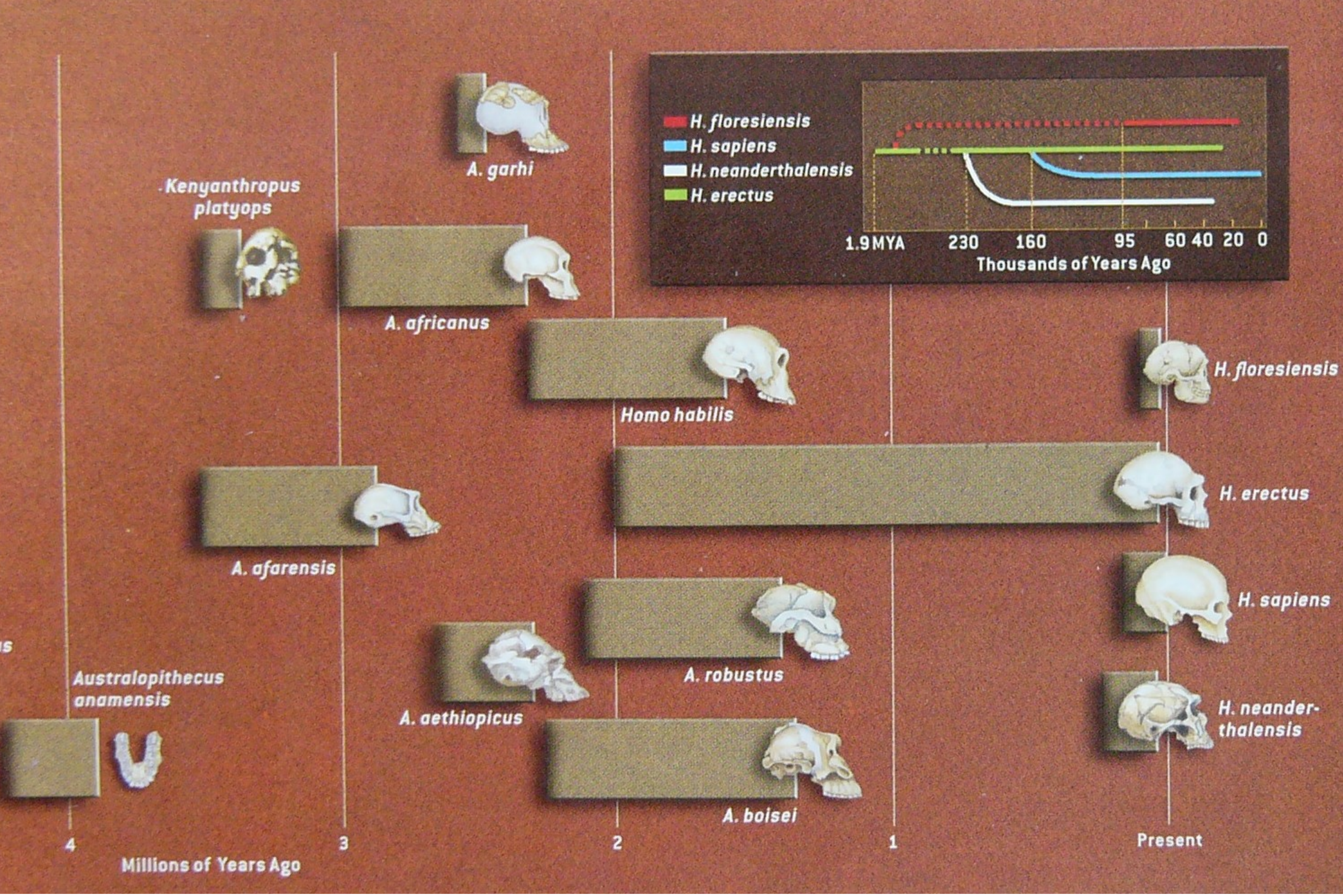
Serkkumme genomi selvitetty

Darwinin syntymäpäivänä 12.02.2009 julkaistiin hämmästyttävä tieto: Neanderthal-ihmisen geenit on luettu Saksassa.

Onko Neanderthalukko myös kloonattu? Näyttää siltä. Hallitus ja EU kuitenkin salaa asian. Kuva napattiin salaa Max Planck -instituutin aidan takaa entisessä DDR:ssä, aurinko paistaa tyytyväisen hepun kasvoille.

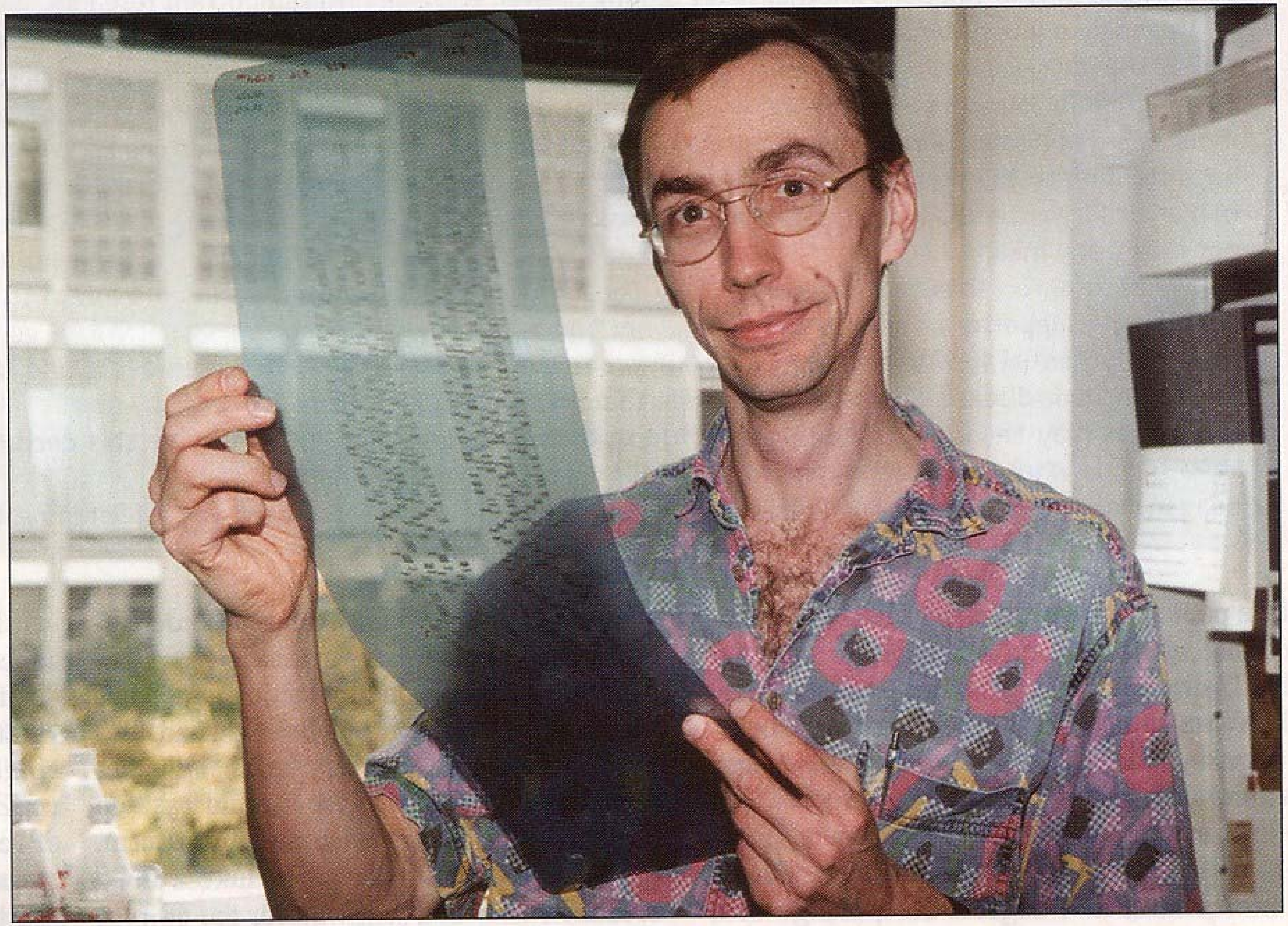
http://blog.wired.com/wiredscience/2009/02/rough-draft-of.html


H. floresiensis
H. sapiens
H. neanderthalensis
H. erectus
1.9 MYA
230
160
95
60
40
20
0
Thousands of Years Ago
A. garhi
Kenyanthropus platyops
A. africanus
Homo habilis
H. floresiensis
H. erectus
A. afarensis
H. sapiens
A. robustus
Australopithecus anamensis
A. aethiopicus
H. neander-thalensis
A. boisei
4
3
2
1
Present
Millions of Years Ago

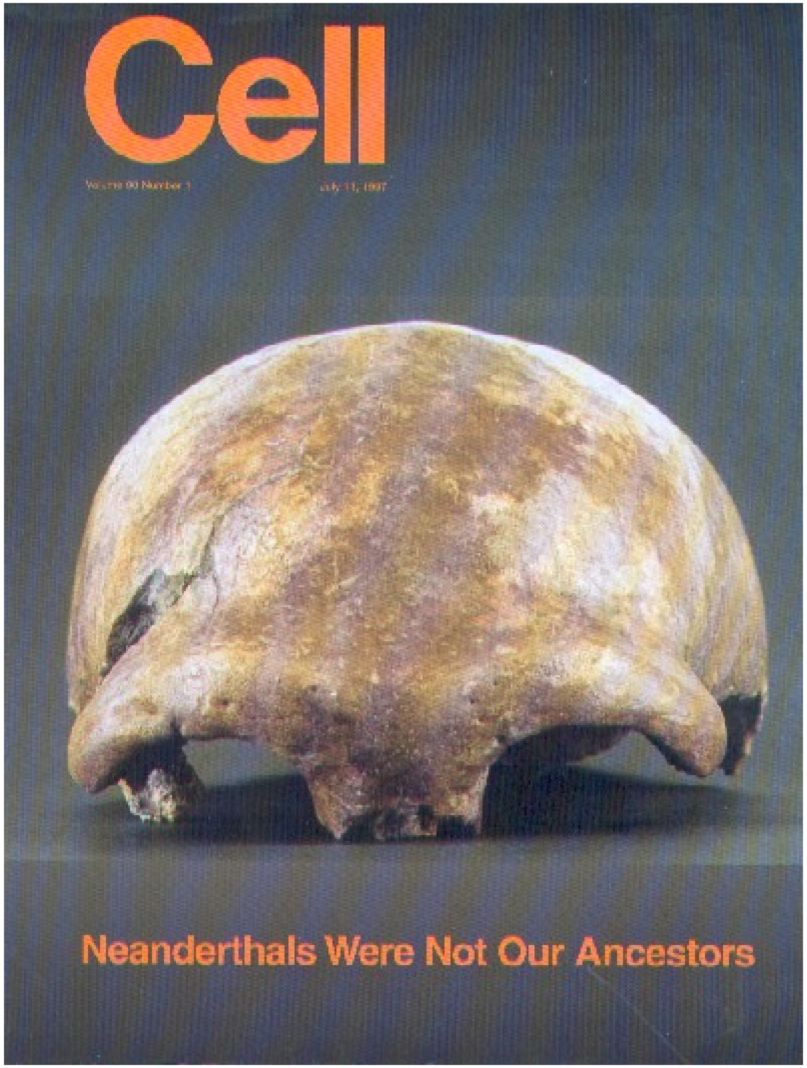
Nykyihmisen ja neanderthalilaisen kallot eroavat hiukan. N. olivat aika paljon isompia kuin meikäläiset ruipelot

Täytettyjä yksilöitä

Ingman, Kaessmann, Pääbo & Gyllensten (2000) Mitochondrial genome variation and the origin of modern humans. - *Nature 408: 708-709*



Ancient DNA wizard. The Max Planck hired geneticist Svante Pääbo to get the ball rolling at its new Leipzig institute, designed to probe human and primate origins and culture.



Cell

Volume 90 Number 1

July 11, 1997

Neanderthals Were Not Our Ancestors

Krings, Stone, Schmitz, Krainitzki, Stoneking & Pääbo (1997) Neanderthal DNA sequences and the origins of modern humans. - Cell 90: 19-30

Tutkijat kaivoivat 3.5 g kudosta humeruksen sisäpuolisesta ontelosta äärimmäisen puhtaissa olosuhteissa (ja kahdella mantereella erikseen!) vuonna 1856 löydetystä tyyppiyksilöstä.

Mitokondrion kontrollialueesta onnistuttiin pikku pätkinä monistamaan 360 nukleotidia. Tällä pätkällä oli 27 eroa (nukleotidisubstituutio) nykyihmiseen verrattuna. Nykyihmiset eroavat toisistaan keskimäärin 8 substituution ja simpanssista noin 55 substituution verran.

Ovchinnikov, Götherström, Romanova, Kharitonov, Lidén & Goodwin (2000) Molecular analysis of Neanderthal DNA from the northern Caucasus. - Nature 404: 490-493

Kaukasukselta Neanderthalilaisia on myös löydetty, tämä työ tehtiin Mezmaiskaya Cavesta löydetystä 29 000 vuotta vanhasta lapsen luurangosta. Kylkiluusta kaivettiin 90 ja 123 mg nöftää ja tutkittin kahdessa eri labrassa.

Nyt nämä 2, Feldhofer- ja Mezmaiskaya-yksilöt erovat 19 yhteisen substituution suhteen nykyihmisen standardisekvenssistä. Ne eroavat toisistaan aika paljon, 3.5% (niinkuin nykyihmisetkin)

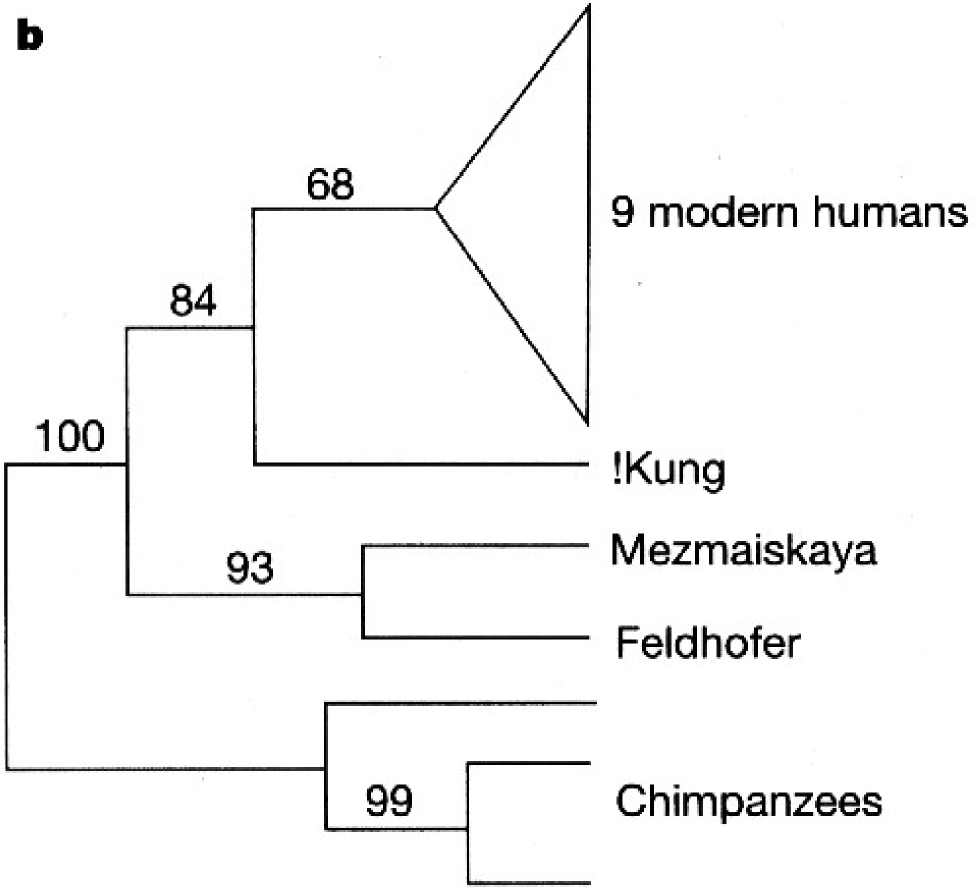


Figure 3 Phylogenetic relationship of the two Neanderthals and modern humans. **a**, A neighbour-joining tree computed using a total of 1,897 haplotypes derived from 5,846 modern humans[19]. **b**, A maximum parsimony branch and bound search with the two Neanderthal sequences along with the sequences of one !Kung, three other Africans, three Asians and three Europeans, all randomly selected[19]. This result is congruent with four additional data sets that were analysed. In both analyses, three chimpanzee sequences[13] were used as an outgroup. The numbers in both diagrams refer to the bootstrap frequencies (%) obtained from 1,000 replicates.

http://www.dnaancestryproject.com/?gclid=CNLd_eGD45gCFRdatAodrHnqcA

http://ngm.nationalgeographic.com/2008/10/neanderthals/hall-text

http://blog.wired.com/wiredscience/2009/02/rough-draft-of.html

LEIPZIG, Germany – Researchers in Germany have completed the first draft of the genome, more than 3 billion genetic building blocks that will shed new light on the ancient hominid as well as the origins of its closest relation — modern humans.

The draft covers about 63 percent of the roughly 3.2 billion base pairs in the Neanderthal genome. The team led by geneticist Svante Paabo has actually isolated 3.7 billion base pairs, but that includes many duplications.

Paabo, of the , said the Neanderthal genome will be an important tool for researchers tracing hominid evolution, and for those probing the origins of the genetic traits that make humans so dominant.

"It will help show what the differences are between them and us that allowed us to develop technology, to colonize the planet," he told The Associated Press on Thursday before presenting his findings to attendees of an American Association for the Advancement of Science conference in Chicago by video uplink from Leipzig.

The announcement was planned to coincide with the 200th anniversary of Charles Darwin's birth.

Gene expert of the in , is leading a separate project to sequence targeted segments of the Neanderthal genome. His work has shown that the Neanderthal genome is as much as 99.5 percent the same as modern humans. He said Paabo's complete draft will let him compare segments and genes from his own research to a separate Neanderthal.

"We'll look very carefully at the data they've generated, and it will tell us what areas we really want to look at," Rubin said.

Other researchers are already planning with genes known to influence speech and brain aging in humans. That work could rekindle a debate over whether early humans simply replaced , or whether the two may have interbred while their ranges overlapped in Europe more than 30,000 years ago.

Paabo, who presented DNA evidence in 1997 that Neanderthals were cousins rather than direct ancestors of modern humans, said his research suggests that if there was mixing between Neanderthals and modern humans, it has left minuscule traces in our genome. But he believes the new Neanderthal genome might allow researchers to investigate whether earlier human genes were passed on to the Neanderthal.

"We're currently analyzing if we see evidence in the Neanderthal genome of contribution from human ancestors," Paabo said. "That question I think is still totally open."

Other researchers said the likelihood of contamination and the vast similarities between the two species would make it exceedingly difficult to pinpoint any genetic connection.

"This research is a great technical achievement in itself, but has little implication for the debate concerning a part-Neanderthal ancestry of Europe's earliest modern humans," Joao Zilhao of the in Britain wrote in an e-mail to the AP.

For 2 1/2 years, Paabo ran minute samples of bone — the whole project has required just half a gram — through hulking half-million dollar machines that revealed .

Varastettu: http://news.yahoo.com/s/ap/20090212/ap_on_re_eu/eu_germany_neanderthal_genome

The process was tedious and fraught with challenges. Much of the DNA in the bone had decayed over time, and it was difficult to distinguish what remained from the of bacteria that colonized the after death. Human handling at the excavation site in Croatia and at the laboratory also contaminated the sample.

Paabo's team studied places in the bone where molecules most often broke down over the centuries and used that data to rule out DNA that didn't show similar degradation, meaning it probably belonged to bacteria. They sterilized their lab and attached a synthetic DNA tag to keep track of strands they believed to be genuine. and DNA researchers said the project's success despite those challenges is its most significant achievement.

"What they've shown is it's possible to get that much data from this old, crummy sample," said Tom Gilbert, a geneticist at the in Denmark.

Many more runs will be necessary, Gilbert said, to check each pair by covering it multiple times before it's clear which pairs are unique to the Neanderthal. Paabo hopes to cover each Neanderthal base pair 12 to 15 times in the years ahead.

In the meantime, scientists can compare smaller sections of Neanderthal DNA to data from completed on humans and chimpanzees.

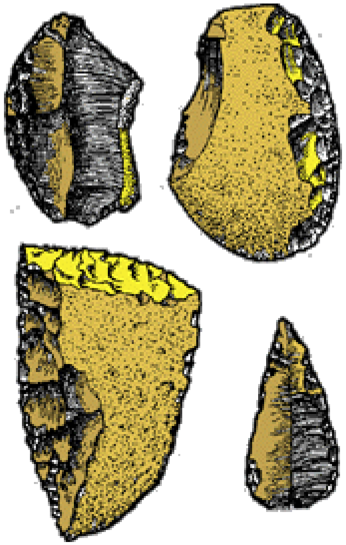
Beth Shapiro, an at Penn State University, said placing the three side by side will make it possible to determine what regions of our genome make us uniquely human.

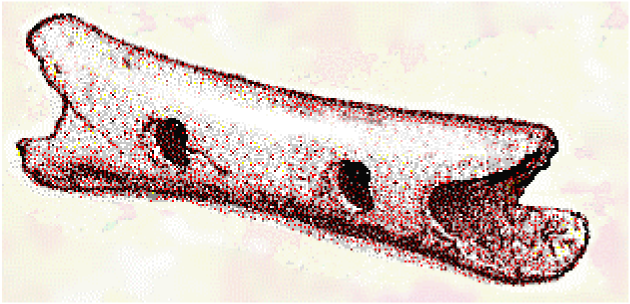
"There are 35 million differences between chimps and us," Shapiro said. "That's a lot, so we don't really know where to look. But this Neanderthal genome gets us that little bit closer."

A three-way comparison will also allow researchers to investigate whether the Neanderthal inherited a certain trait from an ancestor closer to the chimpanzee or one closer to modern humans, Paabo said.

Recent work to map an extinct mammoth's genome using hair preserved in permafrost raised questions about whether it might be possible to clone the mammal using its as a blueprint. Paabo said because the Neanderthal DNA was scattered in imperfect fossils, the notion of cloning a Neanderthal was far-fetched.

"Starting from the DNA extracted from a fossil, it is and will remain impossible," he said. "There is not really an improvement on current technologies that would make that possible."

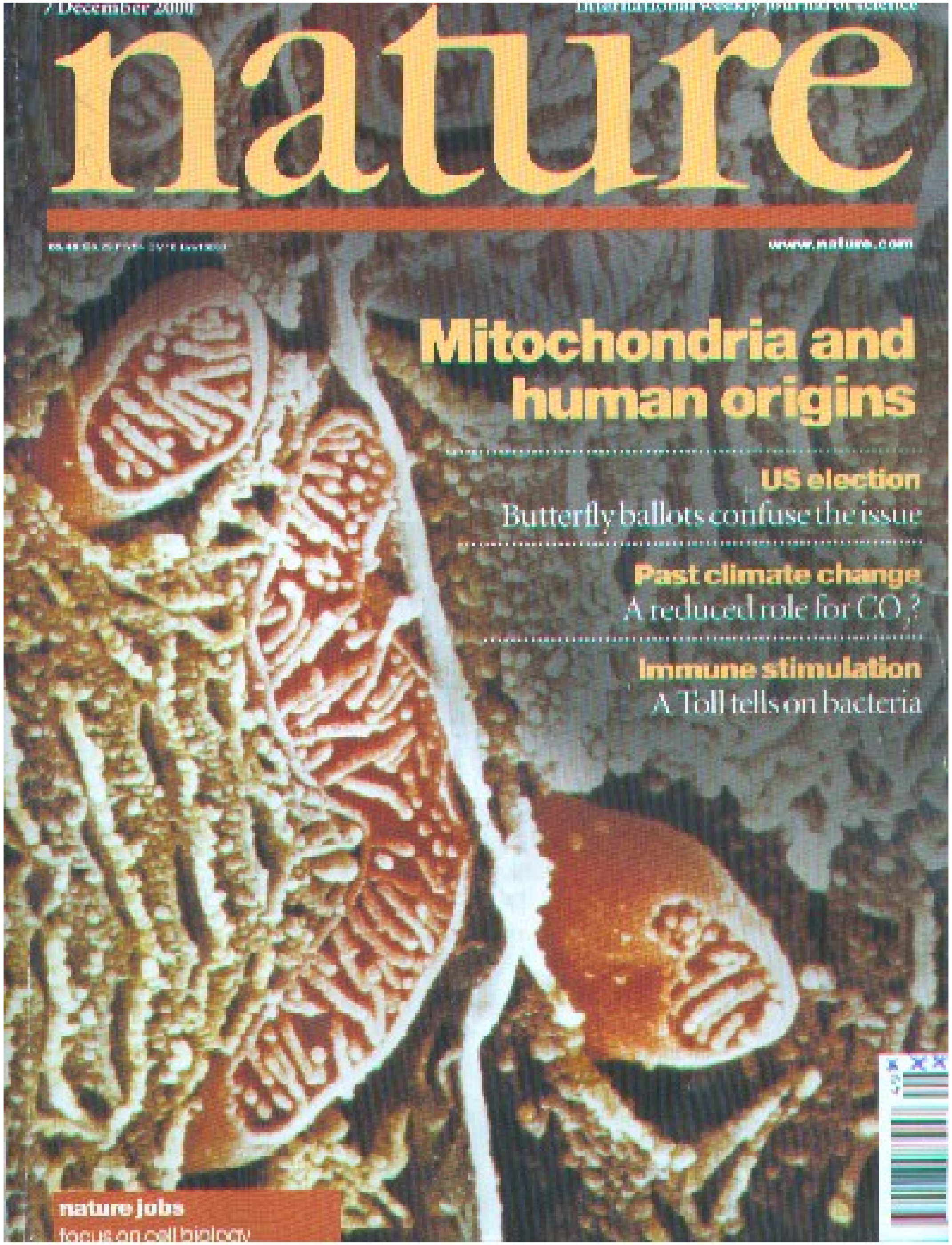




Neanderthalilaiset käyttivät jo työkaluja ja karhunluusta nikerretty huilukin on löytynyt. Ruokana oli mammutteja, sapelihammastiikereitä, luolakarhuja ja muuta maukasta mutta vaarallista.

Fennougrien raaputuksia Vienanmeren rannalta

San-kansan maalauksia Zimbabwesta



7 December 2000

International weekly journal of science

nature

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Mitochondria and human origins

US election
Butterfly ballots confuse the issue

Past climate change
A reduced role for CO$_2$?

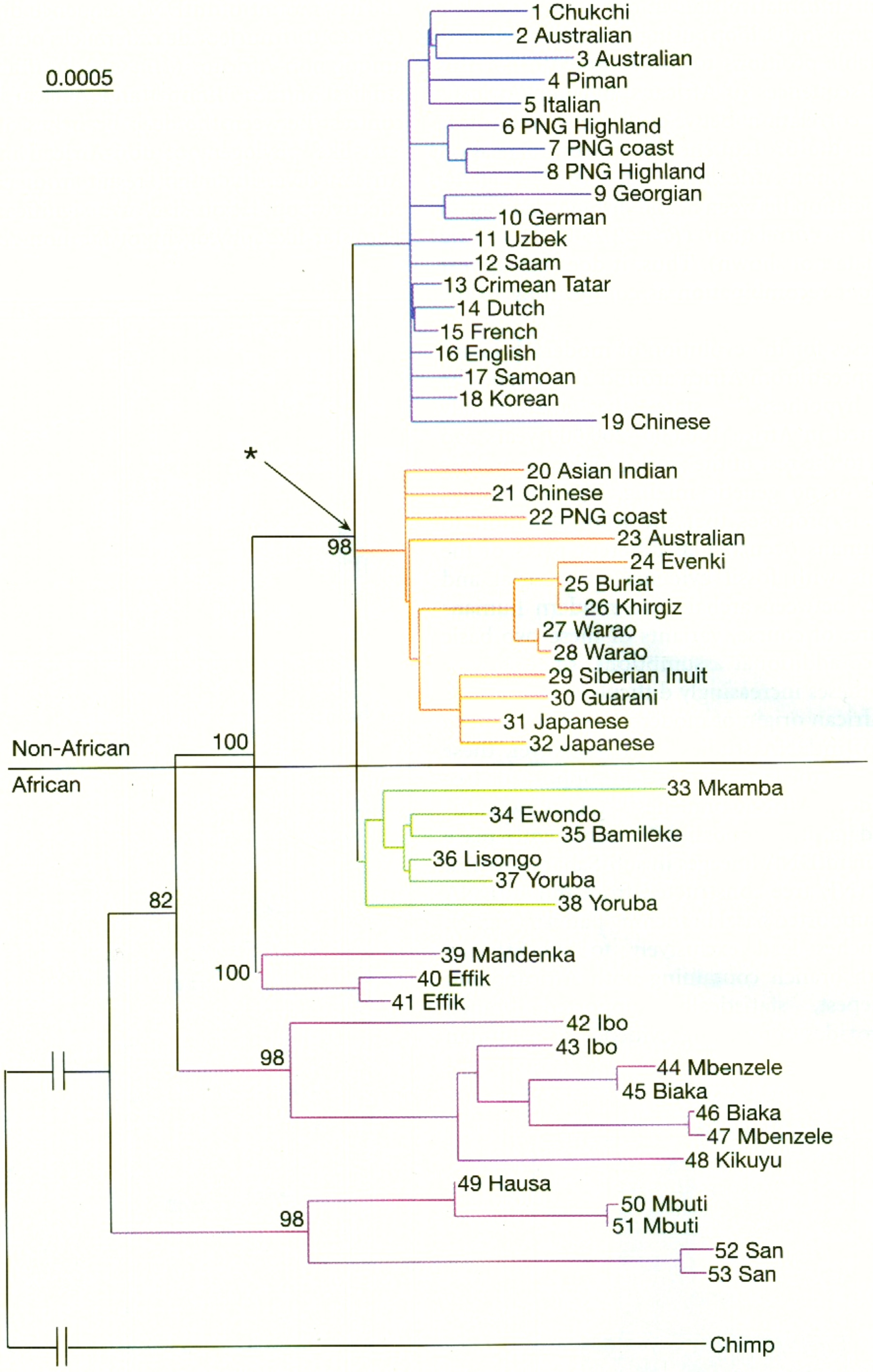
Immune stimulation
A Toll tells on bacteria

nature jobs
focus on cell biology

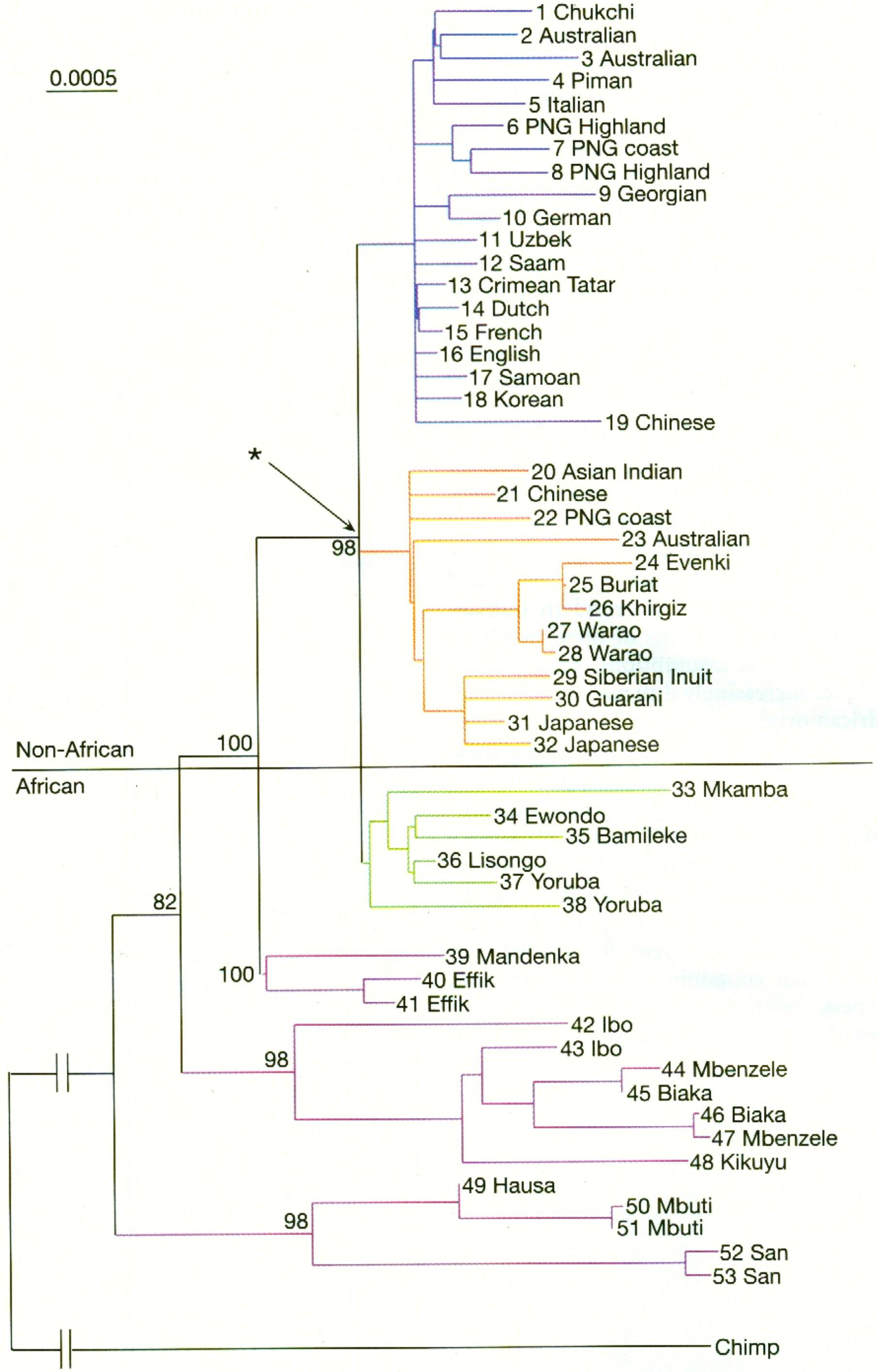
Tavallisista ihmisistä

Ihmisen historiaa on tutkittu paljonkin mtDNA:n avulla, eri mittakaavoissa. Tässä työssä on erikoista se, että sekvensoitiin koko mtDNA-molekyyli eikä vain pientä osaa. Kaikkein muunteleviin, D-looppi, voitiin jopa jättää pois.

Käytettävissä oli 53 kokonaista sekvenssiä.



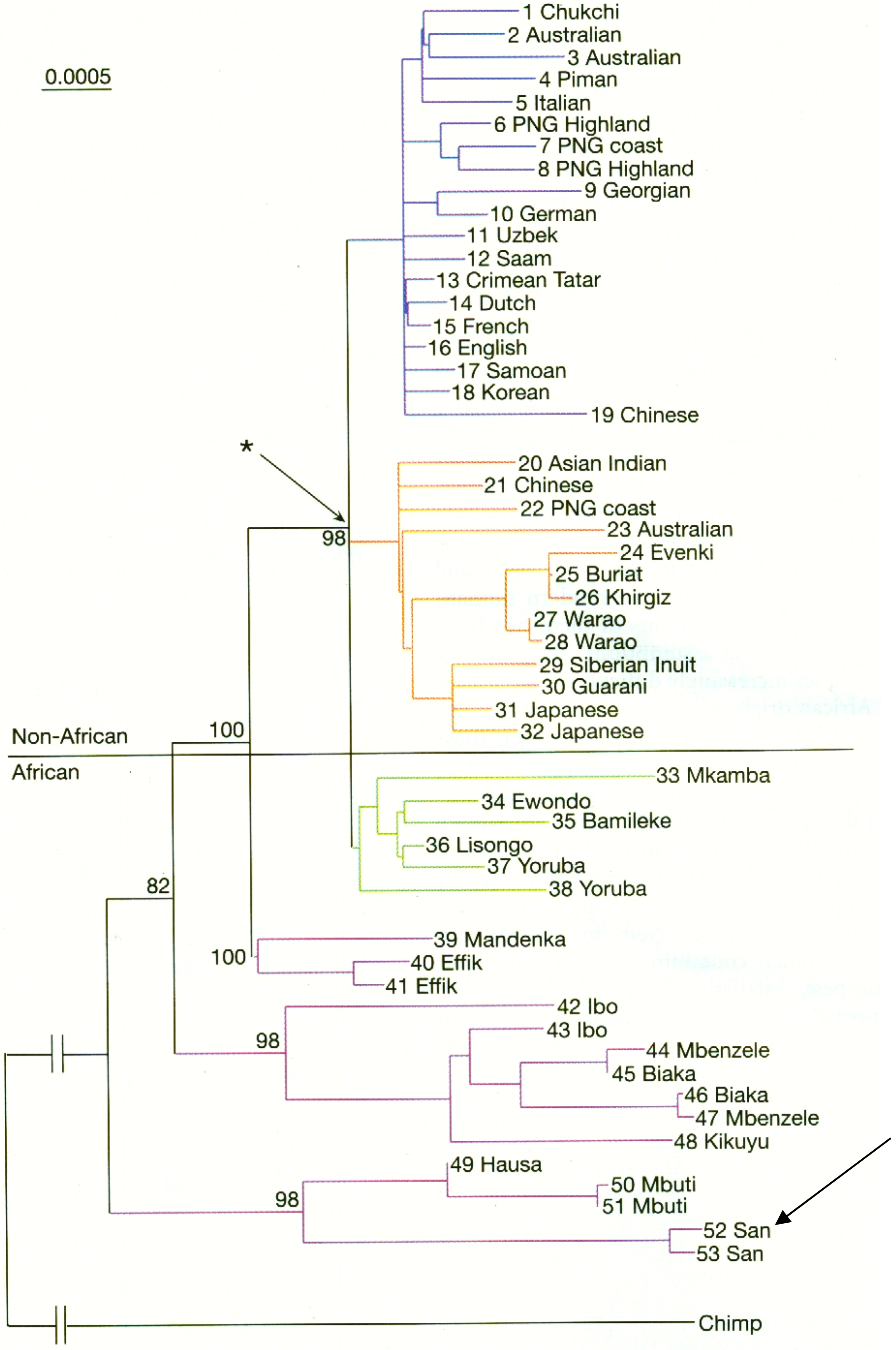
Eri kieliryhmistä tehty mtDNA-fylogenia



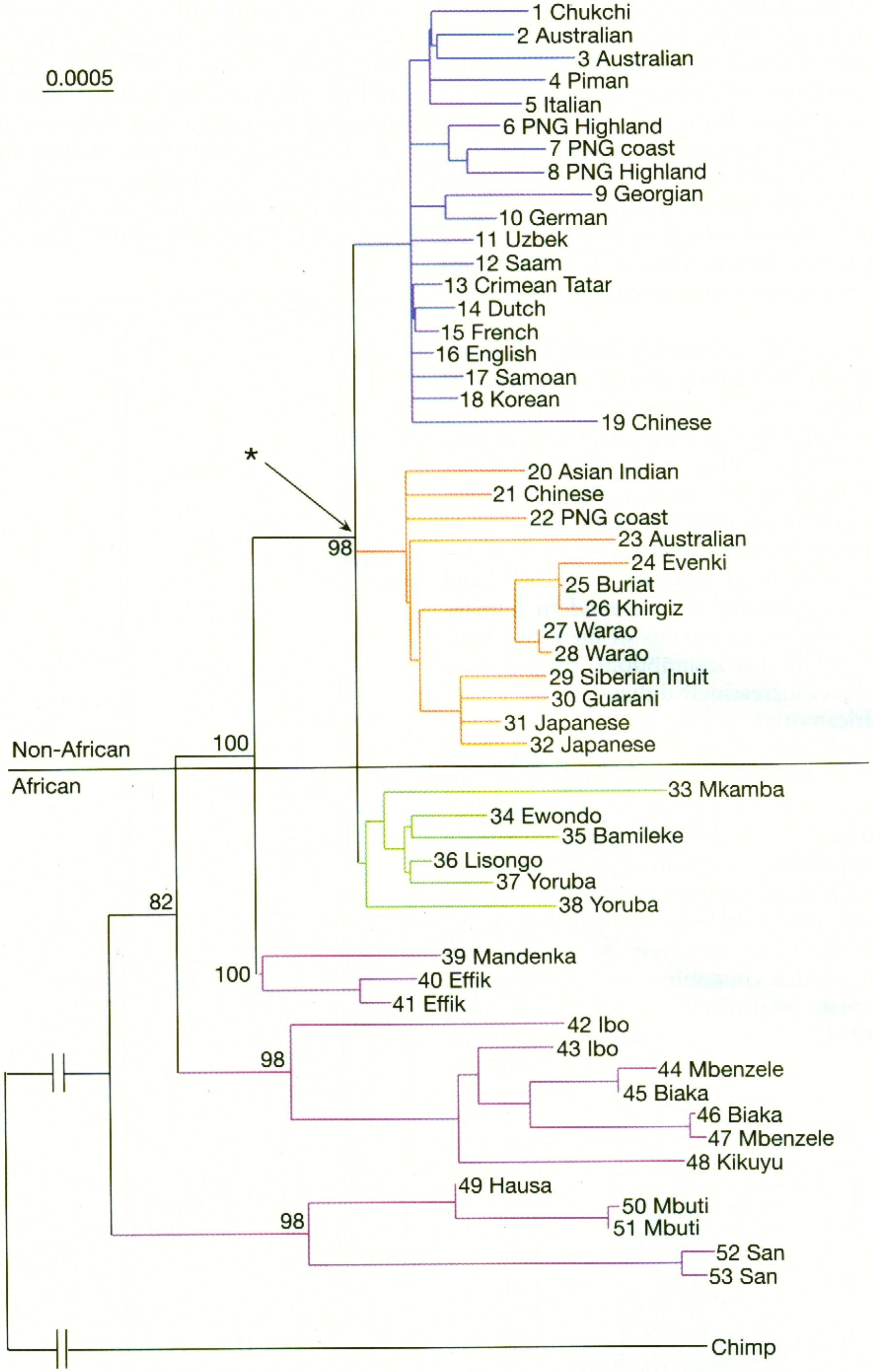
Eri kieliryhmistä tehty mtDNA-fylogenia

Miksi kieliryhmistä?

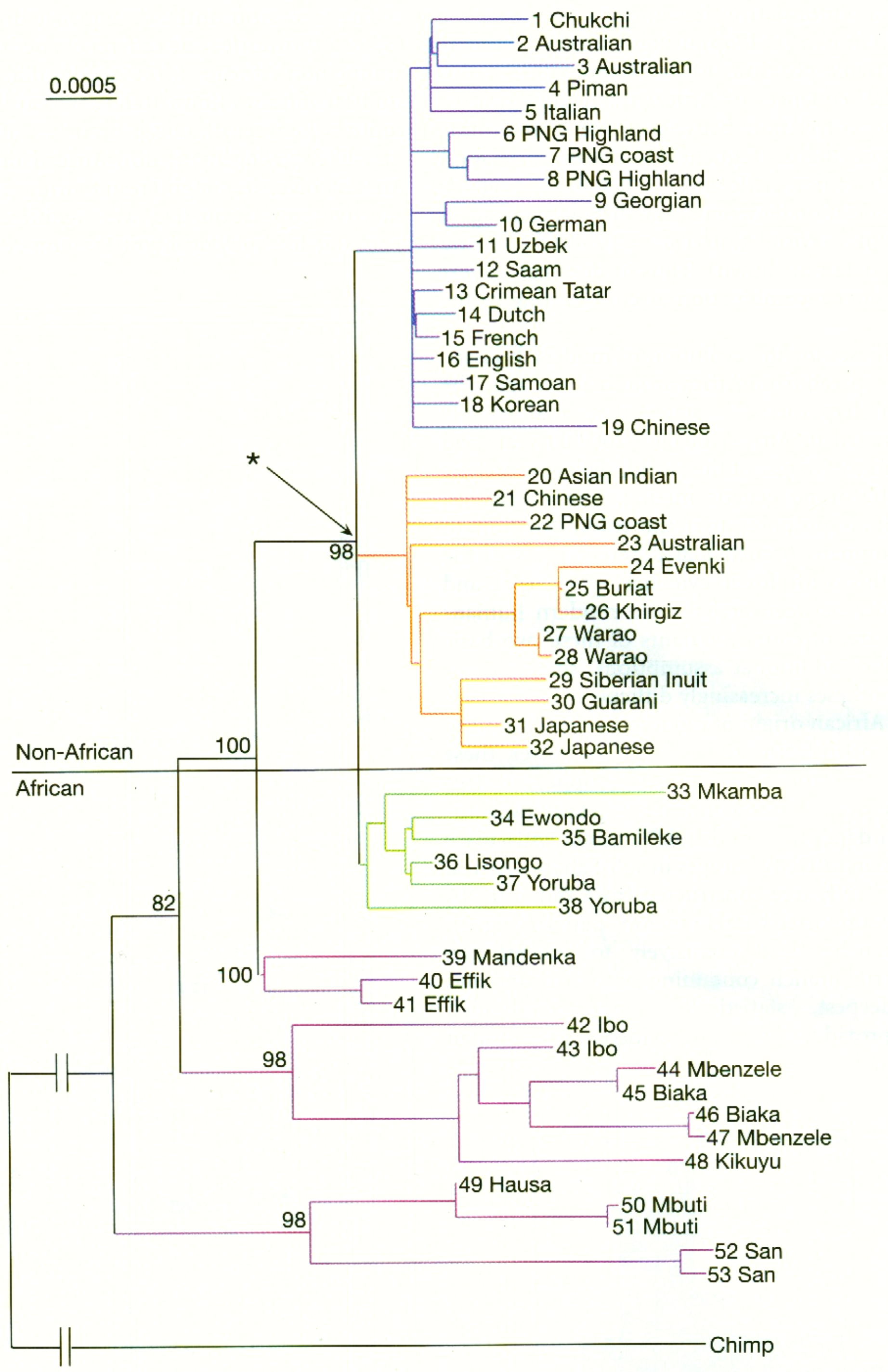
Siksi, että kielet luultavasti liittyvät kansaan (etniseen identiteettiin) sitkeämmin kuin maantieteellinen sijainti, joka on helpommin vaihdettavissa



Syvimmät haarat ***kohtaavat*** afrikkalaisten kieliryhmien välillä, mistä päätellään, että alkukoti oli siellä. Alueella puhutaan vieläkin klik-äänteellisiä ***!Kung*** –kieliä (Taitaa olla nykyisin *San*).



Yksi afrikkalaisista oksista kuuluu yhteen (98% varmuudella) kaikkien ulkoafrikkalaisten kanssa



Tämä haara (clade) edustaa ns. tähtimäistä fylogeniaa, jollainen syntyy kasvavan populaation oloissa

Kasvu liittyy kokonaisten mantereiden valtaukseen

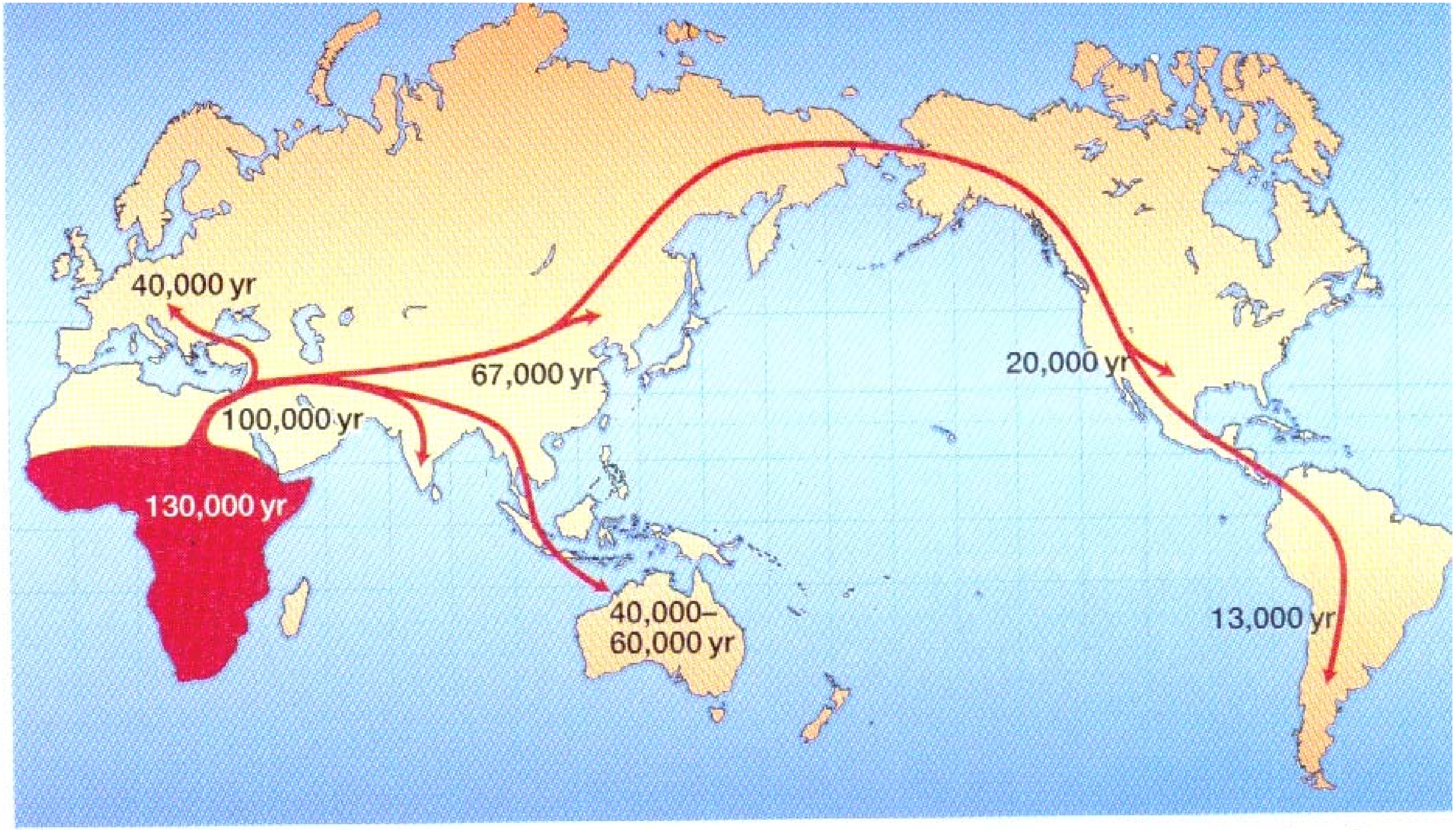
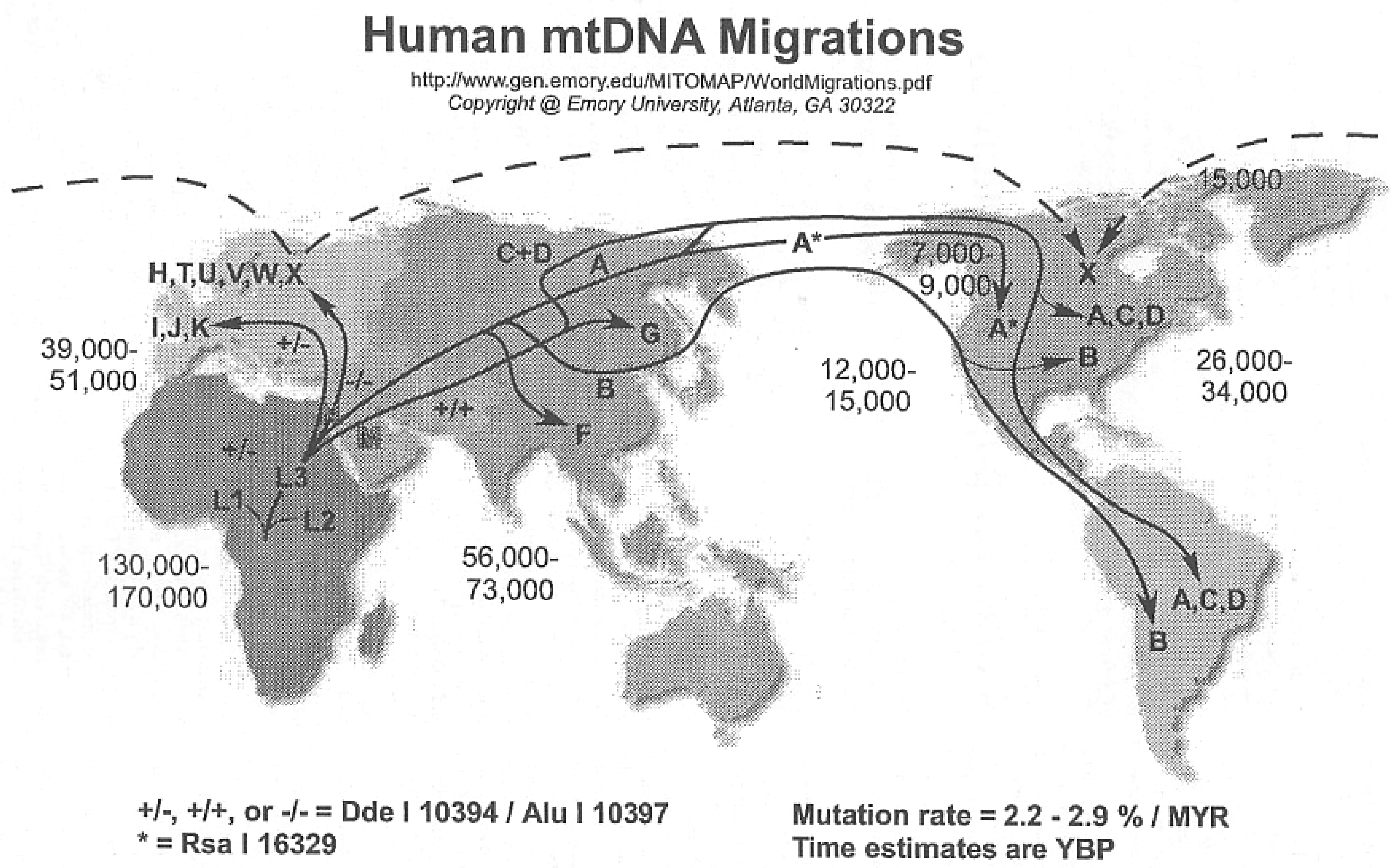


Figure 1 **The origin and dispersal of modern humans, *Homo sapiens*. The time of origin of modern humans is not well known but may have been about 200,000 (130,000–465,000) years ago. New evidence from mitochondrial genomes[5] bolsters the hypothesis that the place of origin was sub-Saharan Africa and that the dispersal from Africa occurred within the past 100,000 years. The earliest known fossil and archaeological evidence on each continent[14], shown on the map, is consistent with this view.**

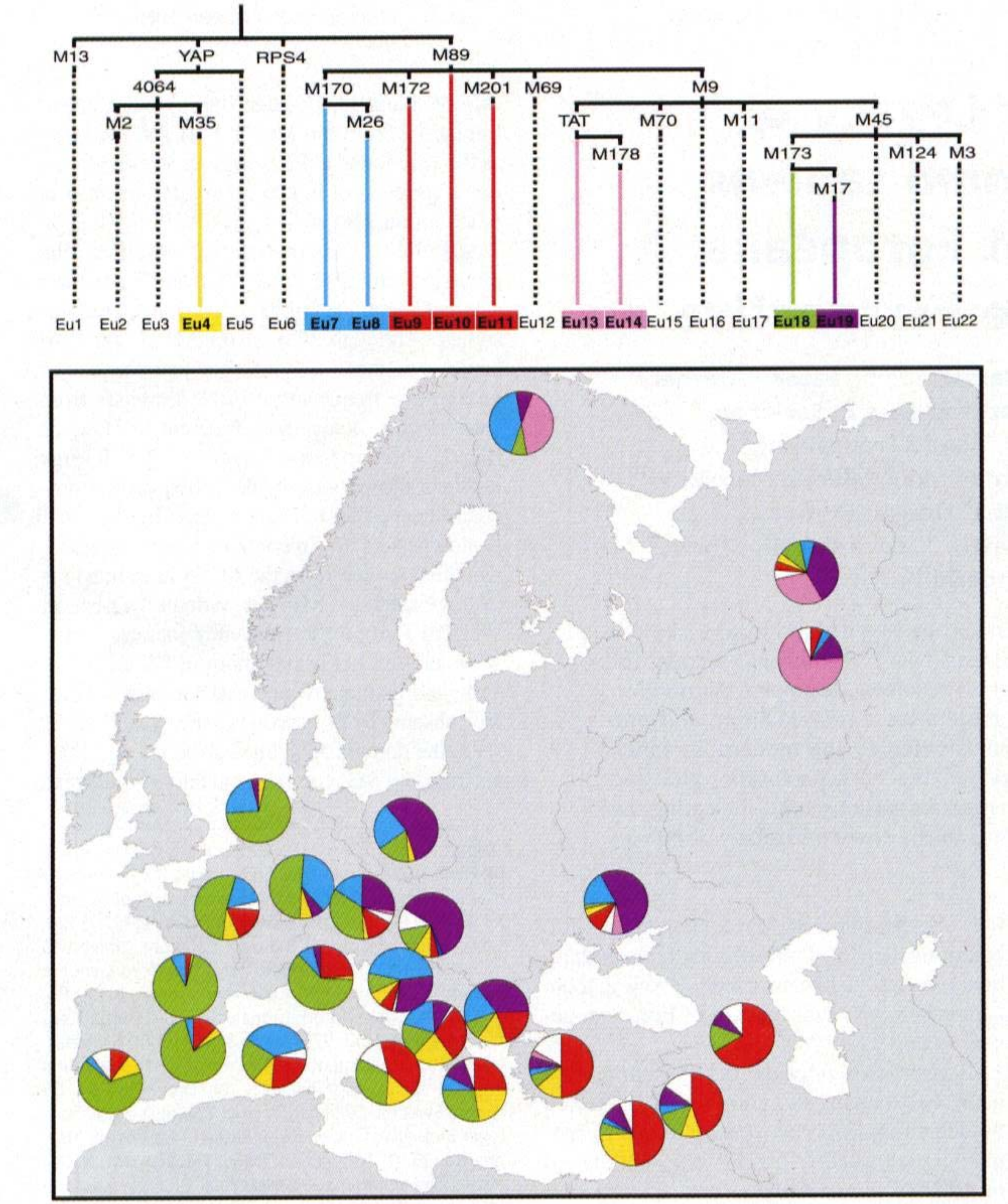


kirjaimet on ns. haplogrouppeja eli puun paksuja haaroja

Y-kromosomi vastaa mitokondriota:

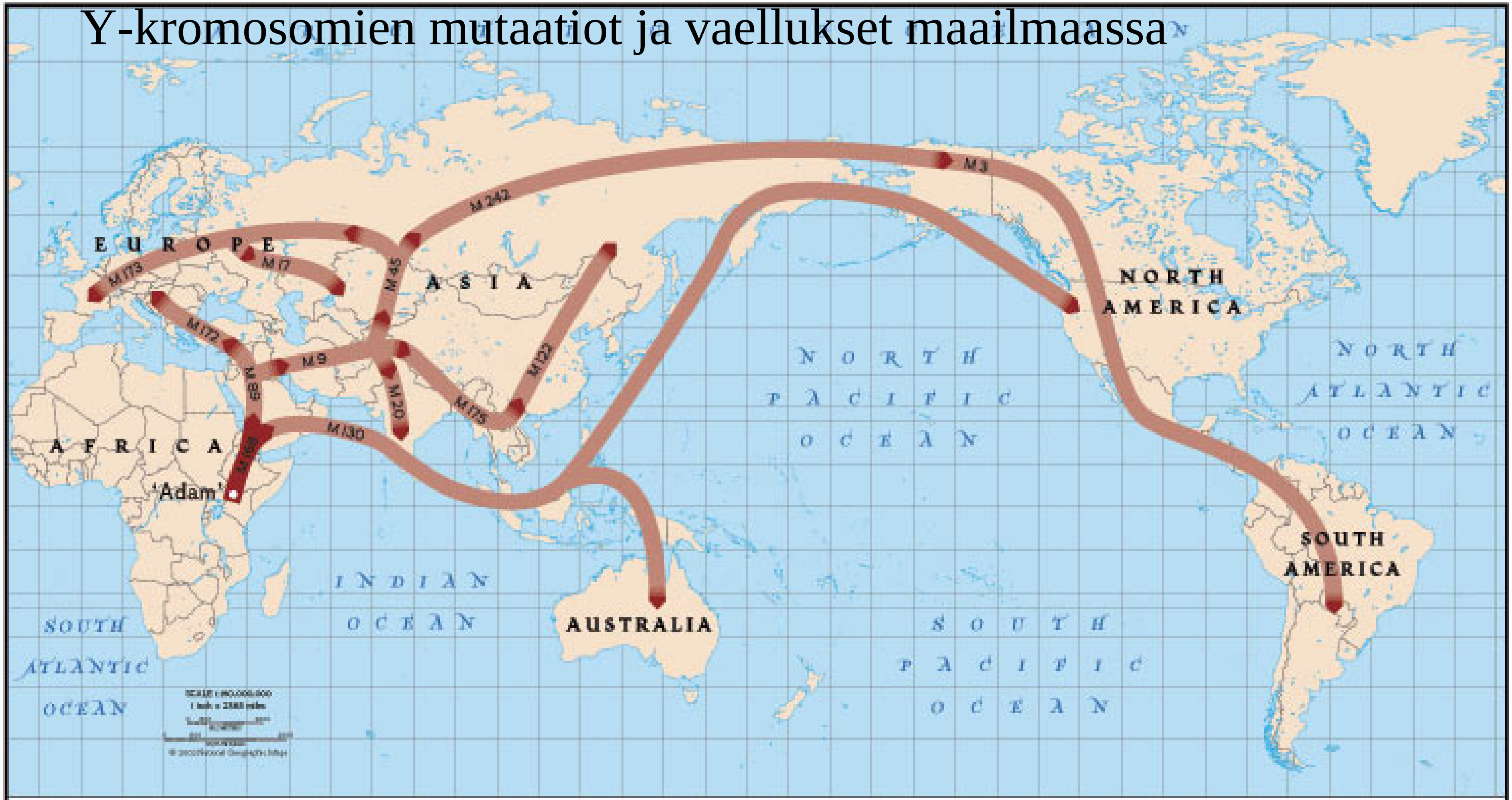
ei rekombinaatiota, vaan mutaatiot kasautuvat aina entisten päälle

Y-tyypit Euroopassa



Science 10 Nov 2000

Y-kromosomien mutaatiot ja vaellukset maailmaassa



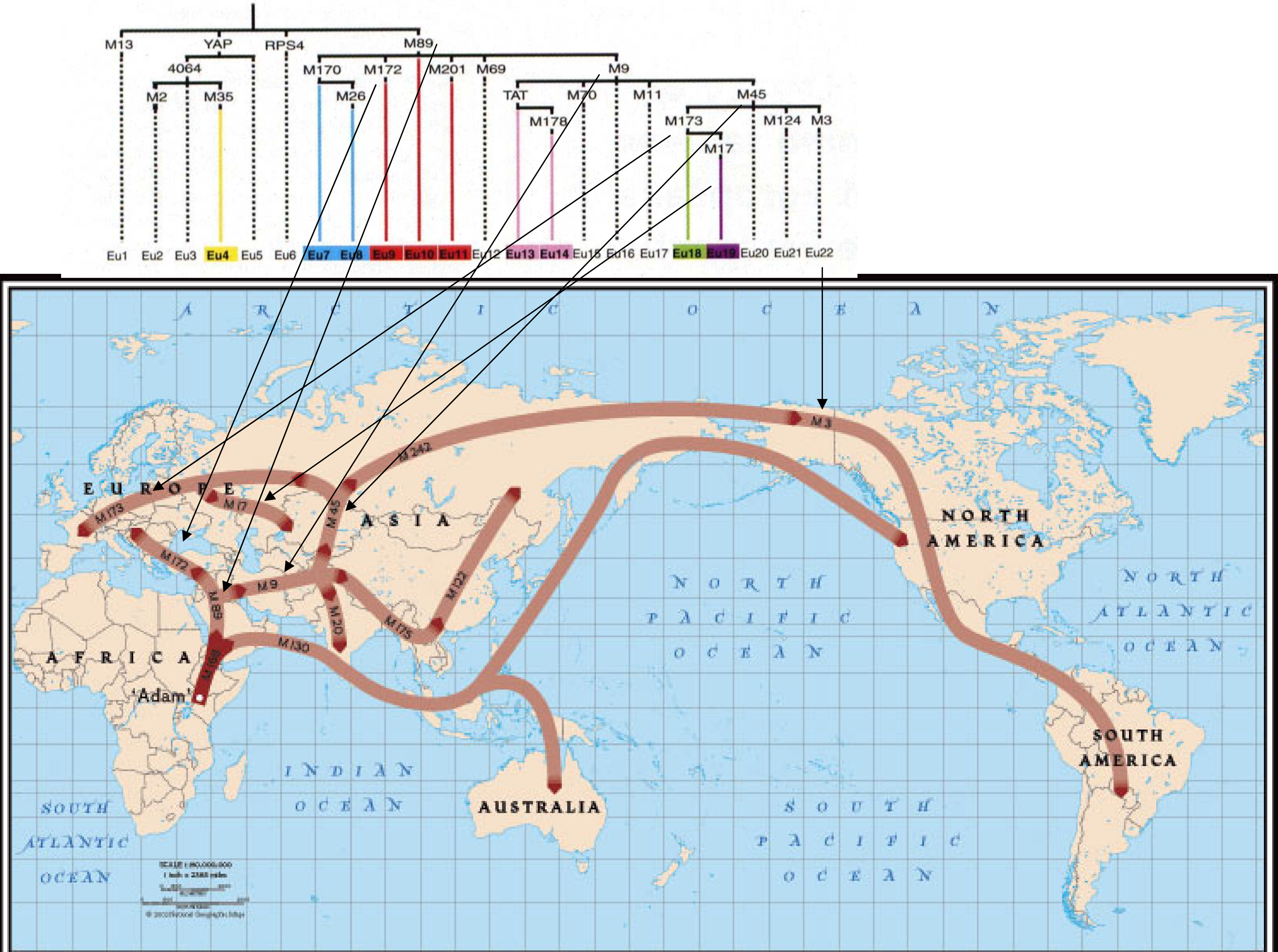
EARLY MAN MIGRATION

M 168: 50,000 years ago
M 130: 50,000 years ago
M 89: 45,000 years ago
M 9: 40,000 years ago
M 175: 35,000 years ago
M 45: 35,000 years ago
M 173: 30,000 years ago
M 20: 30,000 years ago
M 242: 20,000 years ago
M 122: 10,000 years ago
M 3: 10,000 years ago
M 172: 10,000 years ago
M 17: 10,000 years ago

Journey of Man

The markers above represent genetic markers found in DNA as identified by Dr. Spencer Wells in the film *Journey of Man*. Tracing our ancestry back to the people who left Africa some 50,000+ years ago, Dr. Wells tells the story of a remarkable human journey that began in Africa (M168), and divided and expanded into the rest of the world, connecting everyone to a global family tree. Watch *Journey of Man* in December on National Geographic Channel, and visit *www.nationalgeographic.com/channel/intl* to find information specific to your region.

NATIONAL GEOGRAPHIC CHANNEL


M13
YAP
RPS4
M89
4064
M170
M172
M201
M69
M9
M2
M35
M26
TAT
M70
M11
M45
M178
M173
M124
M3
M17
Eu1
Eu2
Eu3
Eu4
Eu5
Eu6
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Eu22
ARCTIC OCEAN
EUROPE
ASIA
AFRICA
NORTH AMERICA
SOUTH AMERICA
AUSTRALIA
NORTH PACIFIC OCEAN
NORTH ATLANTIC OCEAN
INDIAN OCEAN
SOUTH PACIFIC OCEAN
SOUTH ATLANTIC OCEAN
'Adam'
M168
M89
M130
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M172
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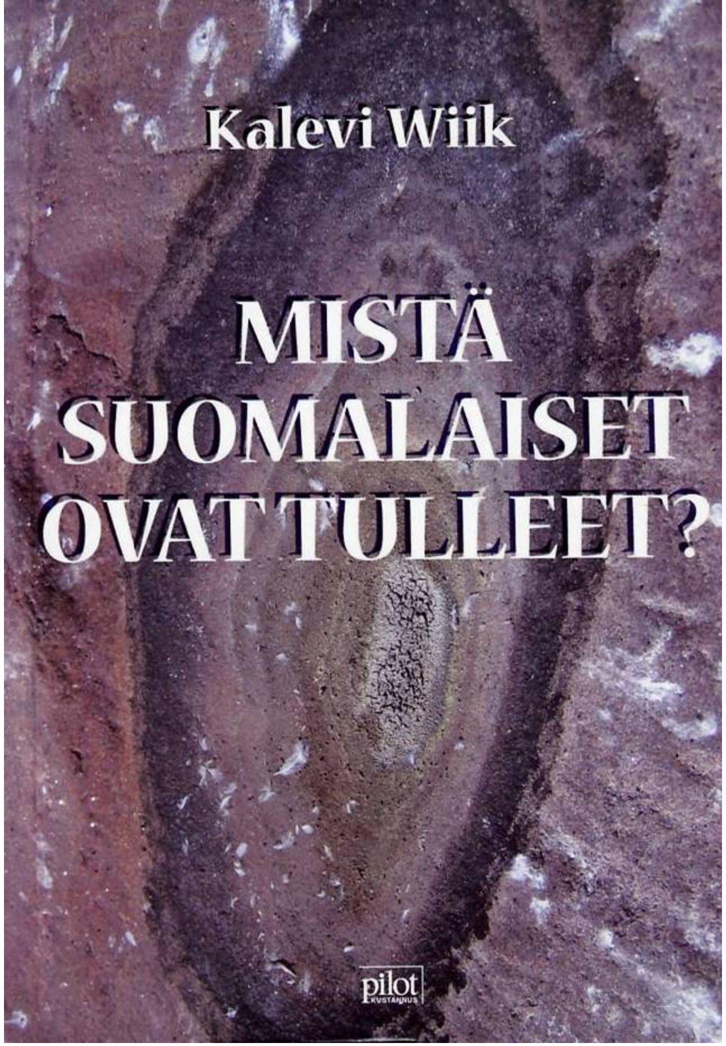
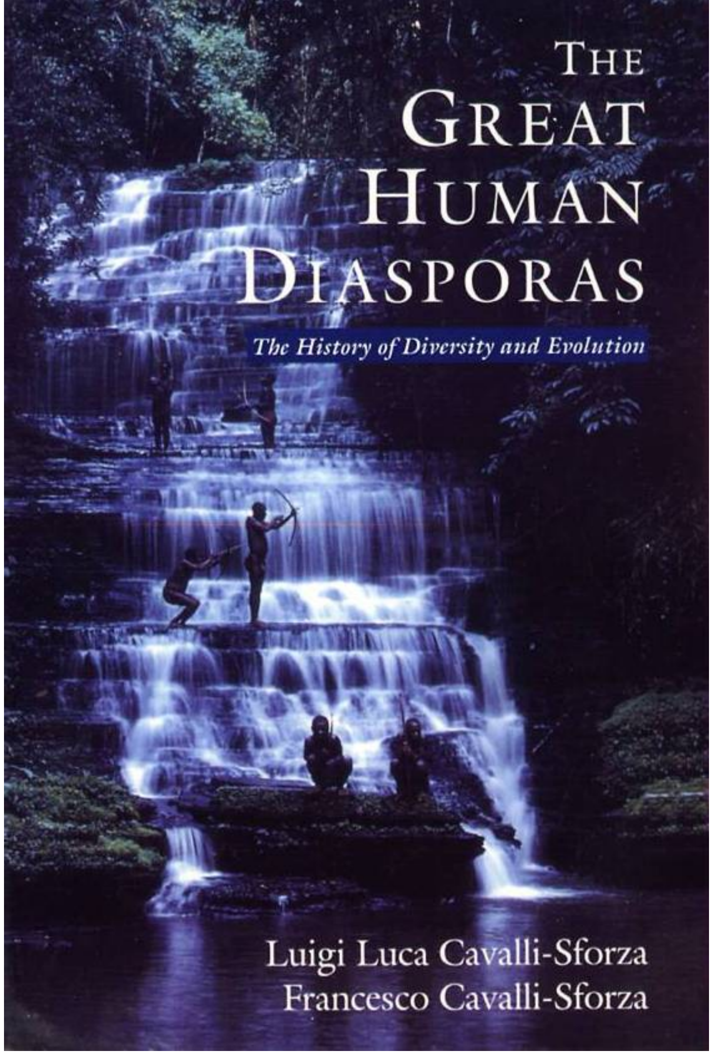
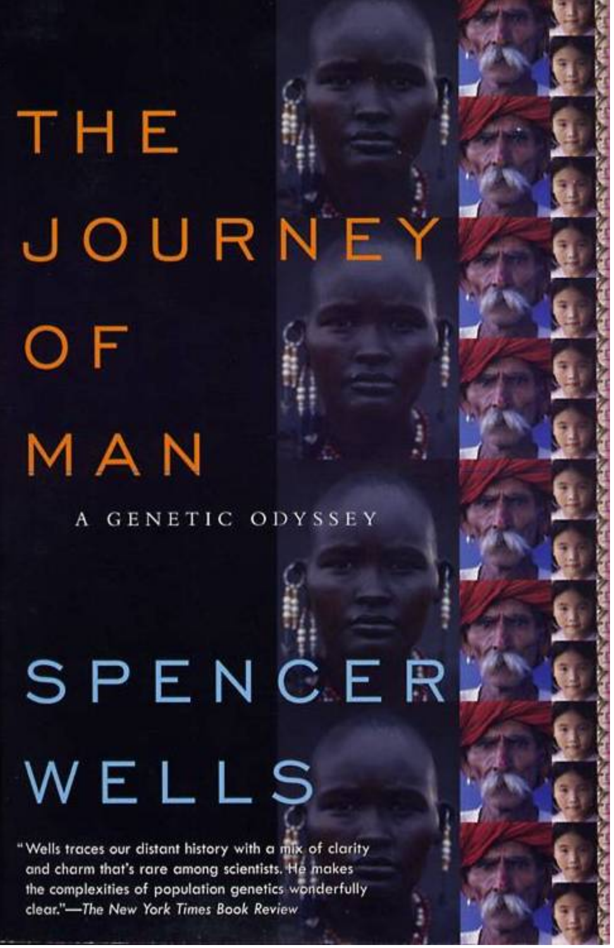
M122

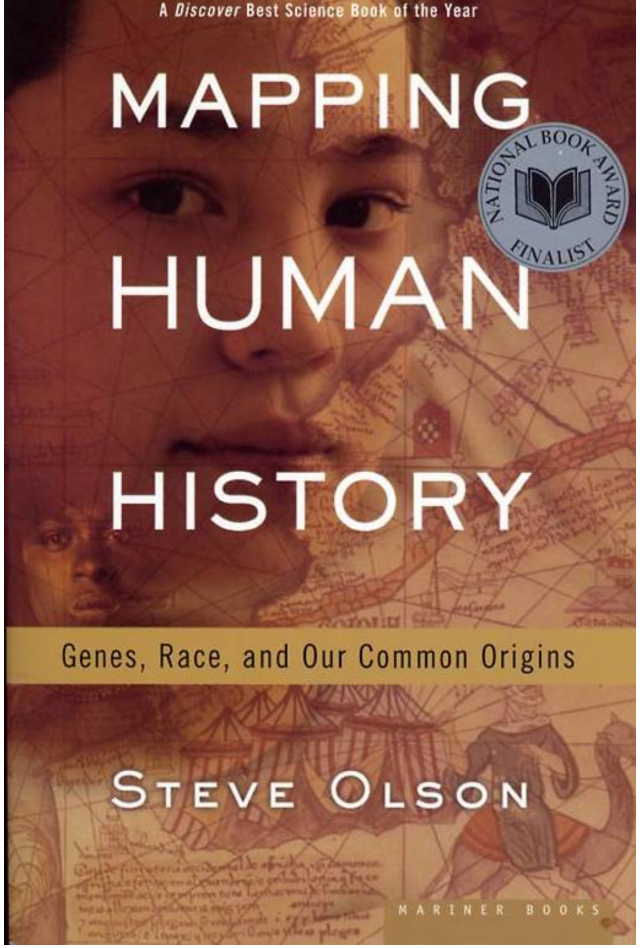


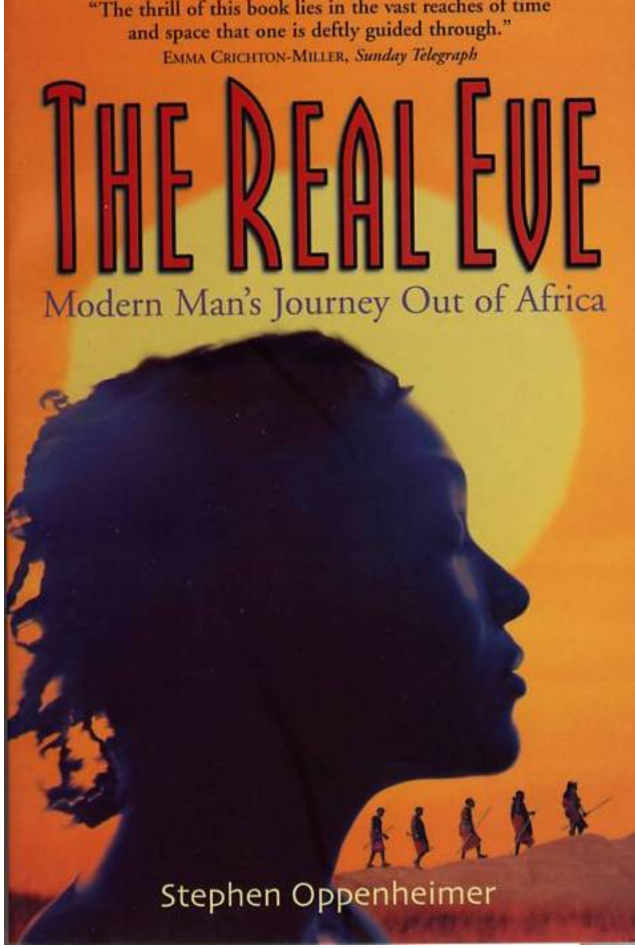


Eurooppakeskeinen, raskas faktaluettelo, tulkinta yksiviivaista, mutta kannattaa opiskella

Alan suurmiehen viisas näkemys pojan viimeistelmänä

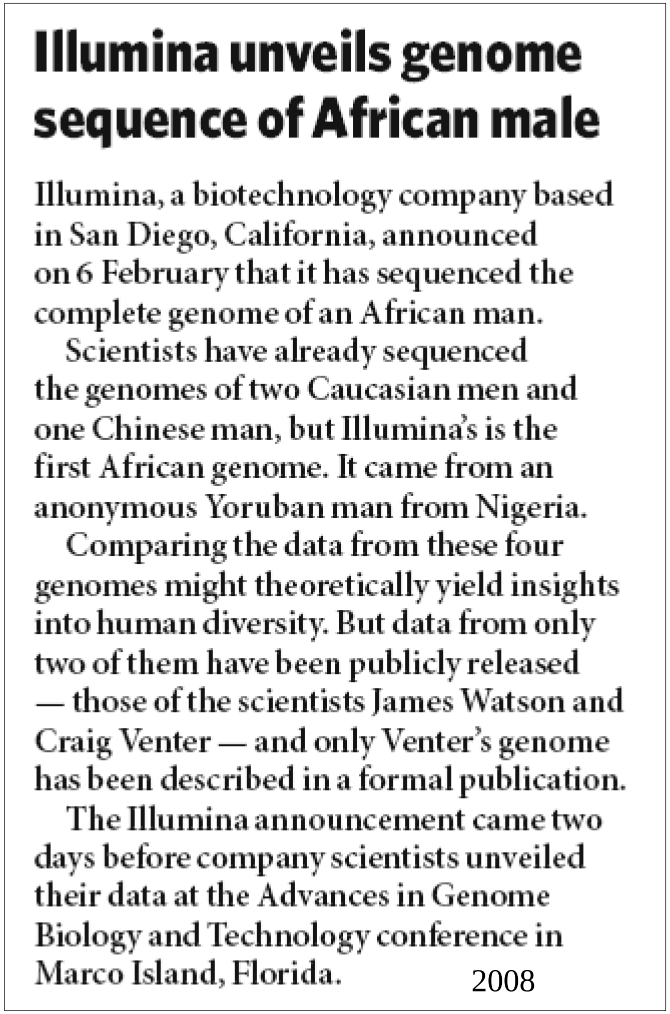






Hyviä kirjoja ovat nämä kaikki, toiset hauskojakin

Muutamia lisämatskuja



Illumina unveils genome sequence of African male

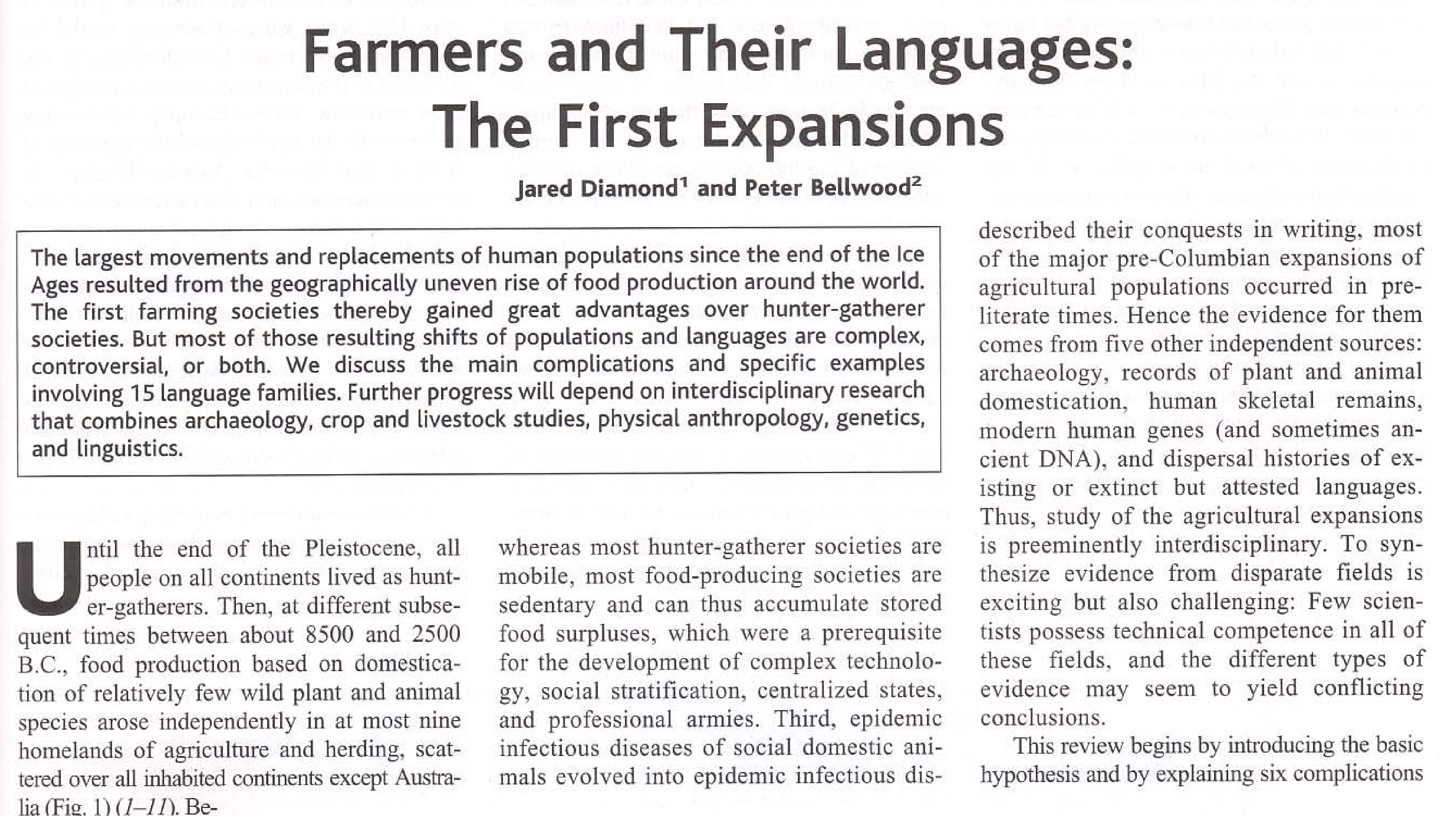
Illumina, a biotechnology company based in San Diego, California, announced on 6 February that it has sequenced the complete genome of an African man.

Scientists have already sequenced the genomes of two Caucasian men and one Chinese man, but Illumina's is the first African genome. It came from an anonymous Yoruban man from Nigeria.

Comparing the data from these four genomes might theoretically yield insights into human diversity. But data from only two of them have been publicly released — those of the scientists James Watson and Craig Venter — and only Venter's genome has been described in a formal publication.

The Illumina announcement came two days before company scientists unveiled their data at the Advances in Genome Biology and Technology conference in Marco Island, Florida.

2008



Farmers and Their Languages: The First Expansions

Jared Diamond[1] and Peter Bellwood[2]

The largest movements and replacements of human populations since the end of the Ice Ages resulted from the geographically uneven rise of food production around the world. The first farming societies thereby gained great advantages over hunter-gatherer societies. But most of those resulting shifts of populations and languages are complex, controversial, or both. We discuss the main complications and specific examples involving 15 language families. Further progress will depend on interdisciplinary research that combines archaeology, crop and livestock studies, physical anthropology, genetics, and linguistics.

Until the end of the Pleistocene, all people on all continents lived as hunter-gatherers. Then, at different subsequent times between about 8500 and 2500 B.C., food production based on domestication of relatively few wild plant and animal species arose independently in at most nine homelands of agriculture and herding, scattered over all inhabited continents except Australia (Fig. 1) *(1–11)*. Be-

whereas most hunter-gatherer societies are mobile, most food-producing societies are sedentary and can thus accumulate stored food surpluses, which were a prerequisite for the development of complex technology, social stratification, centralized states, and professional armies. Third, epidemic infectious diseases of social domestic animals evolved into epidemic infectious dis-

described their conquests in writing, most of the major pre-Columbian expansions of agricultural populations occurred in preliterate times. Hence the evidence for them comes from five other independent sources: archaeology, records of plant and animal domestication, human skeletal remains, modern human genes (and sometimes ancient DNA), and dispersal histories of existing or extinct but attested languages. Thus, study of the agricultural expansions is preeminently interdisciplinary. To synthesize evidence from disparate fields is exciting but also challenging: Few scientists possess technical competence in all of these fields, and the different types of evidence may seem to yield conflicting conclusions.

This review begins by introducing the basic hypothesis and by explaining six complications

Diamond & Bellwood Science 25 April 2003

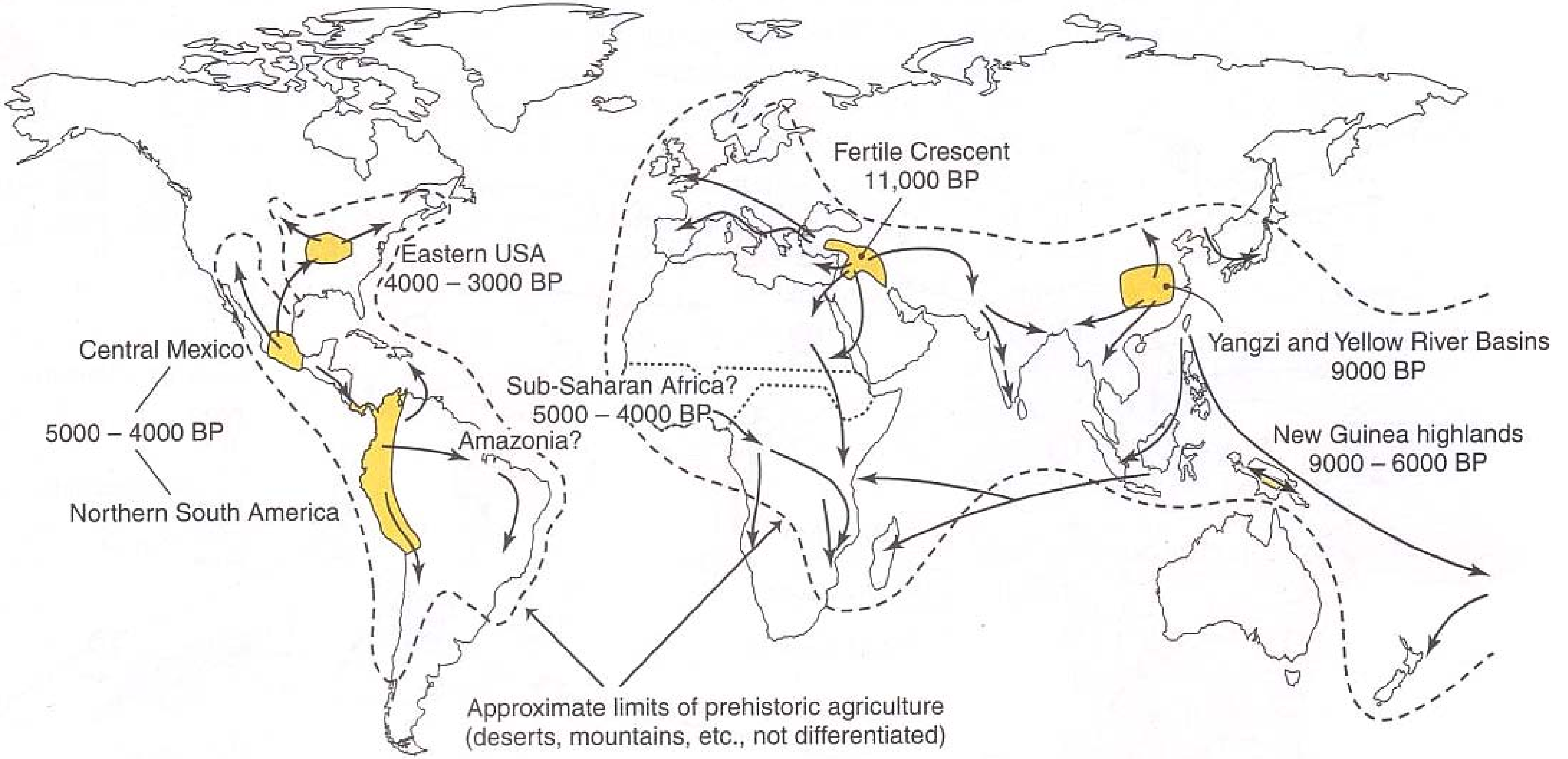


Fig. 1. Archaeological map of agricultural homelands and spreads of Neolithic/Formative cultures, with approximate radiocarbon dates.

Diamond & Bellwood Science 25 April 2003

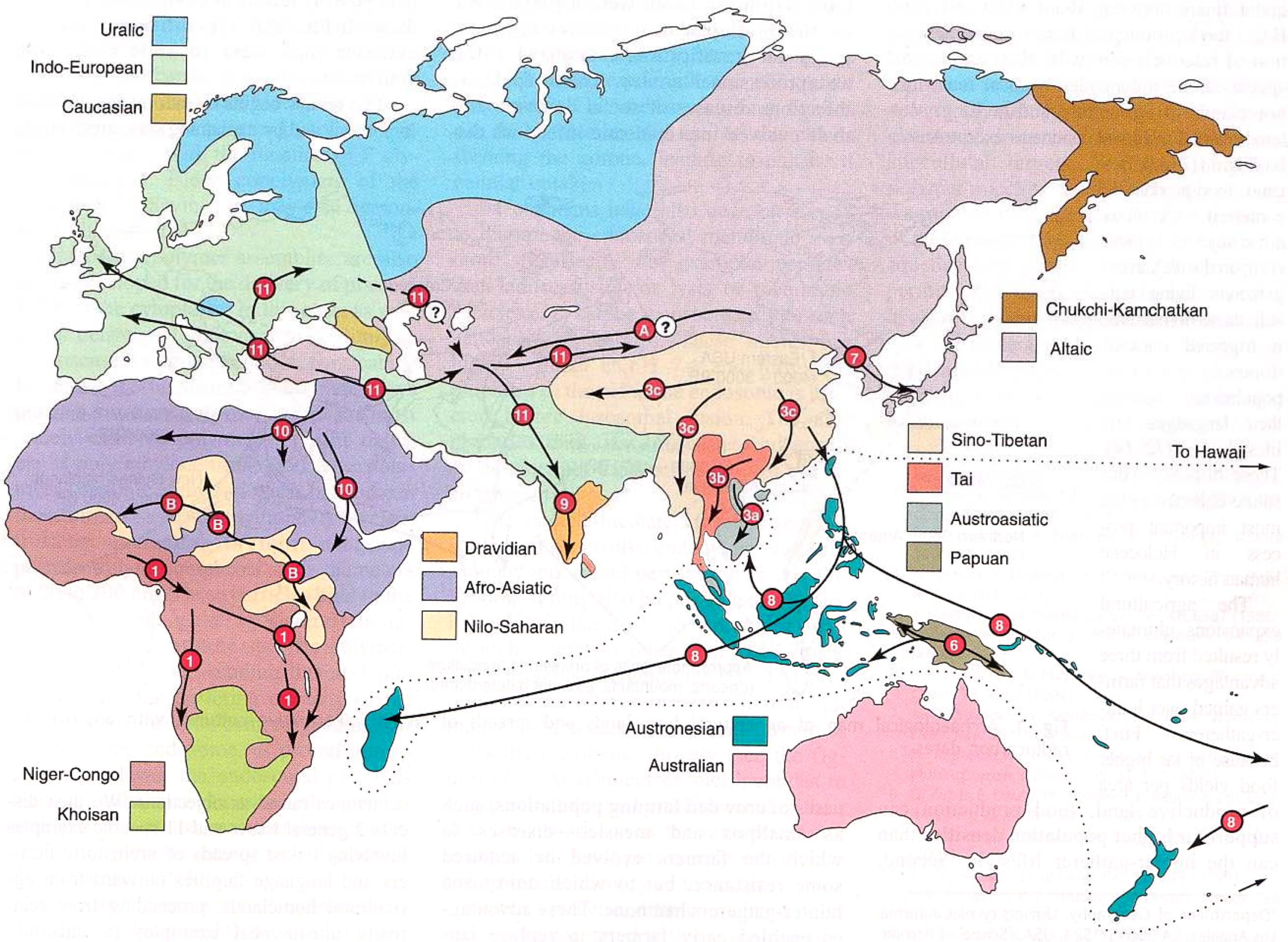


Fig. 2. Language families of the Old World and their suggested expansions. Map based on information in (87) and other sources. Numbered examples discussed in text are 1 (Bantu), 3a to 3c (Austro-Asiatic, Tai, and Sino-Tibetan, respectively), 6 (Trans New Guinea), 7 (Japanese), 8 (Austronesian), 9 (Dravidian), 10 (Afro-Asiatic), 11 (Indo-European). Other possible examples mentioned only briefly: A (Turkic), B (Nilo-Saharan).

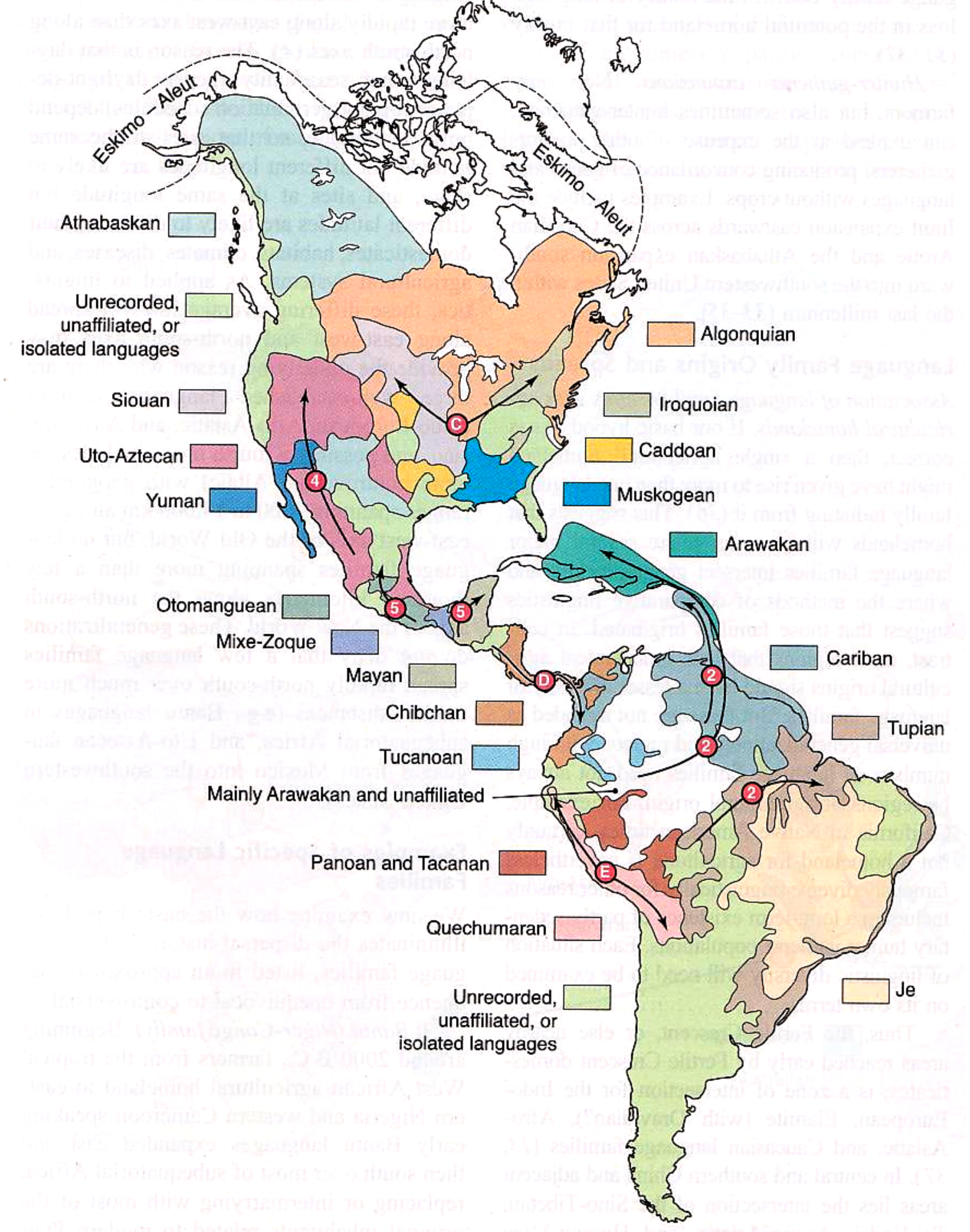


Fig. 3. Language families of the New World and their suggested expansions. Maps based on information in (*89*) and other sources. Numbered examples discussed in text are 2 (Arawakan, Cariban, and Tupian), 4 (Uto-Aztecan), 5 (Oto-Manguean and Mayan). Other possible examples mentioned only briefly: C (Iroquoian and Siouan, with maize after 500 A.D.), D (Chibchan), and E (Quechuan and Aymaran).

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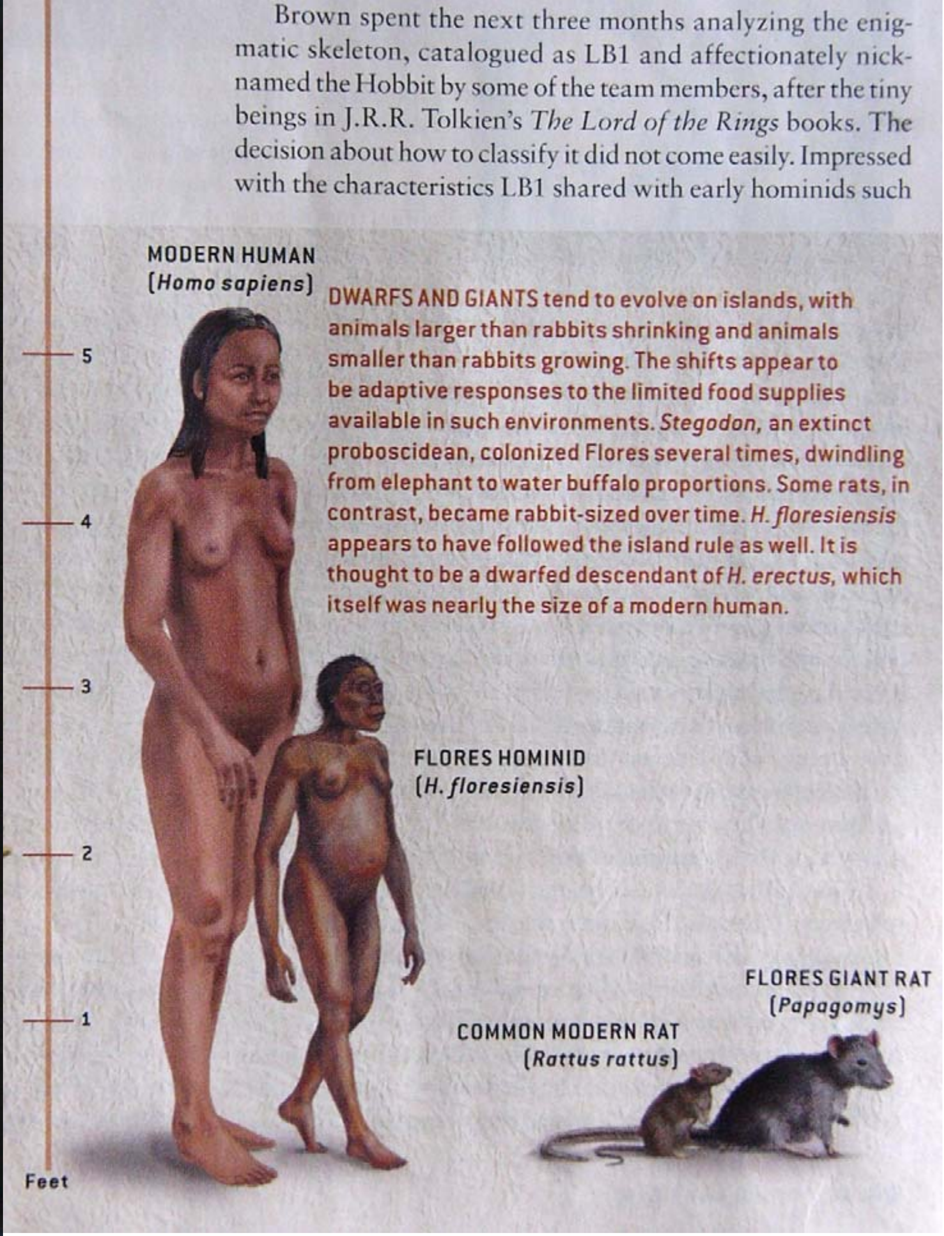
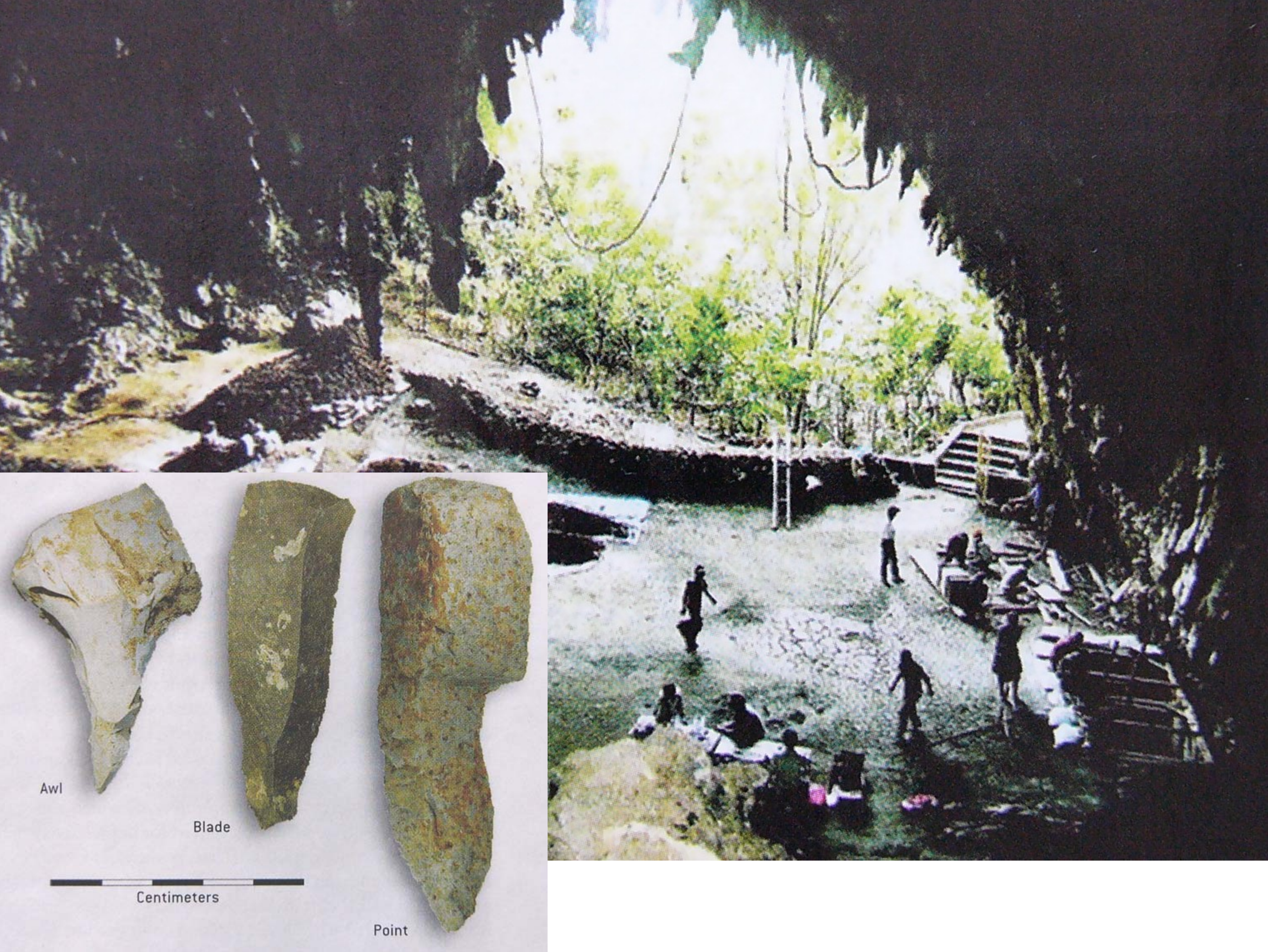


Brown spent the next three months analyzing the enigmatic skeleton, catalogued as LB1 and affectionately nicknamed the Hobbit by some of the team members, after the tiny beings in J.R.R. Tolkien's *The Lord of the Rings* books. The decision about how to classify it did not come easily. Impressed with the characteristics LB1 shared with early hominids such

DWARFS AND GIANTS tend to evolve on islands, with animals larger than rabbits shrinking and animals smaller than rabbits growing. The shifts appear to be adaptive responses to the limited food supplies available in such environments. *Stegodon,* an extinct proboscidean, colonized Flores several times, dwindling from elephant to water buffalo proportions. Some rats, in contrast, became rabbit-sized over time. *H. floresiensis* appears to have followed the island rule as well. It is thought to be a dwarfed descendant of *H. erectus,* which itself was nearly the size of a modern human.

Homo floresiensis


Zafarraya, Spain
28–32 KYA
Vindija, Croatia,
28 KYA
Dmanisi, Georgia
1.75 MYA
Qafzeh
Skūl, Israel
120–80 KYA
Longgupo, China
1.9 MYA?
Liujiang, China
67 KYA?
Bahr el Ghazal, Chad
3.0–3.5 MYA
Hadar, Ethiopia 3.0–3.4 MYA
Herto, Ethiopia 160 KYA
Olorgesailie,
Kenya
970–900 KYA
Turkana, Kenya
1.6–1.9 MYA
Olduvai Gorge,
Tanzania
1.2–1.8 MYA
Laetoli,
Tanzania
3.6 MYA
Sterkfontein,
South Africa
2.5 MYA
Swartkrans,
South Africa
1.5–2.0 MYA
● *Homo floresiensis*
● Early modern humans
○ Late Neandertals
● *Homo erectus*
● *Homo habilis*
● Australopithecines
MYA = million years ago
KYA = thousand years ago
Niah,
Borneo
40 KYA
Java,
Indonesia
1.8 MYA–25 KYA
Flores,
Indonesia
95–13 KYA
Lake Mungo,
Australia
40–60 KYA
SULAWESI
INDONESIA
Jakarta
SUMATRA
JAVA
FLORES
BALI
LOMBOK
SUMBAWA
SUMBA
TIMOR
INDIAN OCEAN

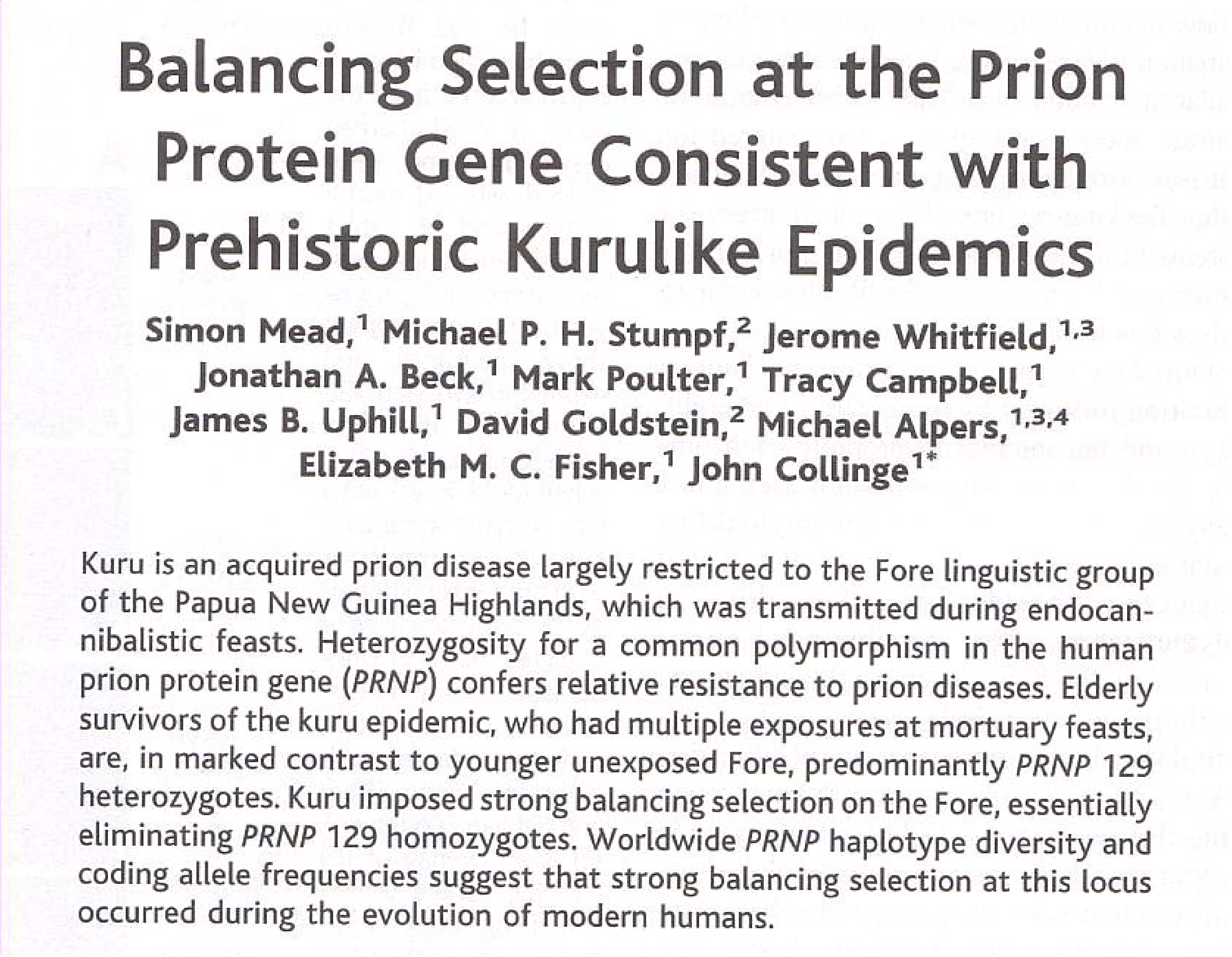

Awl
Blade
Centimeters
Point

Small skull, big discovery: *Homo floresiensis* (left) represents a new branch of human evolution.

Fossil finders in tug of war over analysis of hobbit bones

SHARED FEATURES between LB1 and members of our own genus led to the classification of the Flores hominid as *Homo*, despite its tiny brain size. Noting that the specimen most closely resembles *H. erectus*, the researchers posit that it is a new species, *H. floresiensis*, that dwarfed from a *H. erectus* ancestor. *H. floresiensis* differs from *H. sapiens* in having, among other characteristics, no chin, a relatively projecting face, a prominent brow and a low braincase.

Kaikki me oltiin ihmissyöjiä ennen vanhaan, todisteet selvät



Balancing Selection at the Prion Protein Gene Consistent with Prehistoric Kurulike Epidemics

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Kuru is an acquired prion disease largely restricted to the Fore linguistic group of the Papua New Guinea Highlands, which was transmitted during endocannibalistic feasts. Heterozygosity for a common polymorphism in the human prion protein gene (*PRNP*) confers relative resistance to prion diseases. Elderly survivors of the kuru epidemic, who had multiple exposures at mortuary feasts, are, in marked contrast to younger unexposed Fore, predominantly *PRNP* 129 heterozygotes. Kuru imposed strong balancing selection on the Fore, essentially eliminating *PRNP* 129 homozygotes. Worldwide *PRNP* haplotype diversity and coding allele frequencies suggest that strong balancing selection at this locus occurred during the evolution of modern humans.

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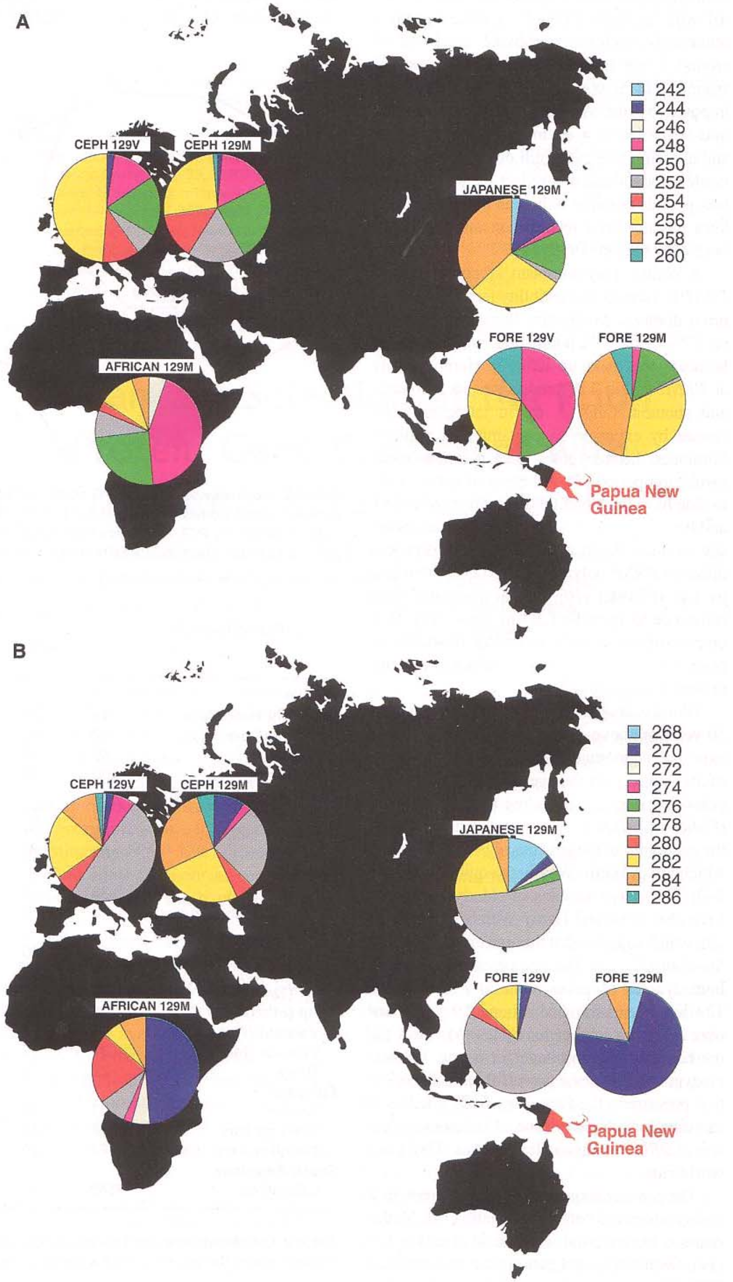

Fig. 2. Allele frequencies at microsatellites tightly linked to *PRNP*. Allele frequency at microsatellites in four populations: (**A**) microsatellite 53, which is 24 kb downstream of codon 129, and (**B**) microsatellite 108, which is 30 kb upstream of codon 129. Note the marked difference between PNG 129M and 129V when compared with CEPH 129M and 129V, although this is less striking for 53 than for 108. Note also the reduced diversity of alleles in PNG compared with other populations. See SOM text, note 5.

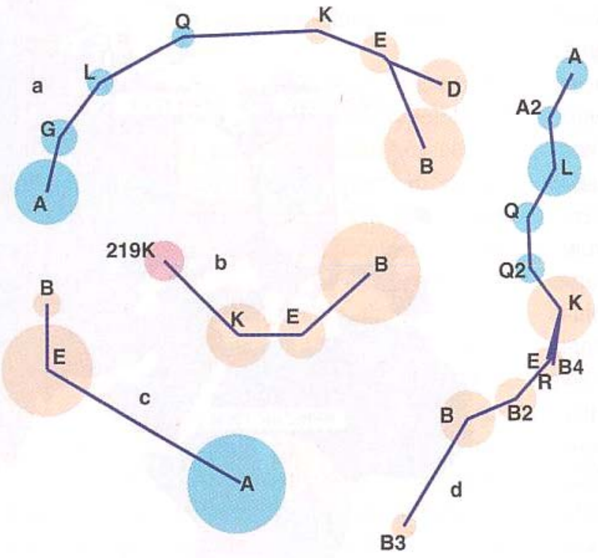

Fig. 1. Examples of predicted haplotype genealogy from four populations: (**a**) European, (**b**) Japanese, (**c**) Fore, and (**d**) African. Haplotypes are colored in orange (129M), blue (129V), or pink (129M, 219K) (*16*). Note the linear structure, loss of diversity in the Fore, and the location of 129V and 219K at extremes of all genealogies. Results are similar using maximum likelihood, parsimony, or distance methods. For method details, see SOM text, note 4.

Science 25 April 2003