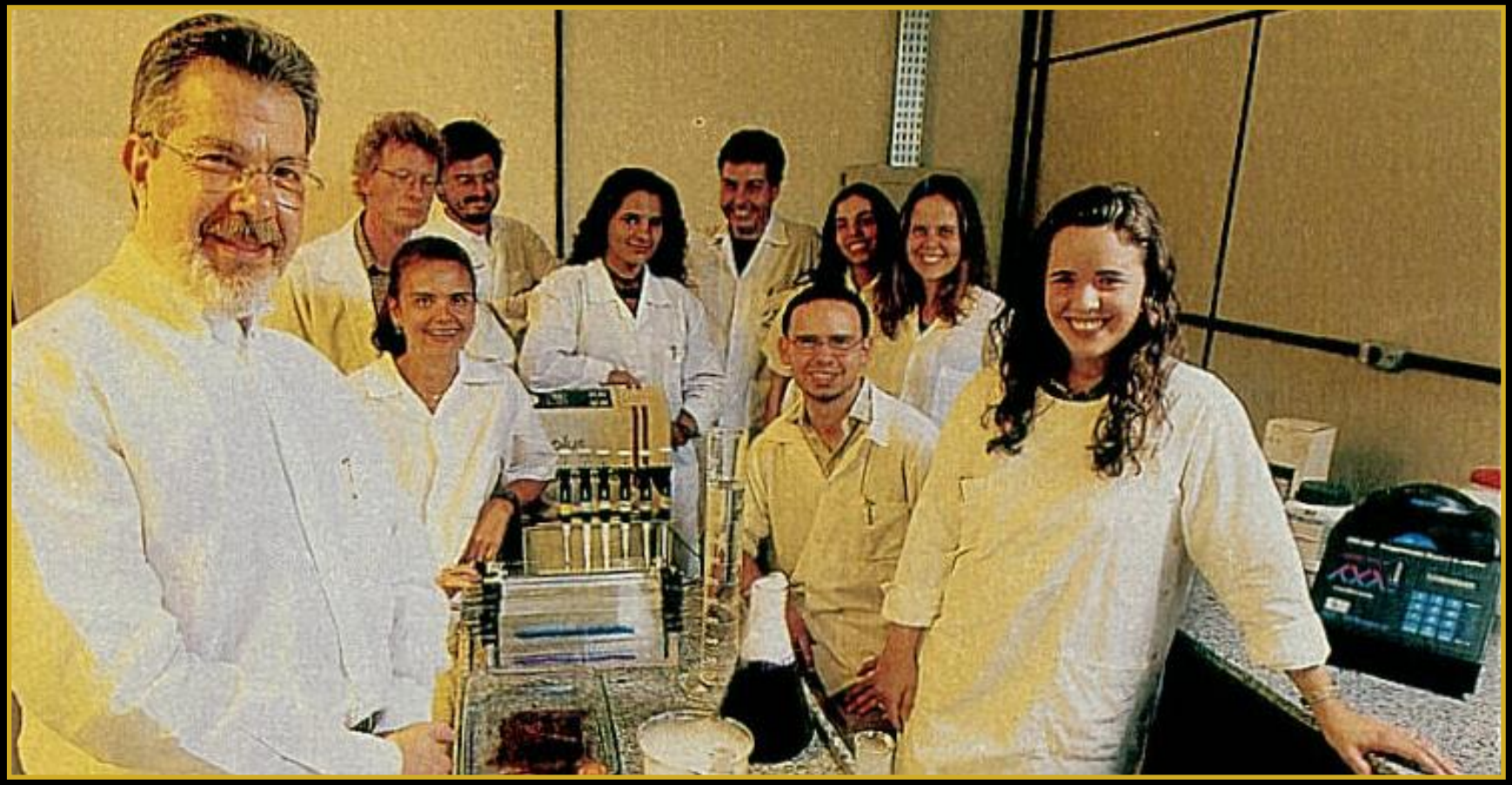
- **Independente da cor de sua pele a vasta maioria dos brasileiros tem um grau significativo de ancestralidade africana**
- **Independente da cor de sua pele a vasta maioria dos brasileiros tem um grau significativo de ancestralidade européia**
- **Independente da cor de sua pele uma grande porção dos brasileiros tem um grau significativo de ancestralidade ameríndia**

Não faz sentido falar sobre “populações” de brasileiros brancos ou de brasileiros negros por causa da pobre correlação entre cor e ancestralidade

Também não faz sentido falar em afrodescendentes ou eurodescendentes porque a vasta maioria dos brasileiros tem uma proporção significativa de ancestralidade africana e européia

(e ameríndia)

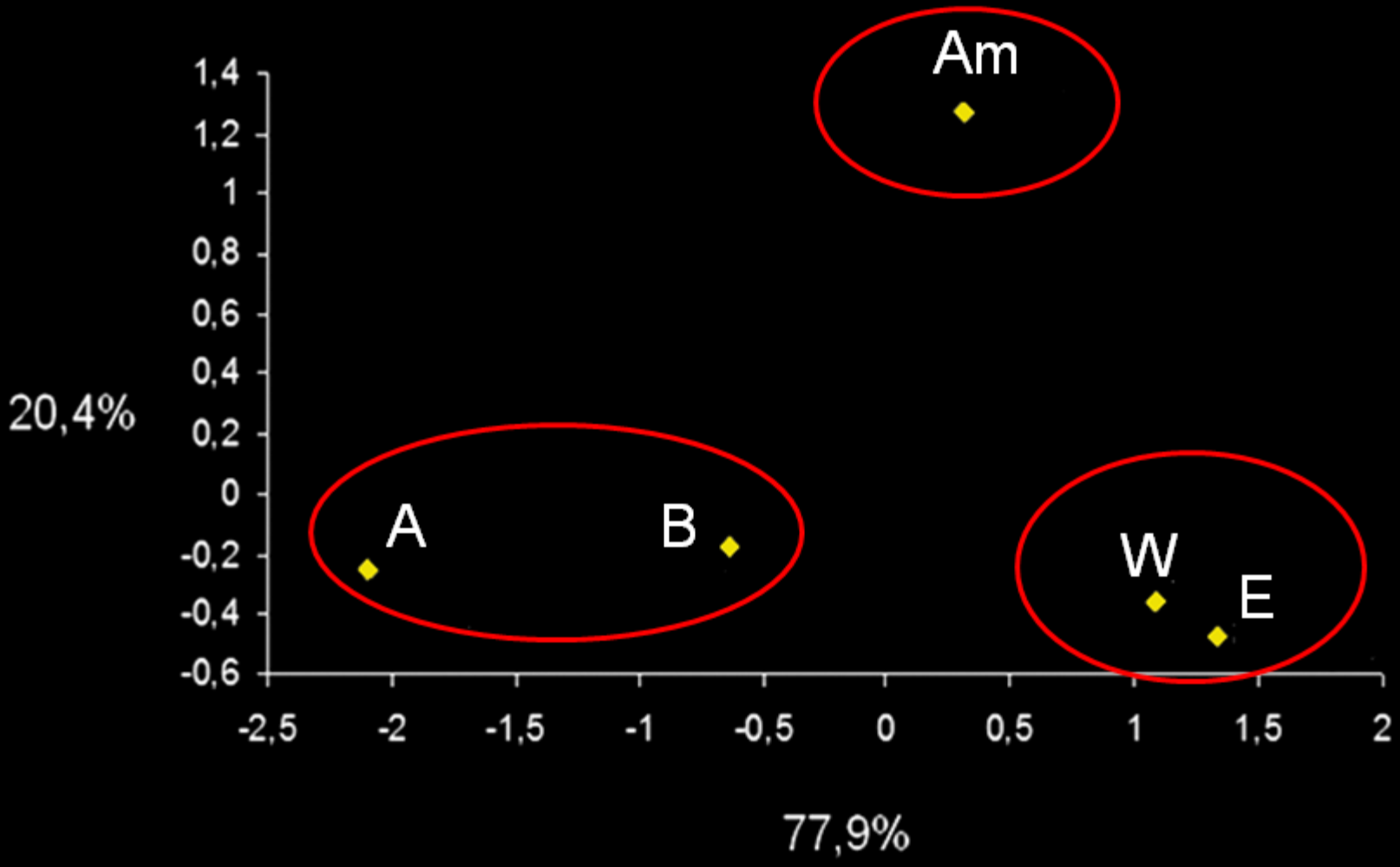
Assim, a única maneira de lidar com a variabilidade genética dos brasileiros é individualmente, como seres humanos únicos e singulares nos seus genomas e nas suas histórias de vida



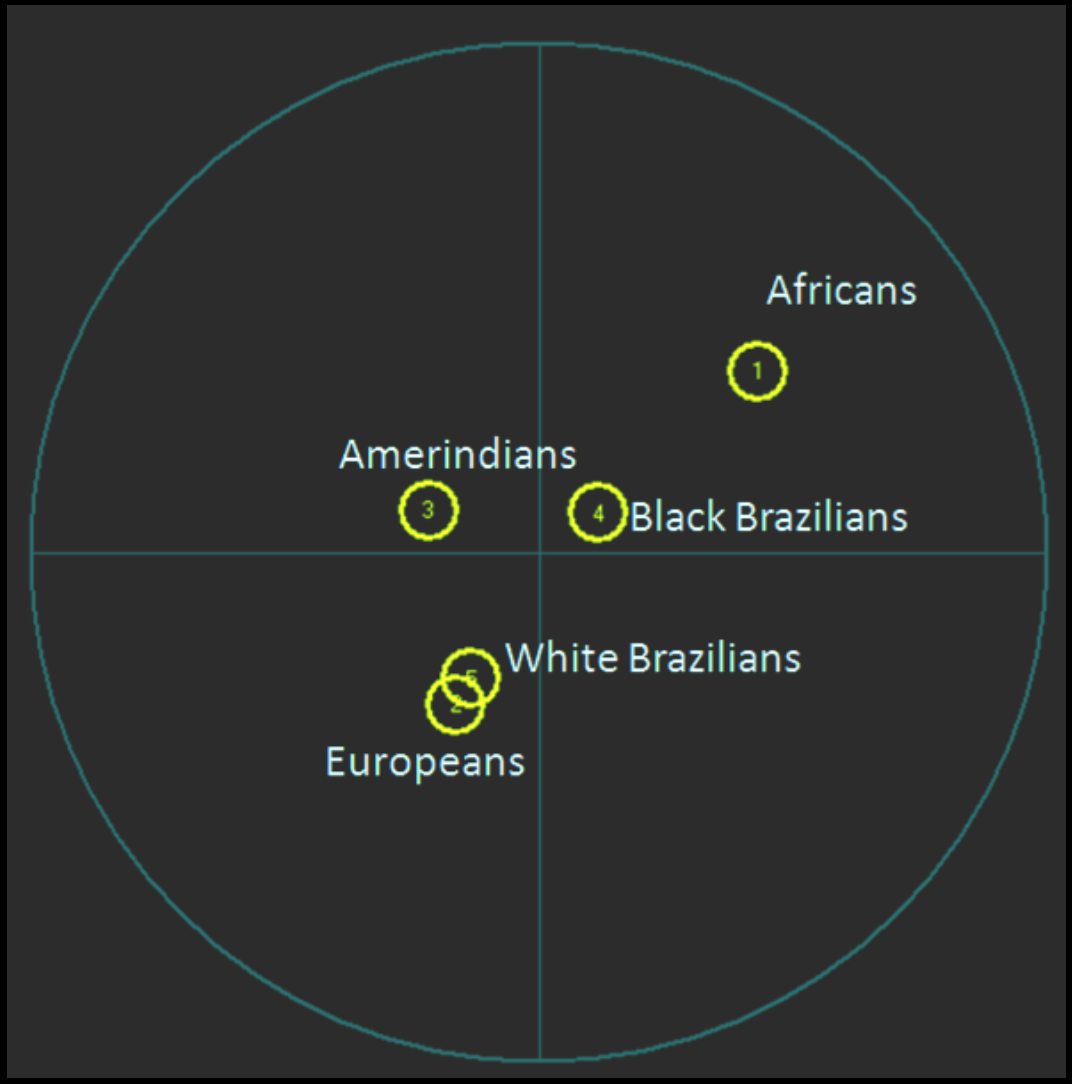
Plus: Juliana Pimenta – Luciana Bastos-Rodrigues – Simone Santos
Vanessa Gonçalves – Fernanda Kehdy – Higgor Dornelas –
Clarice Racioppi – Maria Cátira Bortolini – Guilherme Suarez-Kurtz –
Sergio Bydlowski

The End

PCA



MDS


Africans
1
Amerindians
3
4
Black Brazilians
White Brazilians
5
2
Europeans

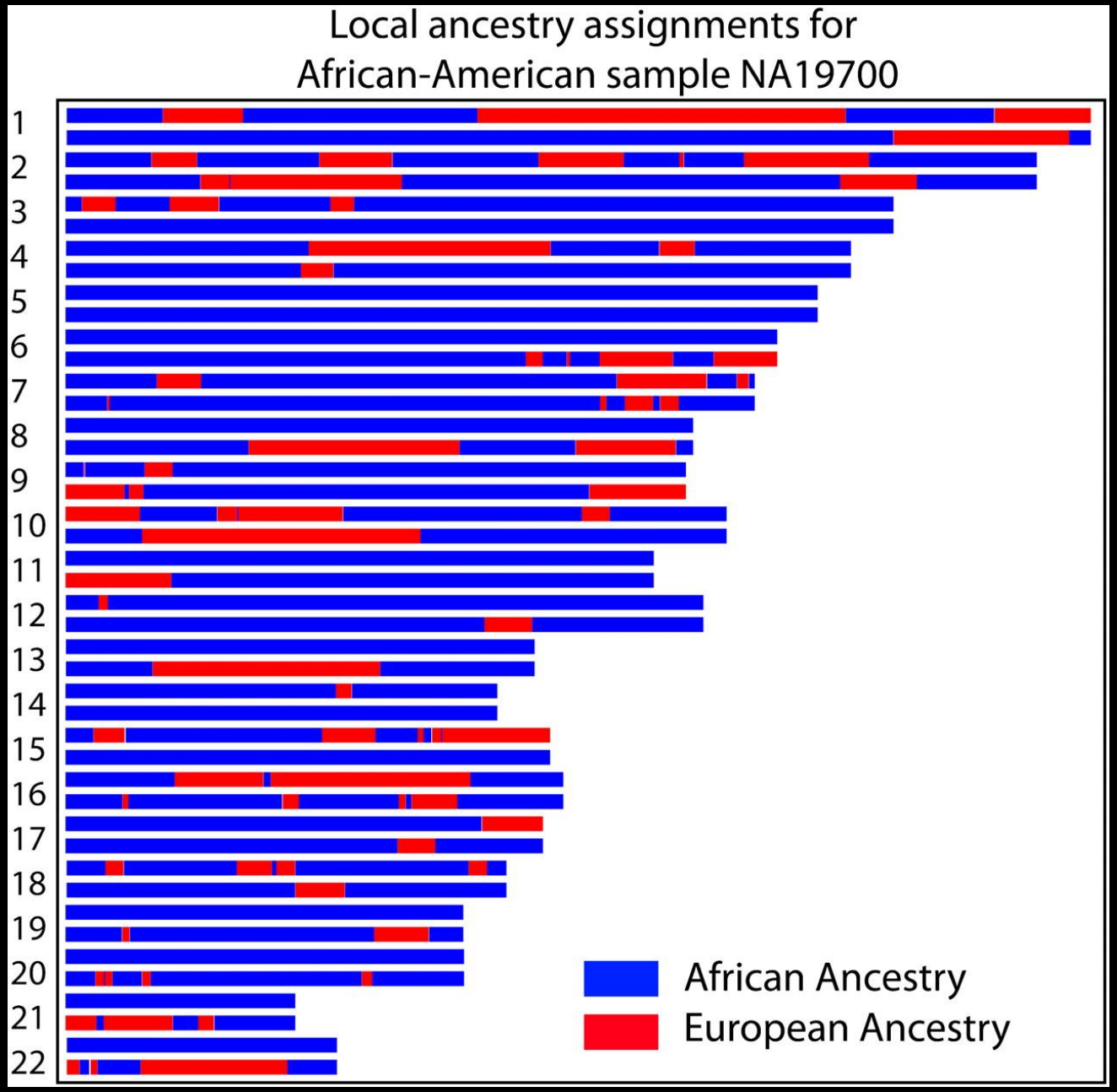
Conclusões Parciais

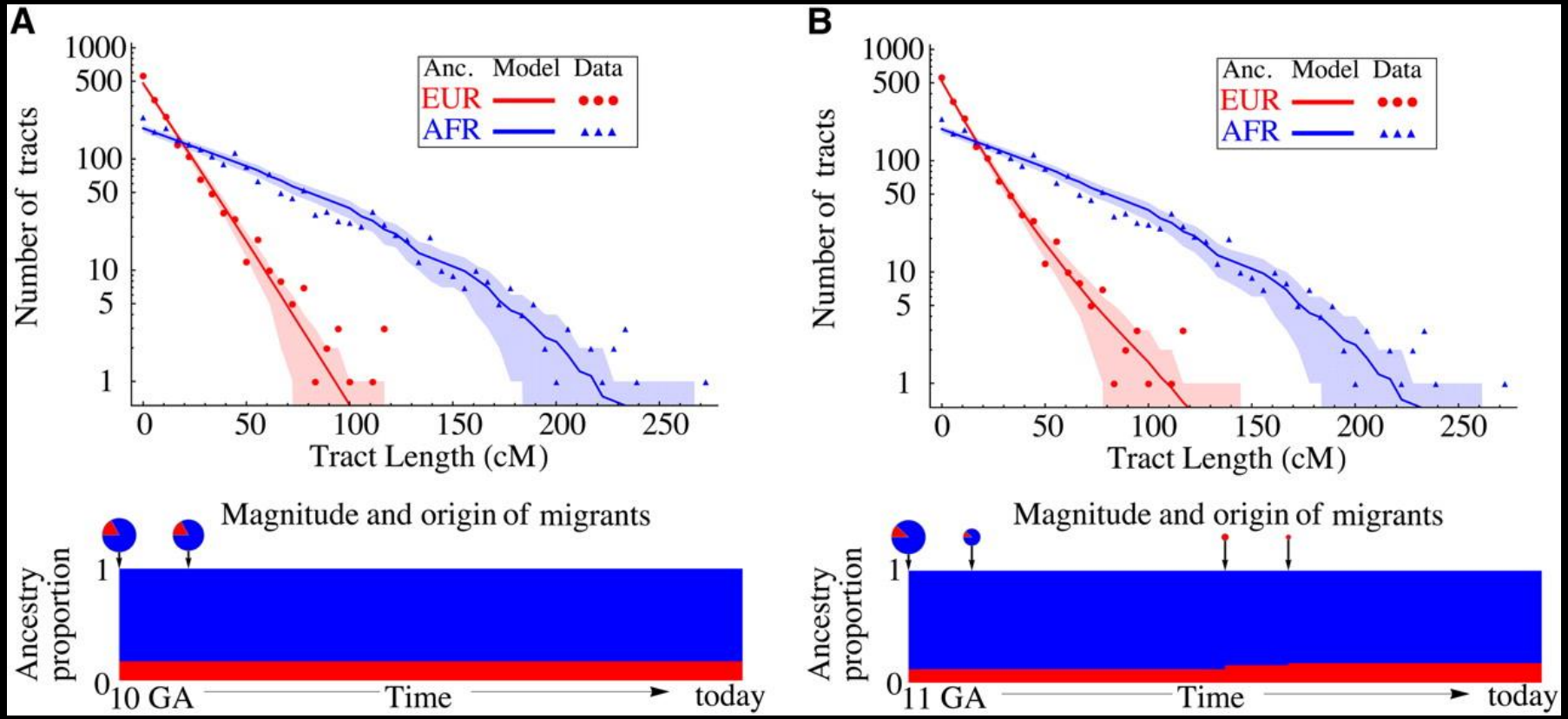
✓ Os *INDELs* selecionados foram capazes de diferenciar as 3 populações parentais (PCA e STRUCTURE)

✓ As populações de pretos de SP se mostraram mais miscigenadas que a população de brancos (PCA. ADMIX e STRUCTURE)

✓ Os cromossomos dos brasileiros são verdadeiros mosaicos constituídos de fragmentos de diferentes origens ancestrais.

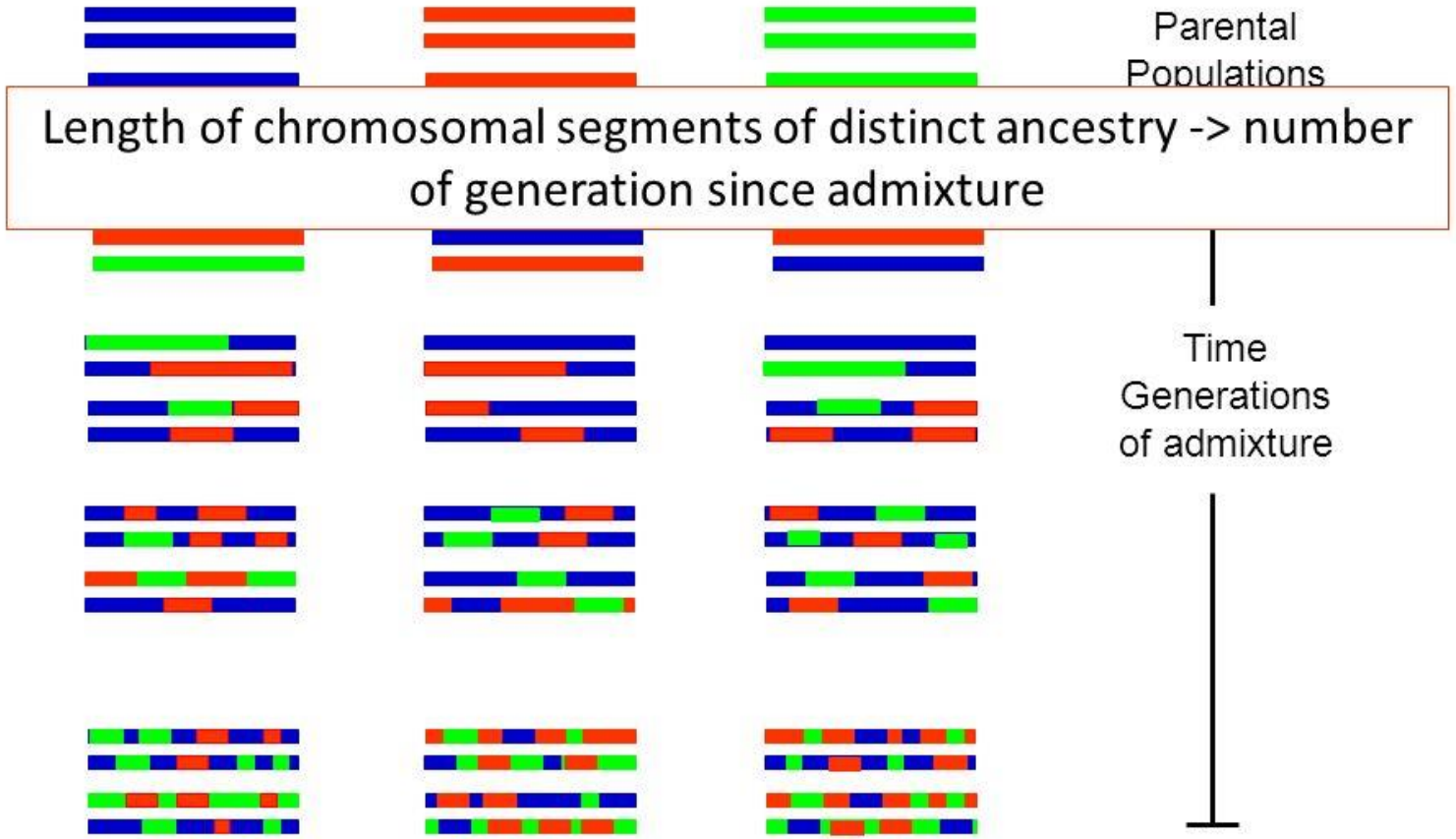
✓ A miscigenação ocorre não apenas a nível individual. mas também a nível cromossômico e que nossos cromossomos são constituídos de fragmentos com diferentes genealogias


Local ancestry assignments for
African-American sample NA19700
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
African Ancestry
European Ancestry


A
B
Number of tracts
1000
500
100
50
10
5
1
0
50
100
150
200
250
Tract Length (cM)
Anc. Model Data
EUR
AFR
Magnitude and origin of migrants
Ancestry proportion
1
0
10 GA
11 GA
Time
today

EpiGen-Brasil

Admixture Dynamics Inference



Differences in Admixture Dynamics. We estimated the continental origin of each allele for each SNP along each chromosome of the EPIGEN individuals (19) (*SI Appendix*, section 6.7) and calculated the lengths of chromosome segments of continuous specific ancestry (CSSA) (Fig. 2*A*), with distribution that informs how admixture occurred over time. By leveraging on the model by Liang and Nielsen (20) of CSSA, we developed an ABC framework to infer admixture dynamics (*SI Appendix*, section 6.8). We simulated CSSA distributions generated by a demographic history of three pulses of trihybrid admixture that occurred 18–16, 12–10, and 6–4 generations ago, conditioning on the observed current admixture proportions of each of the EPIGEN populations. This demographic model conciliates statistical complexity and the real history of admixture. We inferred the posterior distributions of nine parameters $m_{n,P}$, where

large numbers during the last 150 y; Italians (mostly to the So and Southeast); and Germans (mostly to the South). In our P representation (Fig. 3*B*), the European component of the geno of most Brazilians is similar to individuals from the Iberian Peninsula and neighboring regions. The resemblance in within-European ancestry of individuals from Pelotas (South) and Bambuí (Southeast) to central North Europeans and Middle Easters, respectively (Fig. 3*B*), reflects a geographically wider European ancestry of these two populations with respect to Salvador. Considering the total European ancestry estimated by ADMIXTURE, we inferred a higher proportion of North European-associated ancestry in Pelotas (40.2%) than in Bambuí (35.8%) and Salvador (36.7%; $P < 10^{-15}$; Wilcoxon tests) (Fig. 3*A*, red cluster in $K = 7$). We confirmed these results by analyzing a reduced number of SNPs with a larger set of

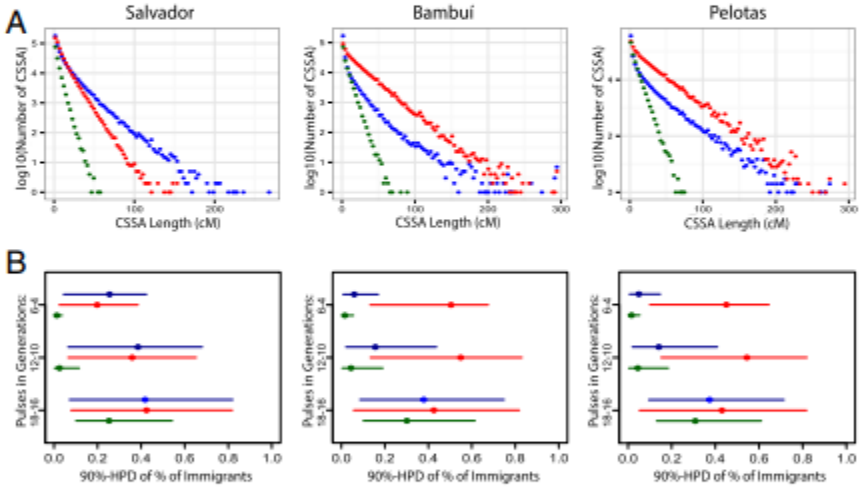


Fig. 2. Distributions of lengths of chromosomal segments of (*A*) CSSA and (*B*) admixture dynamics inferences estimated for three EPIGEN Brazilian populations. (*A*) CSSA lengths were distributed in 50 equally spaced bins per population. Red, blue, and green dots represent a European, an African, and a Native-American CSSA, respectively. (*B*) We inferred the posterior densities of the proportions of immigrants (with respect to the admixed population) from each origin, and we show their 90% highest posterior density (HPD) intervals. Inferences are based on a model of three pulses of admixture (vertical axis) simulated based on the model of CSSAs evolution by Liang and Nielsen (20). Inferences are based on approximate Bayesian computation. Ancestry color codes are red for European, blue for African, and green for Native American.

PNAS PNAS PNAS

Origin and dynamics of admixture in Brazilians and its effect on the pattern of deleterious mutations

Fernanda S. G. Kehdy[a,1], Mateus H. Gouveia[a,1], Moara Machado[a,1], Wagner C. S. Magalhães[a,1], Andrea R. Horimoto[b], Bernardo L. Horta[c], Rennan G. Moreira[a], Thiago P. Leal[a], Marilia O. Scliar[a], Giordano B. Soares-Souza[a], Fernanda Rodrigues-Soares[a], Gilderlanio S. Araújo[a], Roxana Zamudio[a], Hanaisa P. Sant Anna[a], Hadassa C. Santos[b], Nubia E. Duarte[b], Rosemeire L. Fiaccone[d], Camila A. Figueiredo[e], Thiago M. Silva[f], Gustavo N. O. Costa[f], Sandra Beleza[g], Douglas E. Berg[h,i], Lilia Cabrera[j], Guilherme Debortoli[k], Denise Duarte[l], Silvia Ghirotto[m], Robert H. Gilman[n,o], Vanessa F. Gonçalves[p], Andrea R. Marrero[k], Yara C. Muniz[k], Hansi Weissensteiner[q], Meredith Yeager[r], Laura C. Rodrigues[s], Mauricio L. Barreto[f], M. Fernanda Lima-Costa[t,2], Alexandre C. Pereira[b,2], Maíra R. Rodrigues[a,2], Eduardo Tarazona-Santos[a,2,3], and The Brazilian EPIGEN Project Consortium[4]

[a]Departamento de Biologia Geral, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, 31270-901, Belo Horizonte, Minas Gerais, Brazil; [b]Instituto do Coração, Universidade de São Paulo, 05403-900, São Paulo, Sao Paulo, Brazil; [c]Programa de Pós-Graduação em Epidemiologia, Universidade Federal de Pelotas, 464, 96001-970 Pelotas, Rio Grande do Sul, Brazil; [d]Departamento de Estatística, Instituto de Matemática, Universidade Federal da Bahia, 40170-110, Salvador, Bahia, Brazil; [e]Departamento de Ciências da Biointeração, Instituto de Ciências da Saúde, Universidade Federal da Bahia, 40110-100, Salvador, Bahia, Brazil; [f]Instituto de Saúde Coletiva, Universidade Federal da Bahia, 40110-040, Salvador, Bahia, Brazil; [g]Department of Genetics, University of Leicester, LE1 7RH, Leicester, United Kingdom; [h]Department of Molecular Microbiology, Washington University School of Medicine, St. Louis, MO 63110; [i]Department of Medicine, University of California, San Diego, CA 92093; [j]Biomedical Research Unit, Asociación Benéfica Proyectos en Informática, Salud, Medicina y Agricultura (AB PRISMA), 170070, Lima, Peru; [k]Departamento de Biologia Celular, Embriologia e Genética, Universidade Federal de Santa Catarina, 88040-900, Florianópolis, Santa Catarina, Brazil; [l]Departamento de Estatística, Universidade Federal de Minas Gerais, 31270-901, Belo Horizonte, Minas Gerais, Brazil; [m]Dipartimento di Scienze della Vita e Biotecnologie, Università di Ferrara, 44121 Ferrara, Italy; [n]Bloomberg School of Public Health, International Health, Johns Hopkins University, Baltimore, MD 21205; [o]Laboratorio de Investigación de Enfermedades Infecciosas, Universidade Peruana Cayetano Heredia, 15102, Lima, Peru; [p]Department of Psychiatry and Neuroscience Section, Center for Addiction and Mental Health, University of Toronto, Toronto, ON, Canada M5T 1R8; [q]Division of Genetic Epidemiology, Department of Medical Genetics, Molecular and Clinical Pharmacology, Innsbruck Medical University, 6020 Innsbruck, Austria; [r]Cancer Genomics Research Laboratory, Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research, Frederick, MD 20850; [s]Department of Infectious Disease Epidemiology, Faculty of Epidemiology, London School of Hygiene and Tropical Medicine, London WC1E 7HT, United Kingdom; and [t]Instituto de Pesquisa Rene Rachou, Fundação Oswaldo Cruz, 30190-002, Belo Horizonte, Minas Gerais, Brazil

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While South Americans are underrepresented in human genomic diversity studies, Brazil has been a classical model for population genetics studies on admixture. We present the results of the EPIGEN Brazil Initiative, the most comprehensive up-to-date genomic analysis of any Latin-American population. A population-based genome-

the largest and most populous Latin-American country. Its over 200 million inhabitants are the product of post-Columbian admixture between Amerindians, Europeans colonizers or immigrants, and African slaves (1). Interestingly, Brazil was the destiny of nearly 40% of the African diaspora, receiving seven