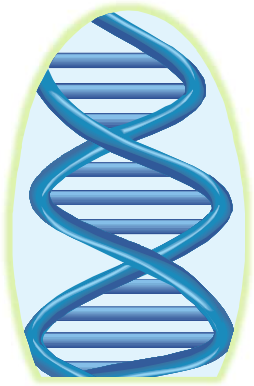
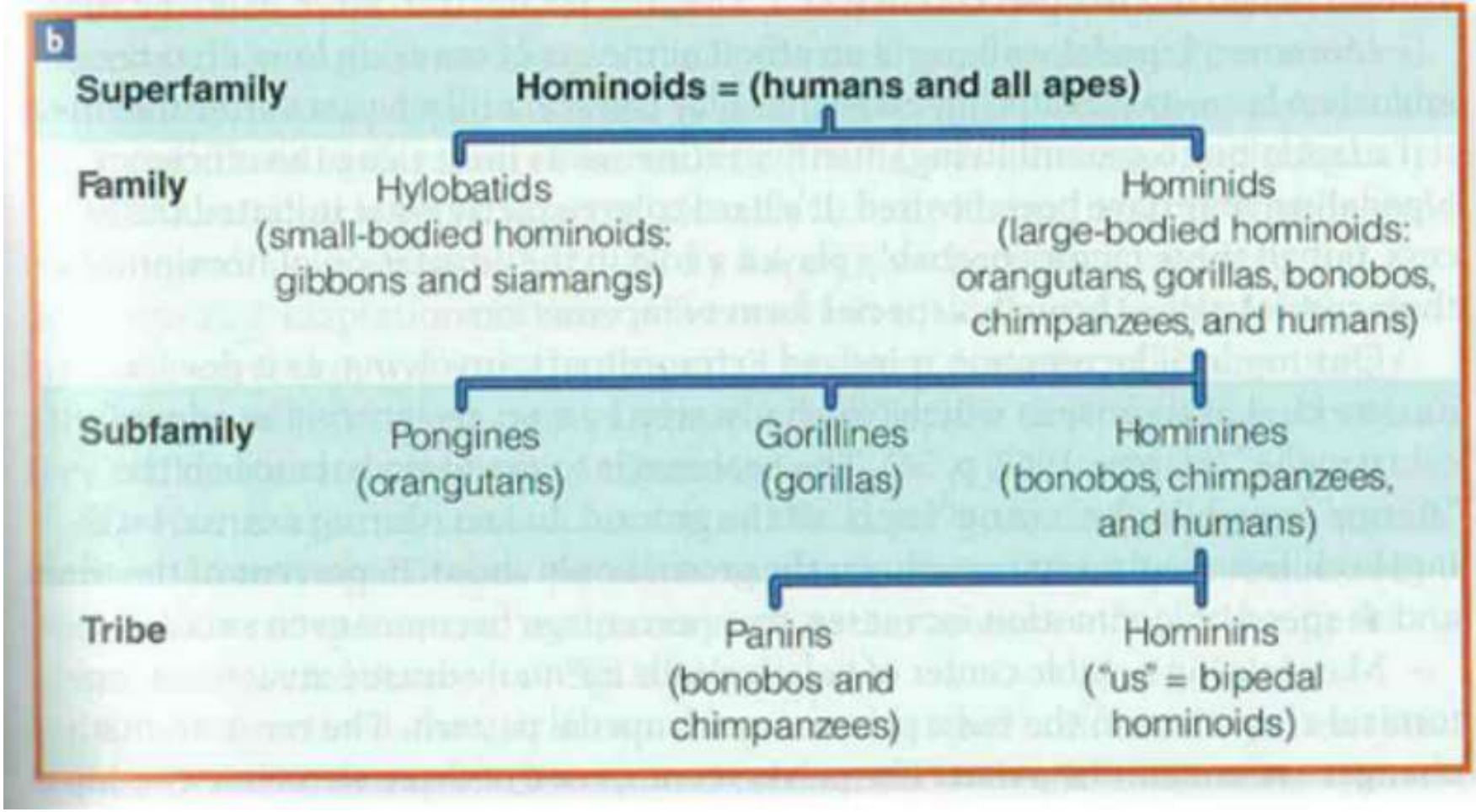
Genetics into History

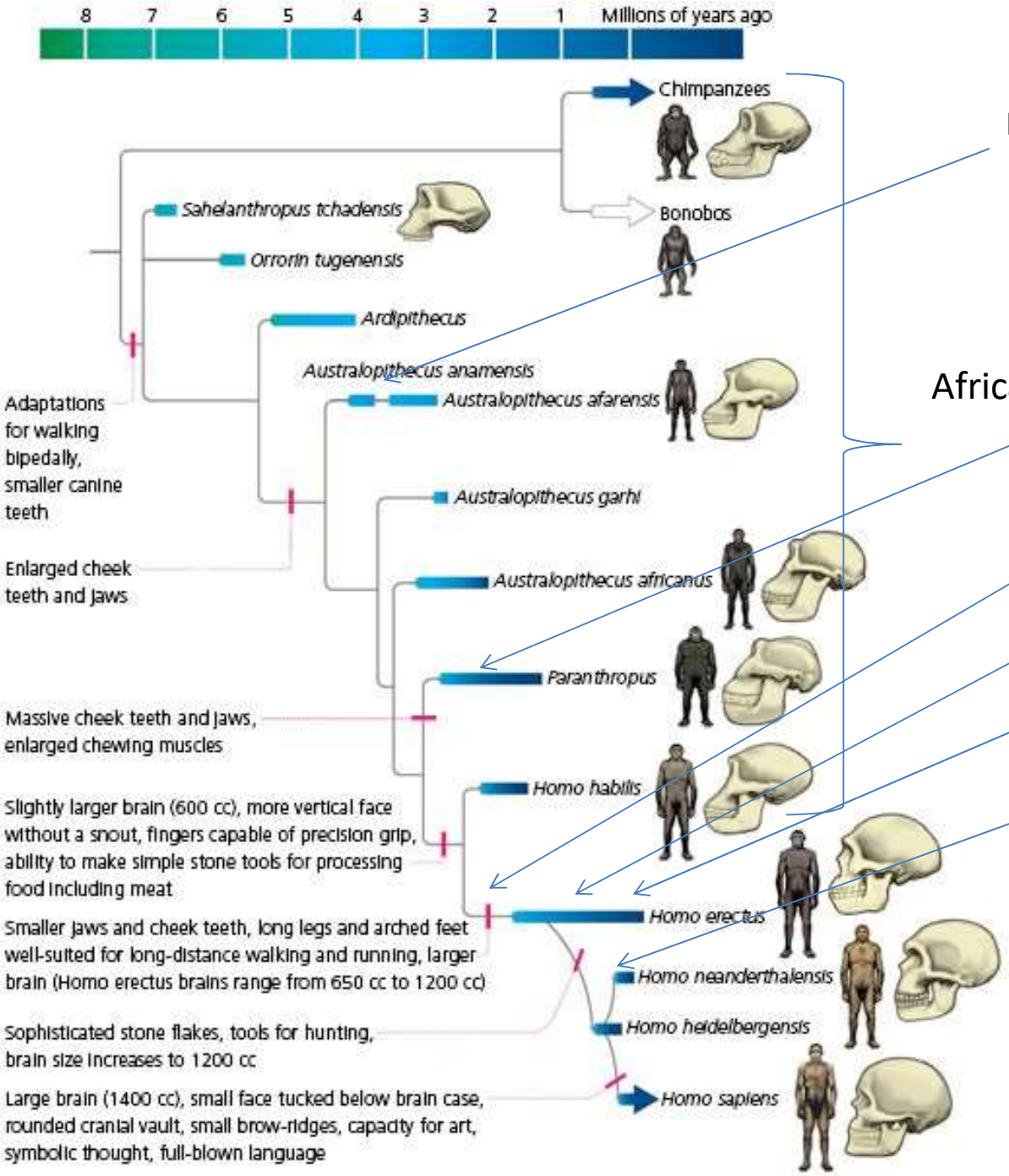


Garry Law

Living Animals Classification



Fossils



Lucy

Africa only

Nutcracker man

Homo naledi (date uncertain)

Turkana Boy

Java Man, Peking Man

Pit of bones

Some others:

Homo ergaster - Africa

Homo antecessor - Europe

- Splitters' groups for some of *Homo erectus* and *Homo heidelbergensis* respectively

Relationships between fossils based on similarity:

- Particular markers believed to have a genetic origin
    - e.g.:
        - Number of cusps on teeth
        - The way bones join at back of skull
        - Position of some blood vessel holes
- Shape / size similarity linked to genes with some credibly

But:

- Sample sizes are often small.
- Shape / size is plastic – varies after birth with diet and the use made of the body in life.
- Bones often disarticulated (one individual or several?) and
- Can be distorted while fossilising
- May not understand gender differences.

Ages without fossils?

- Chimpanzees and humans share 98.8% of DNA
- Humans and Neanderthals share 99.9% of DNA
- Relative order of branch age is obvious – but getting to a splitting off date from gene similarity? It is a bit of an art.

Human fossil experts are notorious for their diversity of views

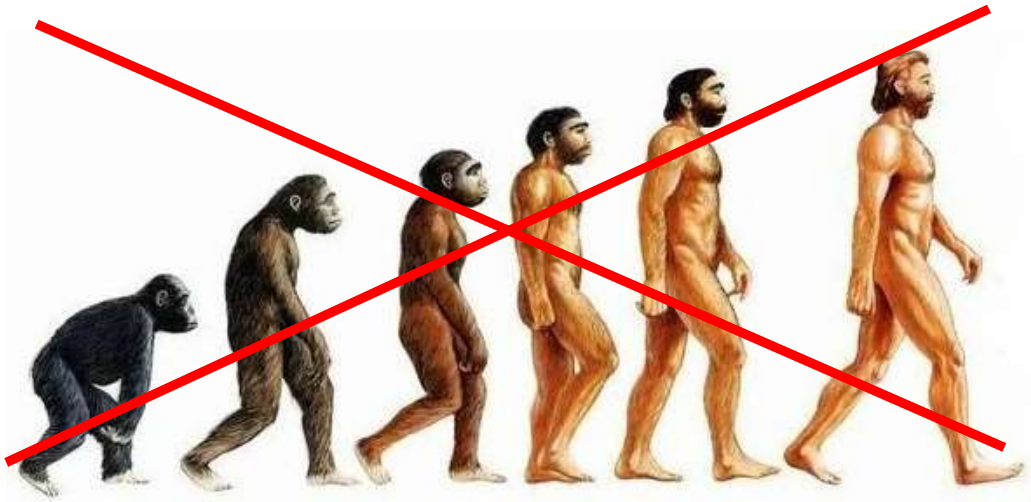
Big egos seem to be a pre-requisite for being paleoanthropologists

Lumper and Splitters (Lumpers using only a few genera / species names, Splitters many)

Even where they agreed on “boxes” to put specimens in they did not agree on their relationship with each other (ancestors or cousins).

All agree there is no straight line linking all fossils in an ancestral line to modern man – there are certainly many outside that line.

For much of the past few million years there were three or more different hominins living at the same time



Forget it – it’s much more complicated

Recent Discoveries

- **“The hobbit” - *Homo floresiensis***
- Flores island – Modern Indonesia
- 9 individuals – only one skull
- Not on the fossil diagram as there is no consensus as to where it fits.
- ~~38,000 to 13,000 years ago~~
- **2016 update 1 – 60,000 to 100,000 years ago**
- **2016 update 2 – second site now known also on Flores – ancestor at 700,000 years ago – even smaller**
- Brain 426cc - tiny
- Two attempts to recover DNA have failed
- ~~Some say it is pathological rather than a human branch – but a population of these?~~ **No, second older site clearly shows was not**

★ Kiwi connection – Was found in a programme lead by NZ born and trained archaeologist Mike Morwood

Homo naledi – South Africa.

2015 announcement.

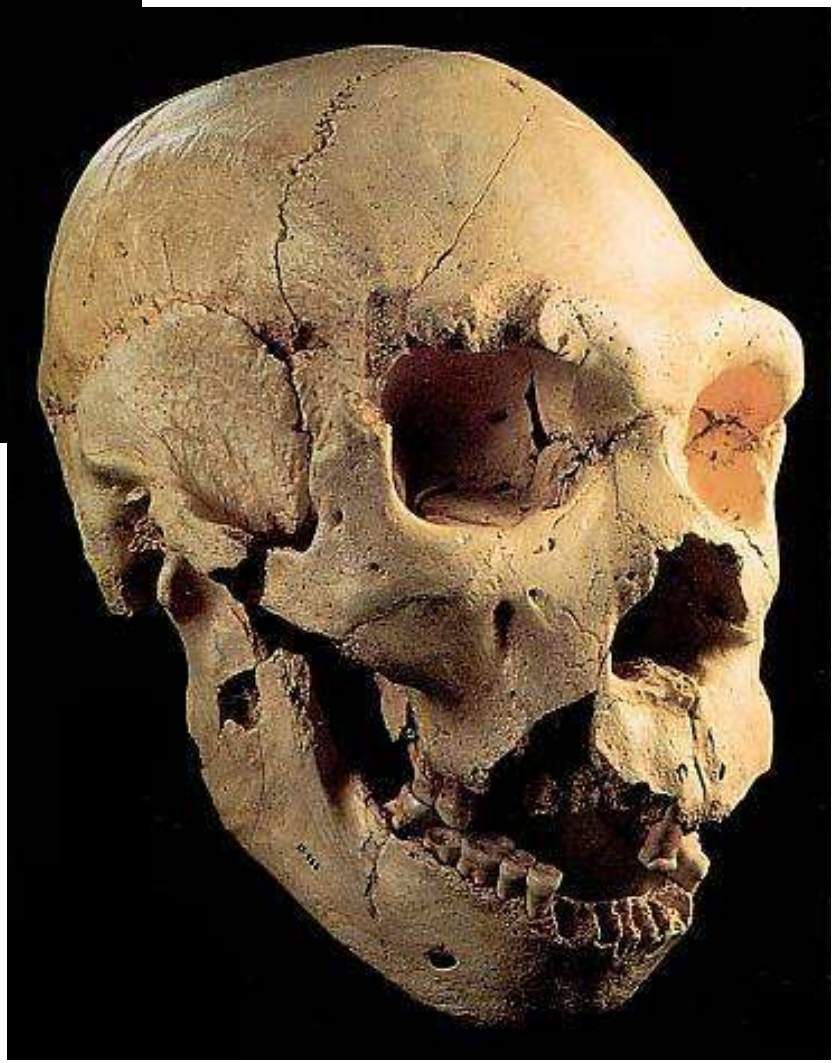
- 1500 bones 15 individuals minimum
- not yet dated
- brain sizes 465cc, & 560cc
- maybe early or pre *erectus.*
- problem is *erectus* now covers three continents and 2M years – can almost anything fit in it?

Investigation and announcement have been controversial.

Neanderthals – “Pit of Bones”, Atapuerca, Spain

- **Oldest fossils 1.2M years, >6500 hominin bones, 28 individuals 17 skulls reassembled - so far**
- **May cover the transition from *Homo heidelbergensis* to Neanderthals**
- **The oldest human DNA from anywhere is from there (2015). Neanderthal of 430,000 years. But only mtDNA so far.**

Pit of Bones -



Some of the skulls

Denisova Cave - Siberia

- **First occupied from 125,000 -180,000 BP**
- **Human remains from a later 1m thick layer, dated 30,000 to 48,000 BP**
  - **Child's phalanx sliver – mtDNA, and later nuclear DNA – female**

  - **Wisdom tooth - described as non-Neanderthal in shape – mtDNA and some nuclear DNA extracted**
  - **DNA is not recent Neanderthal or modern human – people are now called Denisovans**
  - **Their physical form is not known**
  - **But there are Neanderthals as well in the site**

African Origin and Initial Radiation

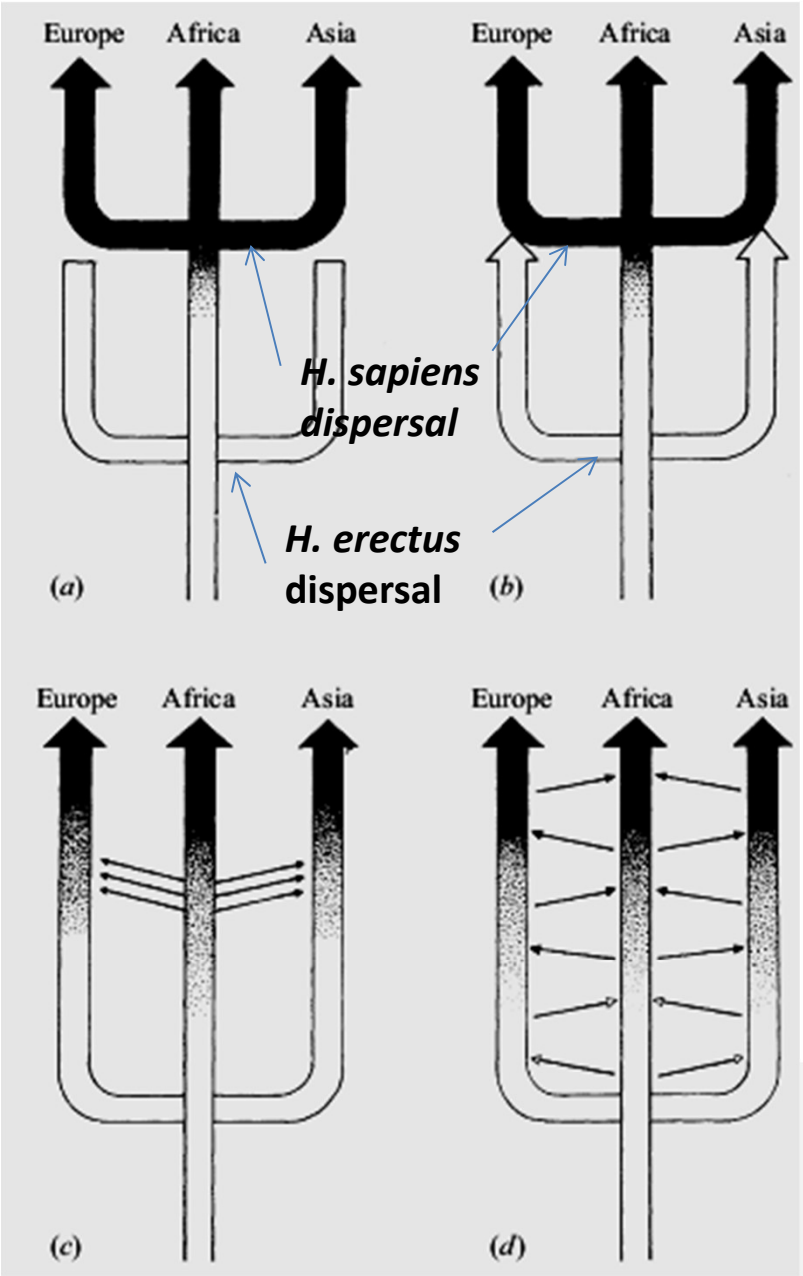
- **The early genetic branches of *Homo sapiens* are exclusive to Africa**
- **The oldest archaeological evidence of developed human behaviour is in (southern) Africa**
- **Early *Homo sapiens* specimens from Africa:**

e.g. Awash, Ethiopia
~160K years ago

- all mean its likely the initial emergence of *H. sapiens* was in Africa and the rest of the world was colonised from there – but ….

Emergence of modern man

- Until very recently the fossil evidence of *H. sapiens* has been scrappy and difficult to interpret
- In part its difficulty was because much lay beyond the reach of C_{14} dating so it has been difficult to fix in time.



How did *Homo erectus* become *Homo sapiens*?

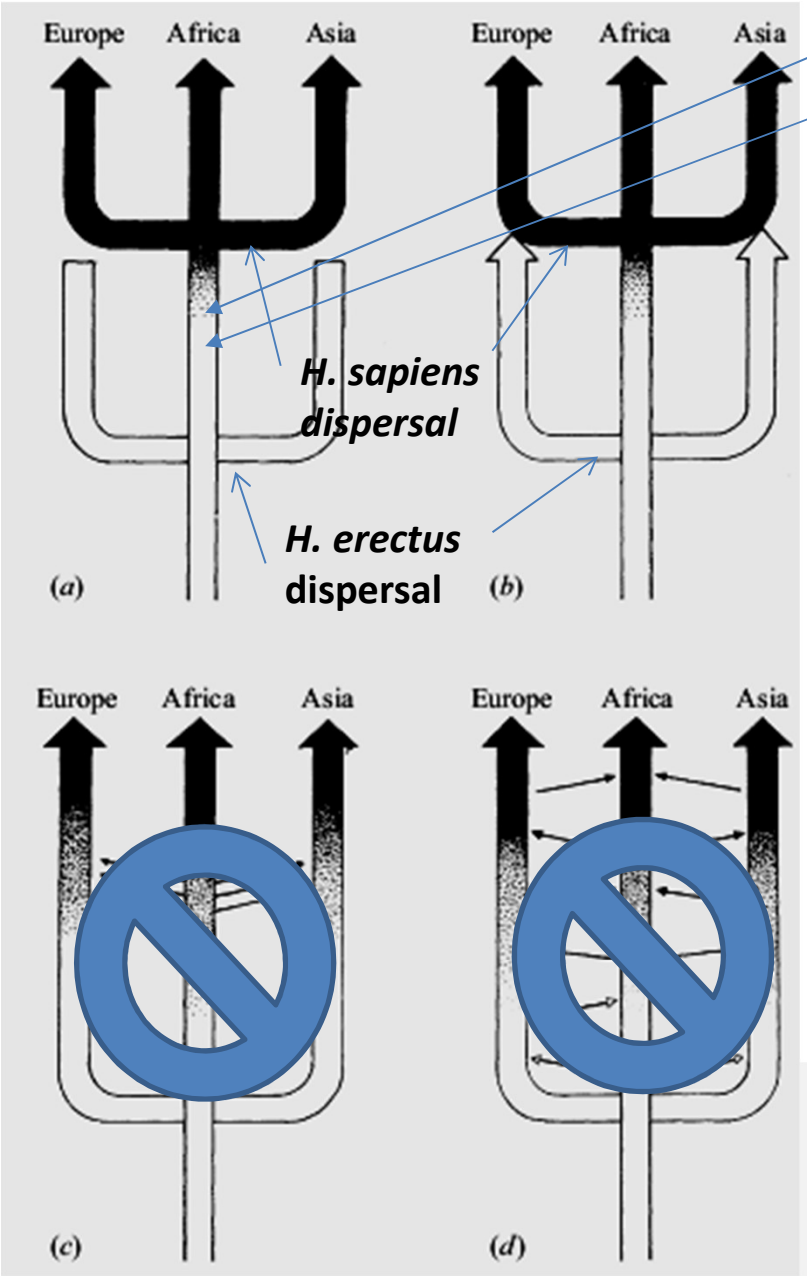
One former view was that humans arrived through parallel processes across the old world – local sequences with some gene flow between passing through primitive moderns to sapiens – the Multi-Regional Hypothesis (d),

(b) and (c) are less extreme versions.

Studying the forms of the fossils was never going to resolve these – the data is too coarse

Figure 2. Evolutionary models of modern human origins (modified from Aiello 1993). (*a*) Recent African Origin; (*b*) (African) Hybridization and Replacement Model; (*c*) Assimilation Model; (*d*) Multiregional Evolution.

Stringer 2002



mtDNA "Eve"

Y Chromosome "Adam"

An early result from DNA analysis of modern people was that we all share common ancestors of quite recent origin 100K – 200K years.

This excludes (c) and (d) as alternatives.

★ **Kiwi Connection – Alan Wilson who led the work that identified the recency of "Eve" was NZ born and trained.**

Figure 2. Evolutionary models of modern human origins (modified from Aiello 1993). (*a*) Recent African Origin; (*b*) (African) Hybridization and Replacement Model; (*c*) Assimilation Model; (*d*) Multiregional Evolution.

Stringer 2002

Newer data

– is more from ancient DNA extracted from fossils

- and closer interpretations of the diversity of modern humans' DNA

It is causing a revolution – hinted at here - and the story about *Homo sapiens* emergence is changing rapidly

That is another talk …….

This Talk:

About the emergence of modern human beings – *Homo sapiens* - and what DNA has to say about it.

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About the emergence of modern human beings – *Homo sapiens* - and what DNA has to say about it.

★ **Kiwi connection:**
Maurice Wilkins, one of the three people that shared the Nobel Prize for finding the helix structure of DNA was New Zealand born.

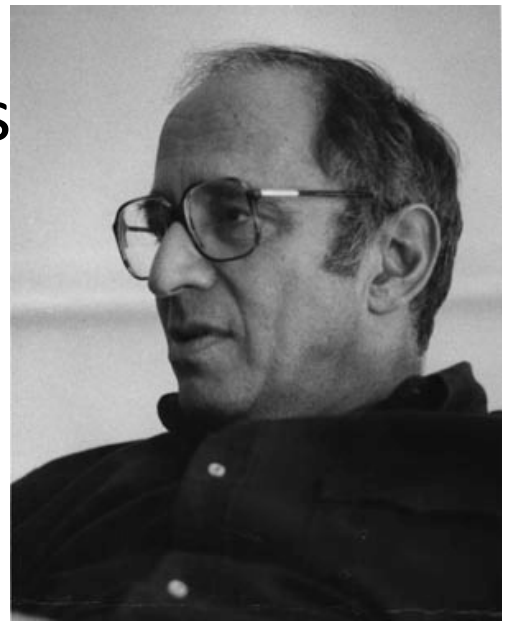
Genetics and human history

Kuhnian paradigm shift:

- Old deep human history – was based on archaeology and fossil forms of hominids
- The new modern human history paradigm – seems to be being dominated by geneticists
- Flood of new reports in the past 6 years

How well are they doing?

Thomas Kuhn ★
Philosopher of science



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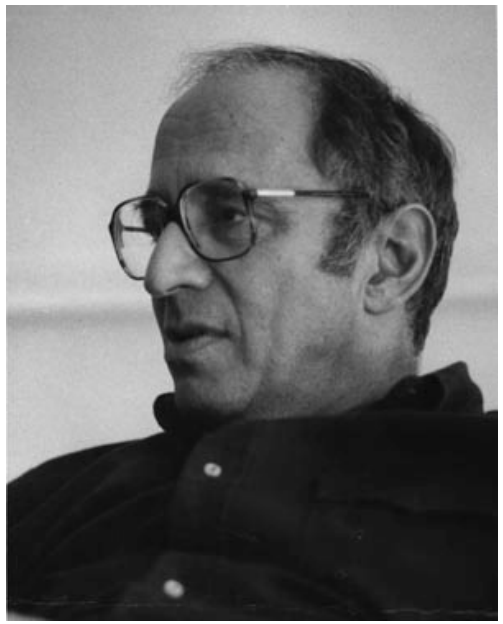
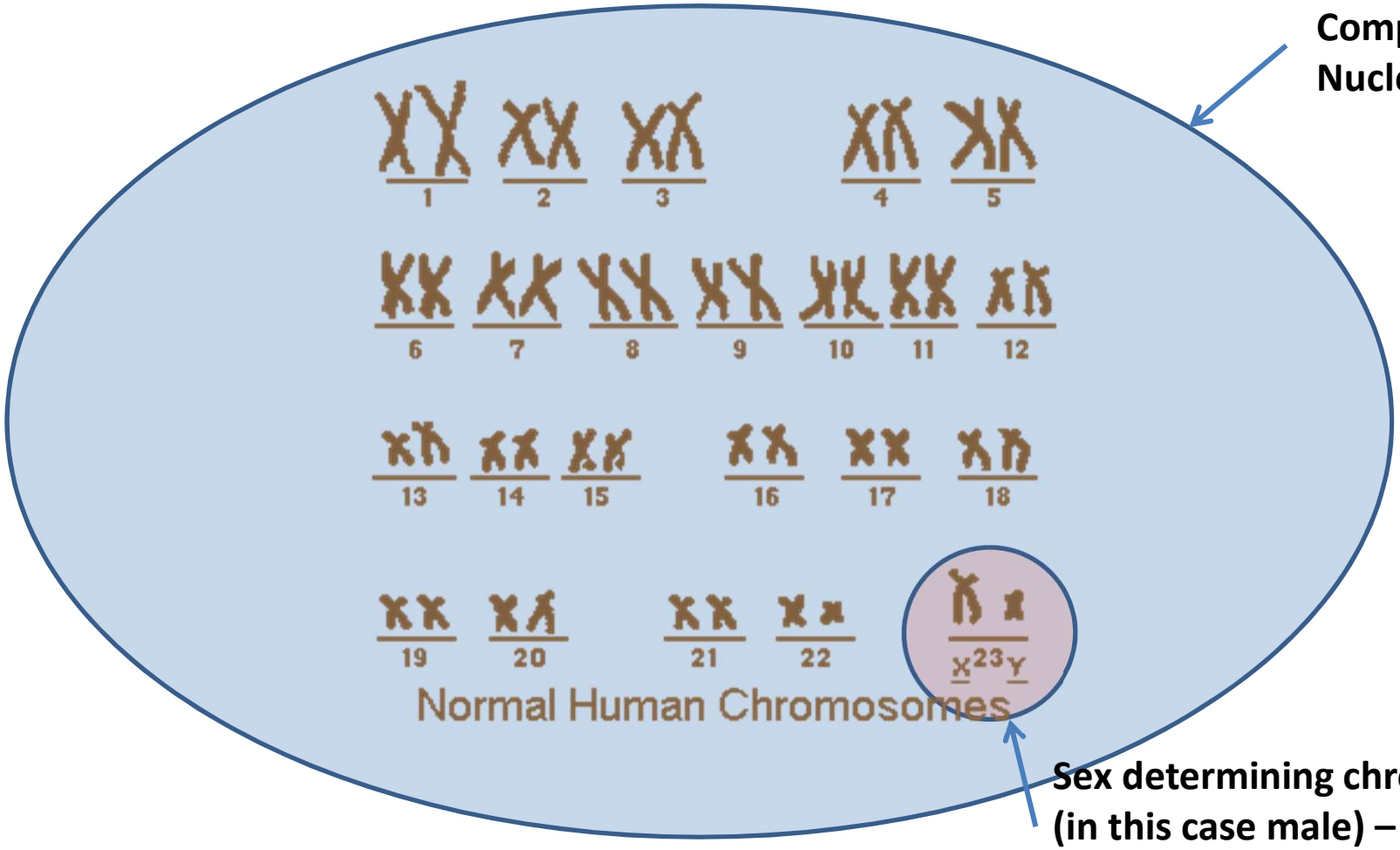


★ **Kiwi connection – the 20th C's other great philosopher of science on whom Kuhn built and challenged, spent WW2 in exile teaching at Canterbury University – Karl Popper**

Diversion into genetics / DNA

Cells have a nucleus and in that nucleus is one copy of the cell's DNA – Nuclear DNA – stored in 23 pairs of chromosomes.

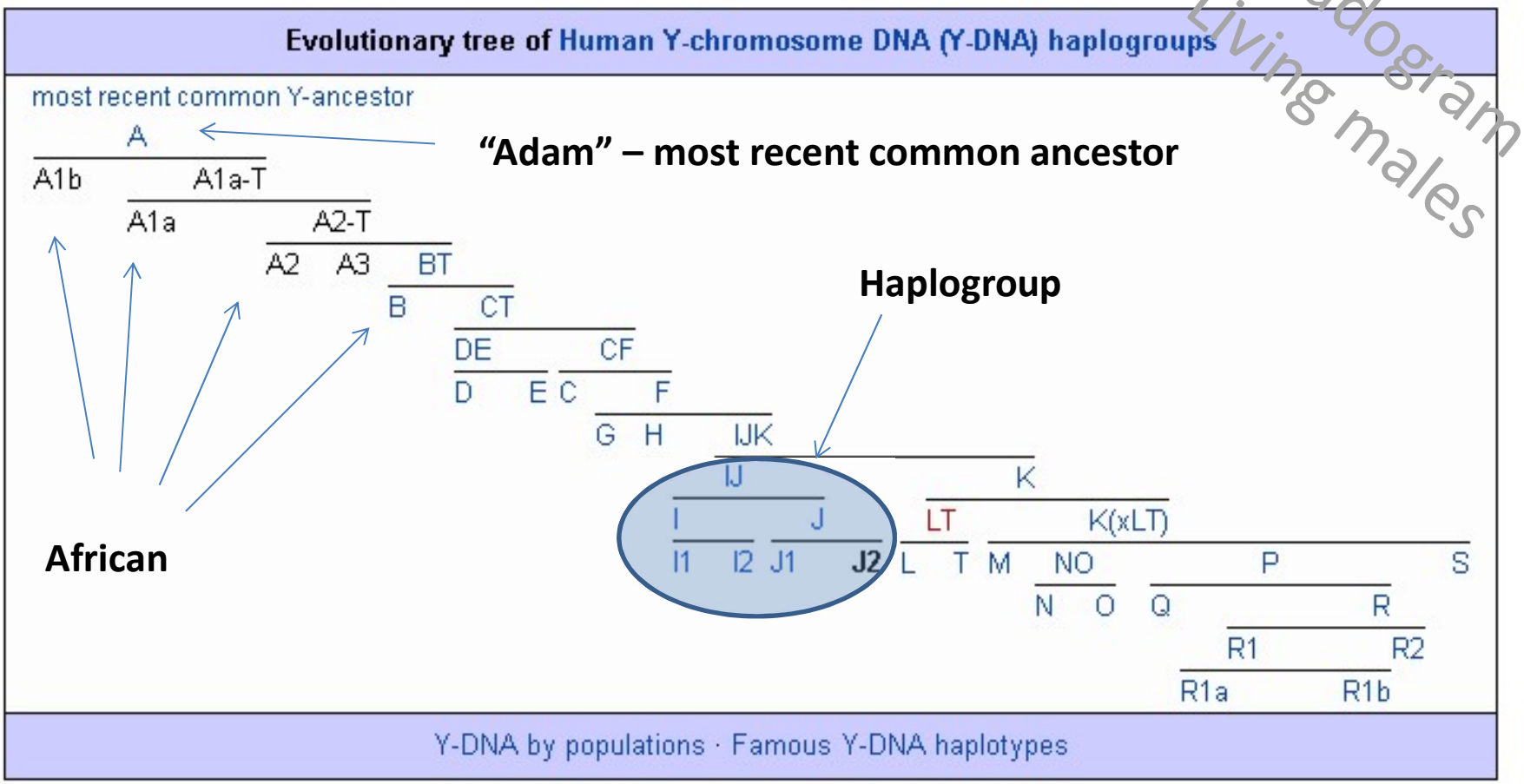


Comprise Nuclear DNA

Sex determining chromosomes (in this case male) – rest are autosomes

- Cells also have Mitochondria – one of their functions is energy conversion.
- Mitochondria have their own DNA - mtDNA
- Human cells have 2 to 2500 mitochondria depending on the cell's function.
- In all of us the mtDNA comes only from the mother
- The others - Autosomes inherited from both parents
- In males the Y chromosome and its DNA comes only from the father

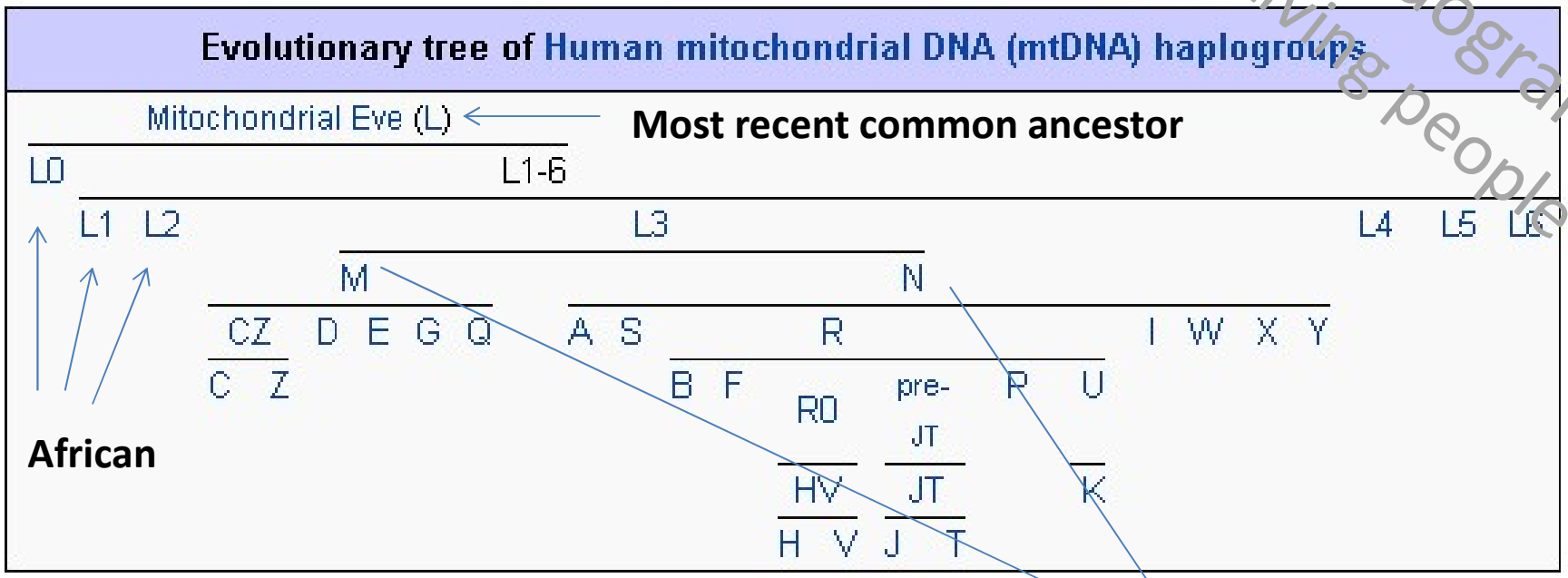
- Because the processes of inheritance of Y Chromosome DNA and mtDNA are simpler they are of the greatest use in studying the history of changes in DNA
- DNA suffers errors in transcription it is possible to look at how changes are shared and build family trees of changes over time for Y and mt DNA
- Because there is some information on the rates at which their errors occur it is also possible to estimate when in the past the errors occurred.
- Can do this by taking samples from living people



Male only descent – only one copy of Y so not subject to chromosome recombination. In males only.

Y chromosome 50M base pairs, ~ 86 genes (out of ~20,000 total)
c.f. average chromosome has ~430 genes

Cladogram
Living people



Female line descent – but in all people. Extra-chromosomal DNA so not subject to chromosome recombination.

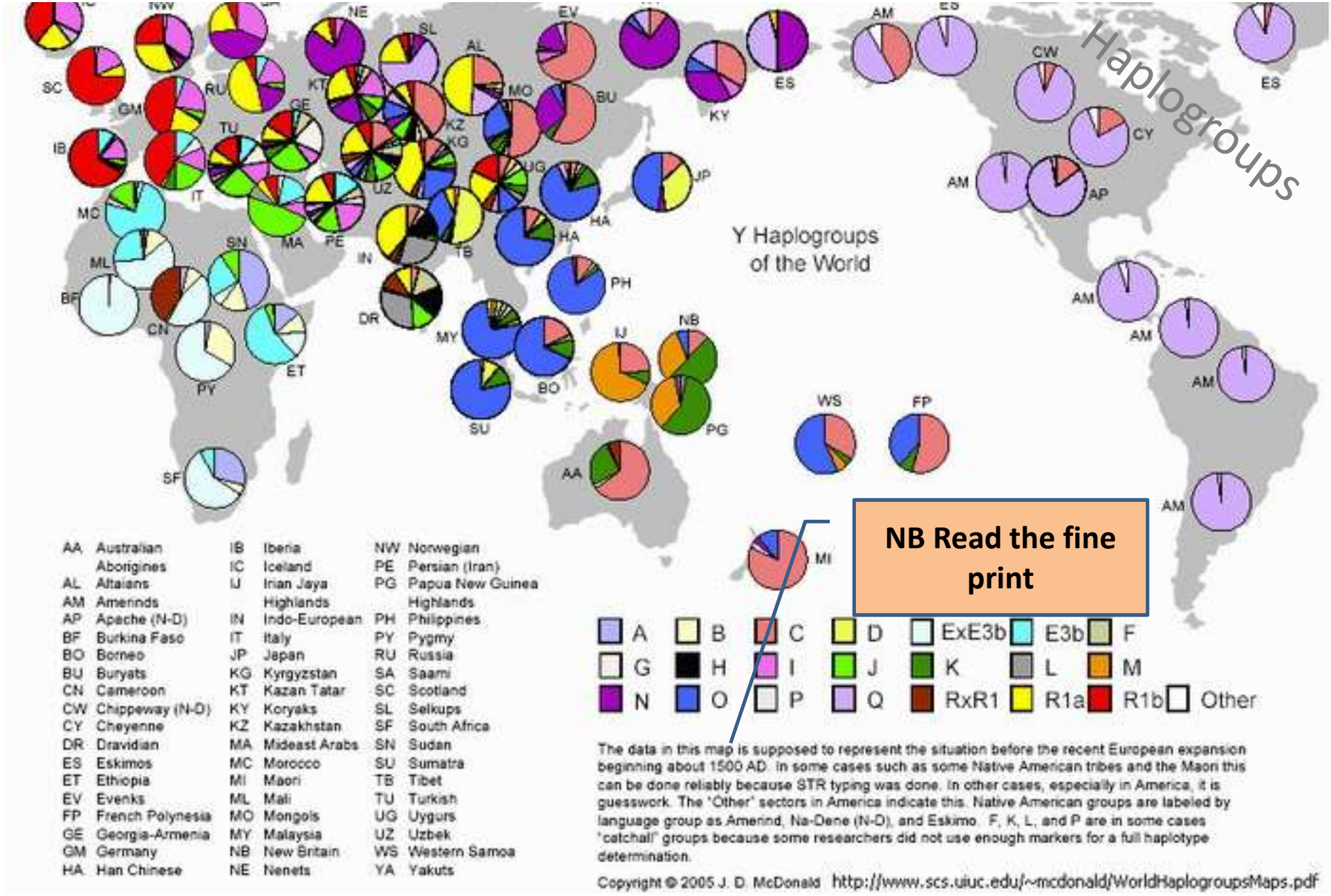
mtDNA 15-17,000 base pairs, 37 genes

Haplogroups

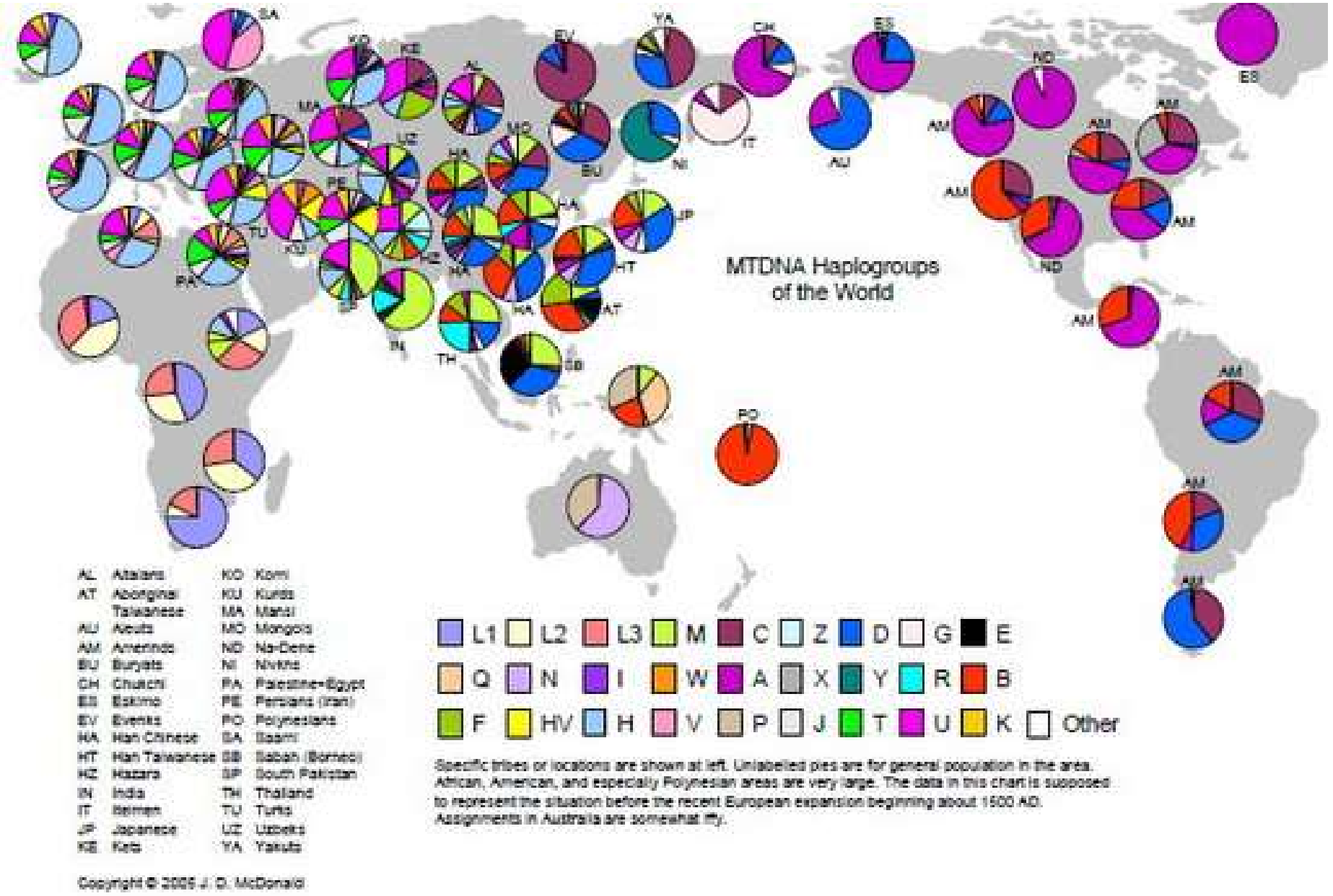
Define Haplogroups from the branching history,
in particular for the male Y chromosome and for mtDNA –

Then **Populations:**
Can have limited Haplogroups, or many diverse ones.

- Limited – the population has been through a bottleneck – or is of recent origin from a small base (founder effect) – or some may have been selected against
- Diverse – population of ancient origin and has retained and augmented its diversity over time - or the diversity comes from the diversity of the population's origins.



Pre-modern populations Y chromosome diversity



Pre-modern populations mitochondrial haplogroup diversity

- These diagrams shout ***'human history here'***
- But here is the fine print:

"The data in this map are supposed to represent the situation before the recent European expansion beginning in 1500AD"

In other words it is someone's interpretation of what they think the past was like.

Cladograms create a history of the different forms of Y and mtDNA found they do not tell us

- where the people of the past lived or
- where the changes that mark different groups took place.

Ancient DNA

- Only DNA from localised and dated fossils can help fix the genetic history to a location.
- Need to find ancient DNA (aDNA) to do this
- Not easy – DNA has a half life of ~ 500 years at ambient temperatures. Most is gone in a few thousand years. Shorter if bacteria active
- There are more copies of mtDNA to start with.
- mtDNA is a much shorter sequence than Y so is easier to sequence - has a good information return
- DNA survives longer in cold and dry places – and a little better in teeth and ear bones.

Ancient DNA

- Sterile collection is vital – no point in sequencing the DNA of the collector. Likewise use laboratories where there is no competing sequencing work that might contaminate samples
- Need to duplicate a large amount of aDNA and then sequence it.
- Analysed in 100 base pair strings by automatic processing and then jig-sawed together to re-assemble larger sequences. Huge computer task.
- Much of what is found is still stray stuff – bacterial DNA in particular

- A lot of DNA is outside genes
- Non-gene DNA once thought to be “junk” – but some is now known to influence the expression of genes – epigenetics
- Calculating species branch dates from changes of DNA not easy – genes and epigenetic code are subject to evolutionary selection - so disadvantageous changes will not survive – and very advantageous changes may become universal quickly
- Rates of DNA change as ”clocks” of are perhaps best applied to DNA code that is not involved in selection
- Need calibration
- There are different approaches and different dates result

What has been happening: 1

	Interpreted as
Mitochondrial "Eve" – all modern people have a most recent common African female ancestor that is surprisingly recent	**Eve" lived in Africa in a small population – in a "population squeeze", from which only one mtDNA haplotype survived, C. 100- 200K**
Y Chromosome "Adam" - the most recent common African male ancestor again shared by all that is surprisingly recent	**"Adam" ditto but a bit older**
All modern non-Africans have less genetic diversity than modern Africans (- has to be through a separation post - "Eve" / "Adam")	**The "Out of Africa" event is the later migration of a founding group exiting Africa ~ 50K BP by replacement rate estimate – but…..**
Ancient DNA has been sequenced from fossils in Europe and Asia that is outside the "Out of Africa" moderns lot, - different / older. However some modern people carry sequences from these ancient people.	**The sequences common to fossils and modern people arose as a result of cross-breeding between the "Out of Africa" lot and more ancient local lineages that were pre "Eve"**

	Interpreted as
There are now enough separate individual Neanderthal mitochondrial determinations to build their family tree (Phylogeny)	There seems to be a western recent subgroup of Neanderthals who replaced older Neanderthal forms
Some modern Africans carry anomalous sequences which seem to derive from different sources from the modern group. (The same thing was also observed outside Africa before it was matched to Neanderthal in-mixing)	Cross-breeding also occurred within Africa with an unidentified older hominin form or forms. Estimate that a form diverged at 700K BP and their DNA introgressed to African moderns at 35K BP. (Replacement rate age estimates)
Aboriginal Australian nuclear DNA sequenced and is closer to Africans than other non-Africans	Aboriginal Australians are an early isolate of modern humans

	Interpreted as
By carrying out 'most recent common ancestor' estimates on replacements on multiple segments of compete individual genomes regional age profiles of the surviving mutations have been developed.	Ancestors to the European and Chinese individuals studied had an age profile on their replacements which suggest their ancestors had a severe population bottleneck 10K-60K BP, the African individual's ancestors' bottleneck was less severe and recovered earlier. (Replacement rate age estimates) (c.f. Marine Isotope Stages 2 and 3: 11K - 60K BP = last glaciation) Other studies support a like bottleneck: One method suggests ~ 12,000 individuals in Africa, ~ 6000 in the non-African old world Another suggests ~ 3000 individuals in Africa and < 1000 in the non-African old world

We *were* an endangered species – lucky to have got here – not the result of some manifest destiny.

“Adam” and “Eve”

Could the mtDNA and Y chromosome DNA have found anything else besides radiation from a single common ancestor?

The short answer is no – because of the way their DNA is inherited *they can show <u>nothing but</u> radiation from a common ancestor*.

It is their dates that are important

To see gene flow from other than this common ancestry have to look at DNA outside mtDNA and Y-DNA (i.e. the non Y chromosomes = autosomes + X).

Dates

- Mitochondrial “Eve” / Y chromosome “Adam” /
  Out of Africa for *H. sapiens*
- are all different dates

- “Adam” oldest 200-300K years ago*
- “Eve” is the middle 100-200K years ago
- Both or these more recent than determined my mtDNA for other primates – we are a young species compared to them
- Out of Africa the youngest ~ 50K years ago – only this one is linked to archaeology
- Out of Africa may be several events – some unsuccessful, dying out again in the middle east, so only the latest is covered by the ~ 50K years ago date estimate.

* It was thought younger than “Eve” but a recent discovery of a whole new Y lineage in moderns changed that.

Hypotheses and Negation

- The more extreme of the geneticists said their mtDNA and Y-DNA data negated all but the recent African model - there was only one stem to all *H. sapiens.*
- But was their view open to negation? – fundamentally *No* - not from within its own data – *because it could only show one stem.*
- However on the very first bits of ancient DNA other than mtDNA the 'one stem' view failed – there was gene flow.

What comparative Genetics on living people alone cannot do:

- Determine ***where*** some genetic innovation event happened.
- On its own, link specific DNA sequences known in moderns to fossil phenotypes *where the fossil genotype is unknown*
- Determine absolutely the genetic diversity of past populations (may give some measure but cannot exclude specific forms)
- Provide absolute dating of genetic events. DNA clocks are approximate and subject to distortions

Neanderthal nuclear DNA

- One primary source is three fully sequenced bones from Vindija Cave, Croatia
- Three individuals – two closely related.
- 38 ~ 44K years ago – i.e. late Neanderthals
- Reinforced by less complete sequences from other sites
- Widely dispersed modern non-Africans often have a small proportion of Neanderthal DNA: 1.5 – 2.1%
- Africans mostly not though some claims otherwise - that north Africans do
- One early 37,000–42,000-year-old *H. sapiens* fossil from Peştera cu Oase, Romania has 6 to 9% of Neanderthal DNA – Also it must have lived soon after cross breeding, but if it has modern descendants the DNA has been diluted.

RIP ~ 39,000 years ago, less a few genes

mtDNA from Neanderthals

- **Now from a lot of late Neanderthal sites**
- **Key source is the Pit of Bones, Atapuerca, Spain**

  Oldest fossils 1.2M years, >6500 hominid bones, 28 individuals 17 skulls reassembled - so far

  May cover the transition from *Homo heidelbergensis* to Neanderthals

  The oldest human DNA from anywhere is from there. Neanderthal of 430,000 years

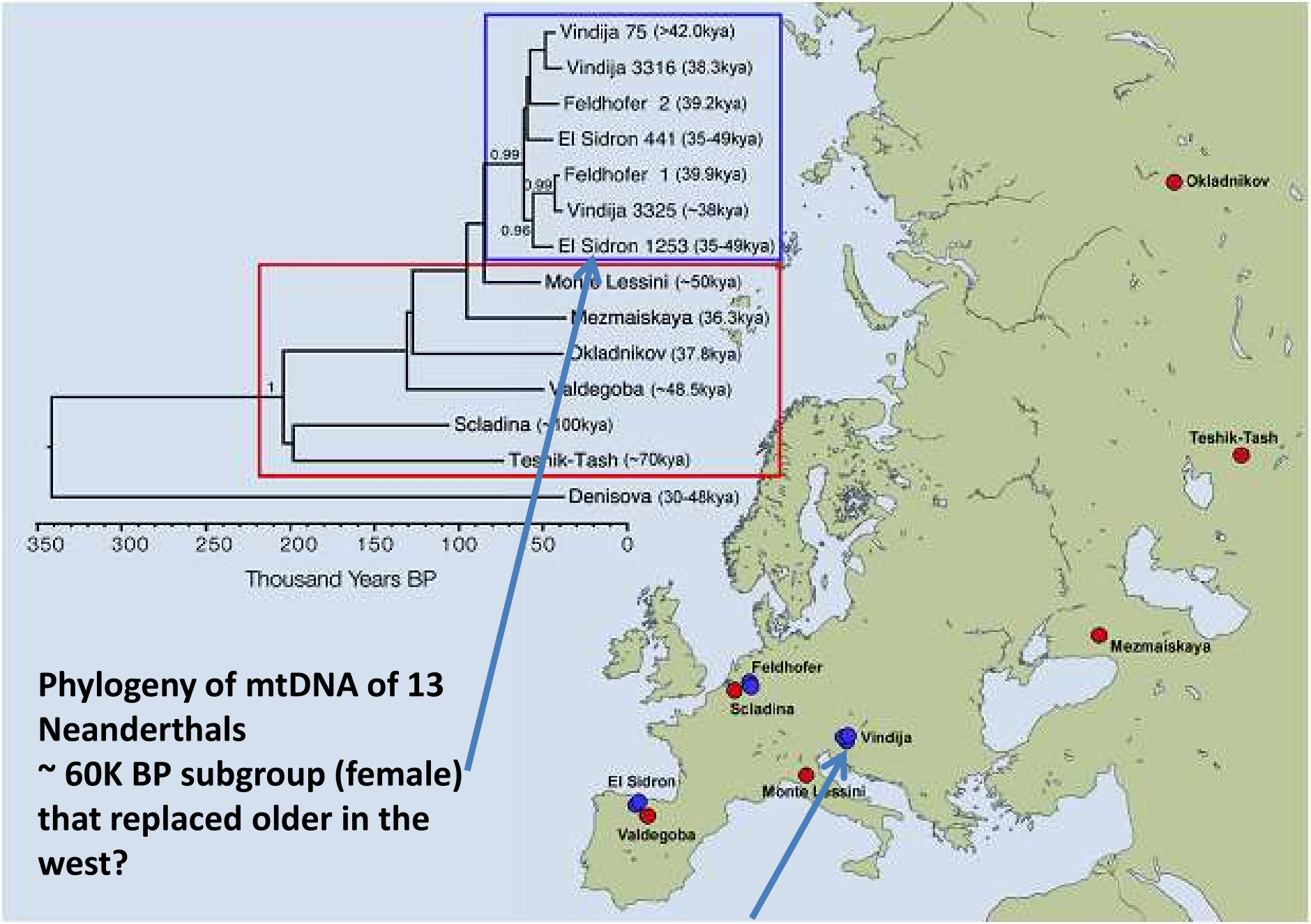
Pit of Bones -

Pit of Bones - more

– Was just mtDNA but –

– *2016 update* - now have nuclear DNA as well

- The mtDNA is “more closely related” to Denisovans than later Neanderthals but the
- Nuclear DNA is clearly Neanderthal
- Revised molecular clock date on nuclear DNA for split between Neanderthal and sapiens ancestor is 550 – 765K Years ago.



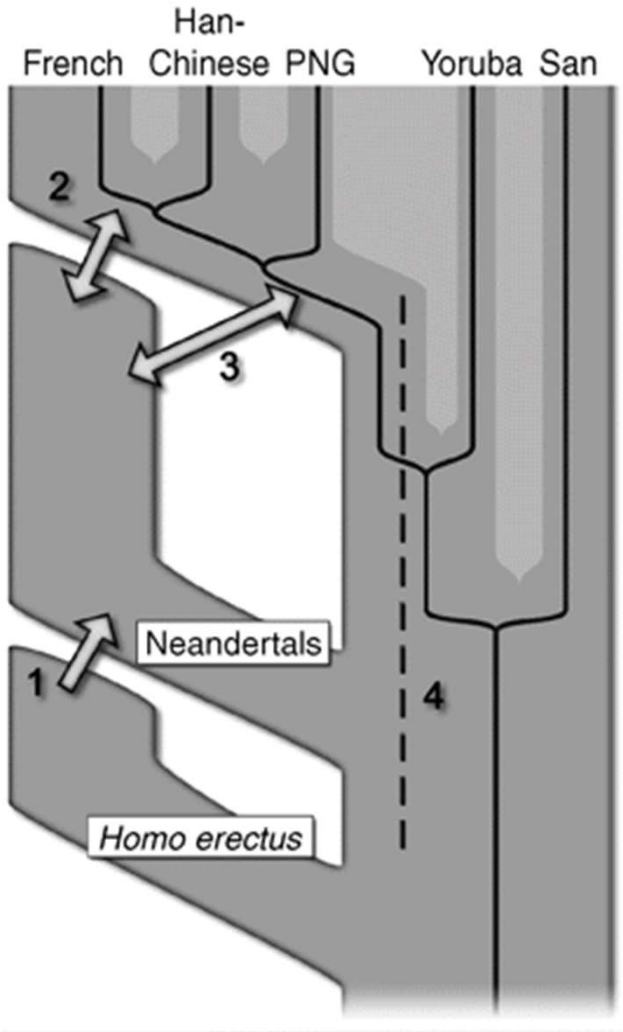
Phylogeny of mtDNA of 13 Neanderthals
~ 60K BP subgroup (female) that replaced older in the west?

Vindija

The apparent contradiction of Pit of Bones DNA relating to Denisovans (mtDNA) and Nuclear to later Neanderthal may be explained by non-Denisovan mtDNA lines becoming dominant in the Neanderthal population later.

Neanderthal introgression into moderns

- Most parsimonious explanation of admixture is interbreeding early in *Homo sapiens* dispersal from Africa (diagram link 3)
- However three other possibilities were considered possible – not that these got a lot of space in science news stories



- and none in the mass media

The cross breeding between Neanderthal and *sapiens* is usually presumed to be in the Middle East, because:

- Recent dating work suggests little overlap in time of *sapiens* and Neanderthals in western Europe ★
- Neanderthal's range included the Middle East and overlapped there with *sapiens* in time and space.
- All non-Africans appear to have a similar small proportion of Neanderthal and hence it was likely early in the *sapiens* dispersal.

However the areal range of the genetic markers associated with Neanderthal is not well known – there may be no exact equivalence of the Neanderthal phenotype and the known marker range.

Hence the cross breeding may have occurred elsewhere, even before the departure from Africa (but been lost in modern African populations if it was there).

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However ★ Kiwi connection. Tom Higham – Professor at Oxford University - is the leading expert on dating Neanderthals. NZ raised and trained.

Neander

equivalence of the Neanderthal phenotype and the known marker range.

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Denisova Cave

- Denis's cave – a former hermit residence
- In Siberia

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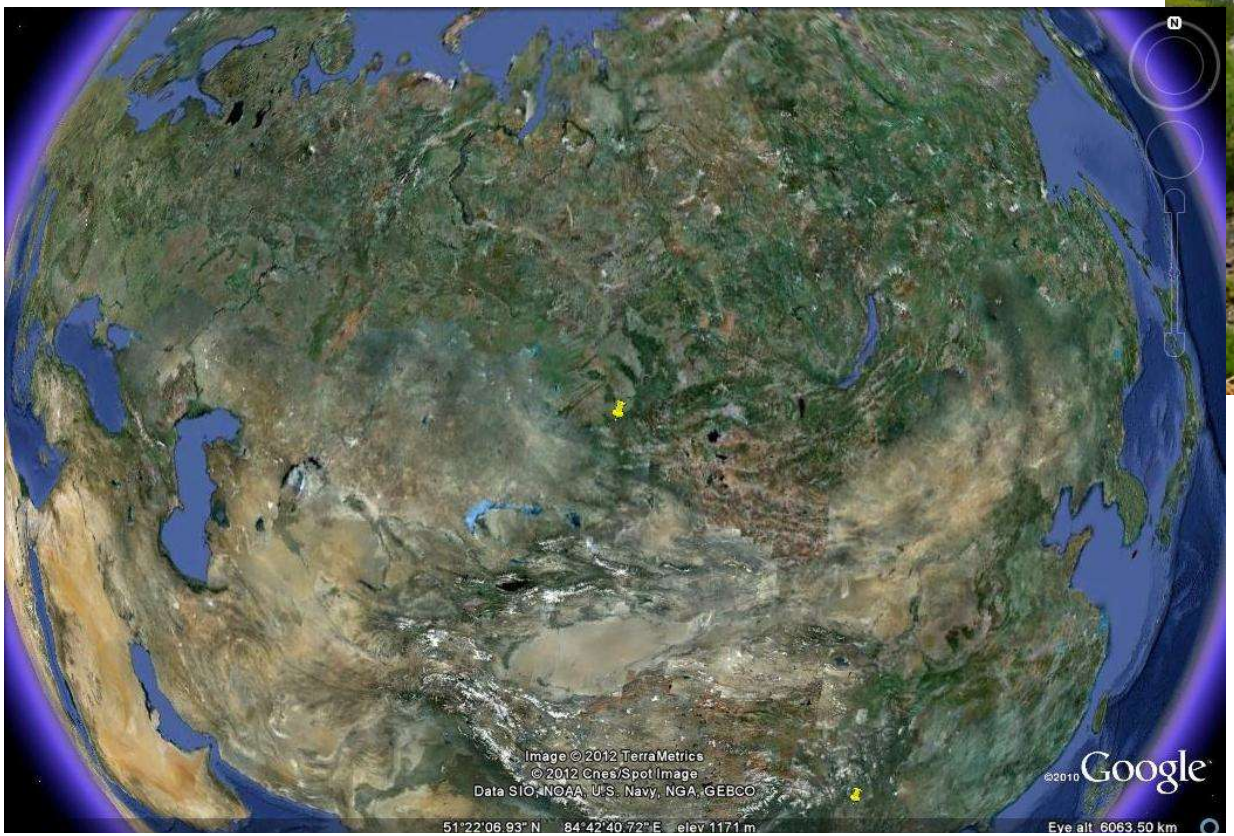

Denisova Cave

- Denis's cave – a former hermit residence
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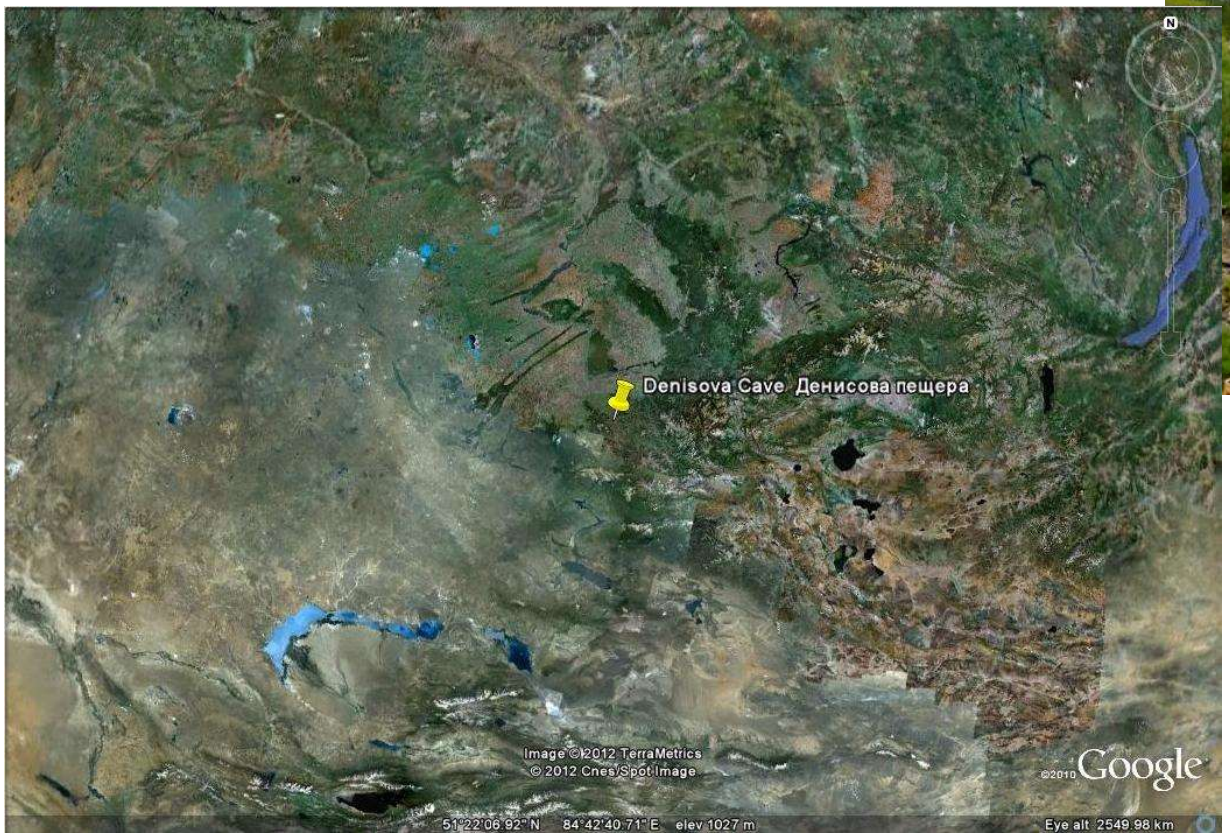

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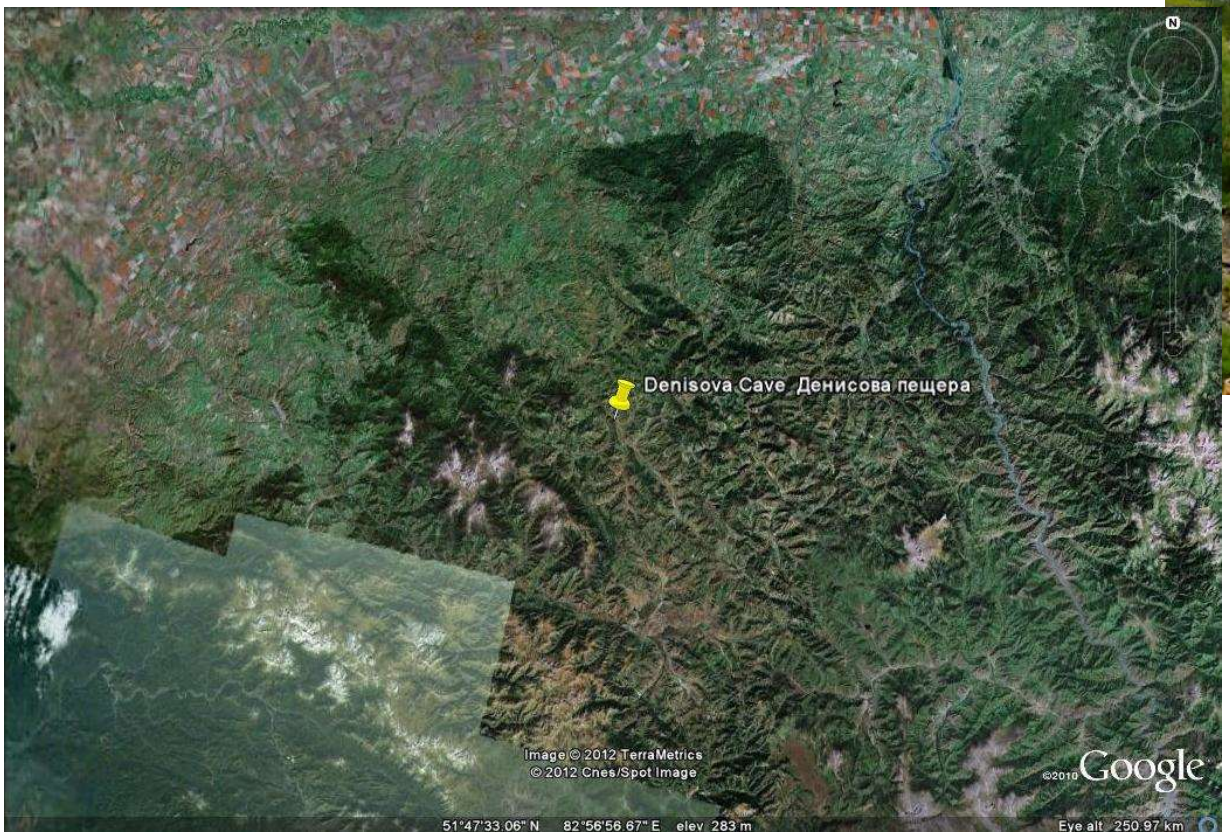

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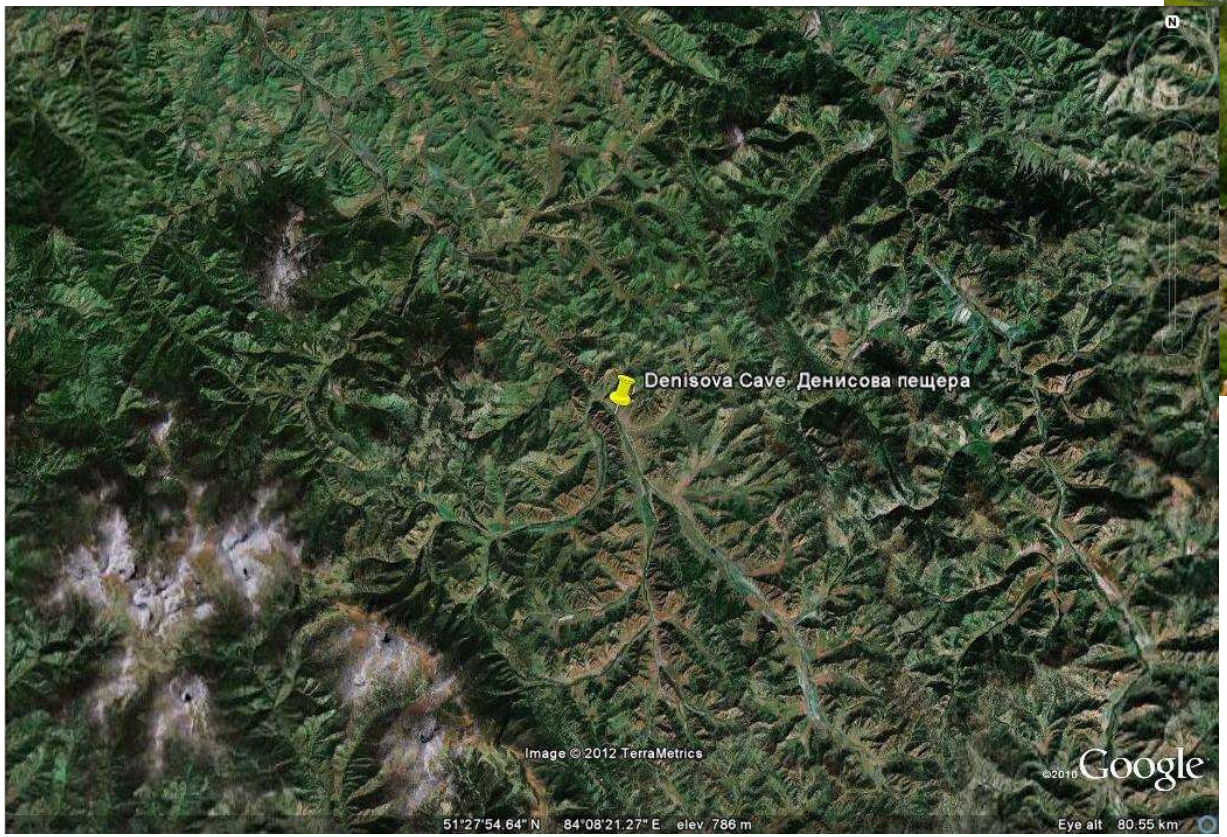

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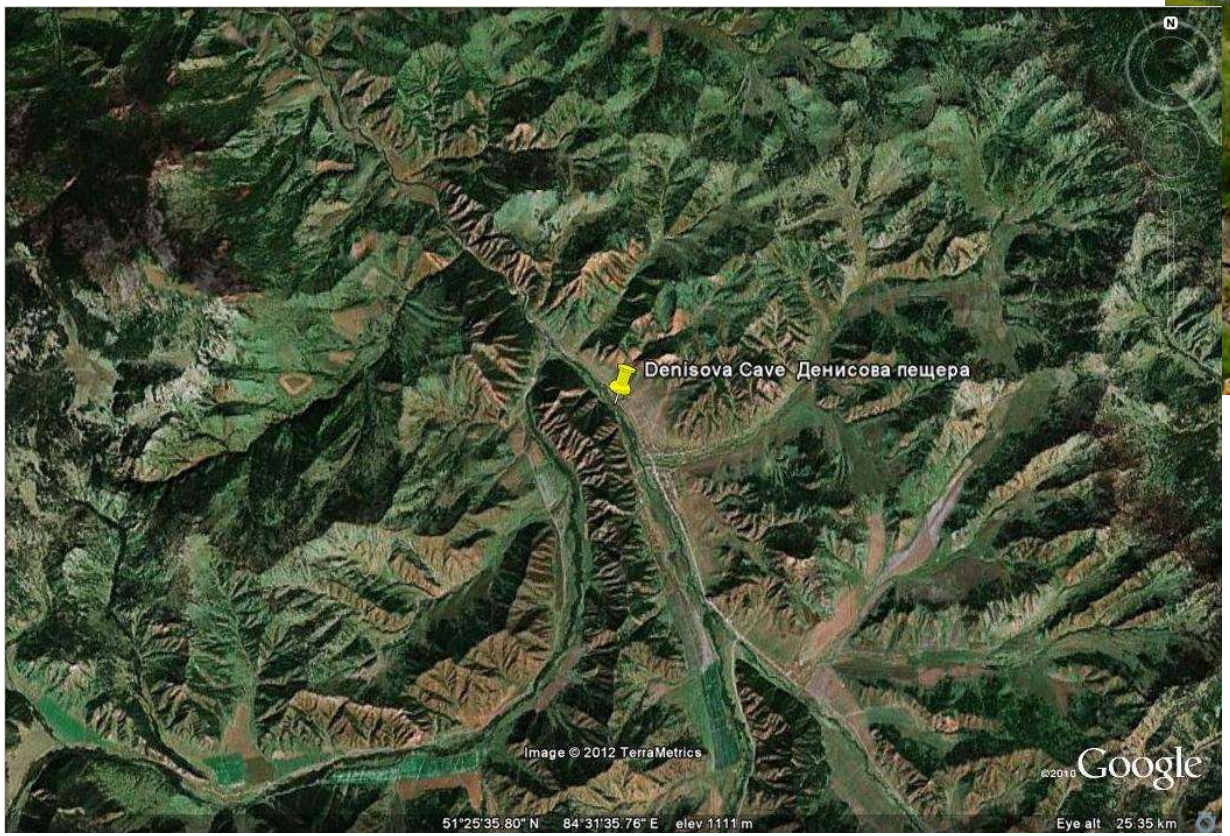


580 km north of Asia's Pole of Inaccessibility

Denisova Cave

- First occupied from 125,000 -180,000 BP
- Original announcement : Human remains from a later 1m thick layer, dated 30,000 to & 48,000 BP
  - Child's phalanx sliver – mtDNA, on later nuclear DNA – **female**

  - Wisdom tooth - described as non-Neanderthal in shape – mtDNA and some nuclear DNA extracted
  - Another molar, Toe bone Neanderthal(?)

Denisova Cave

2015 Announcement:

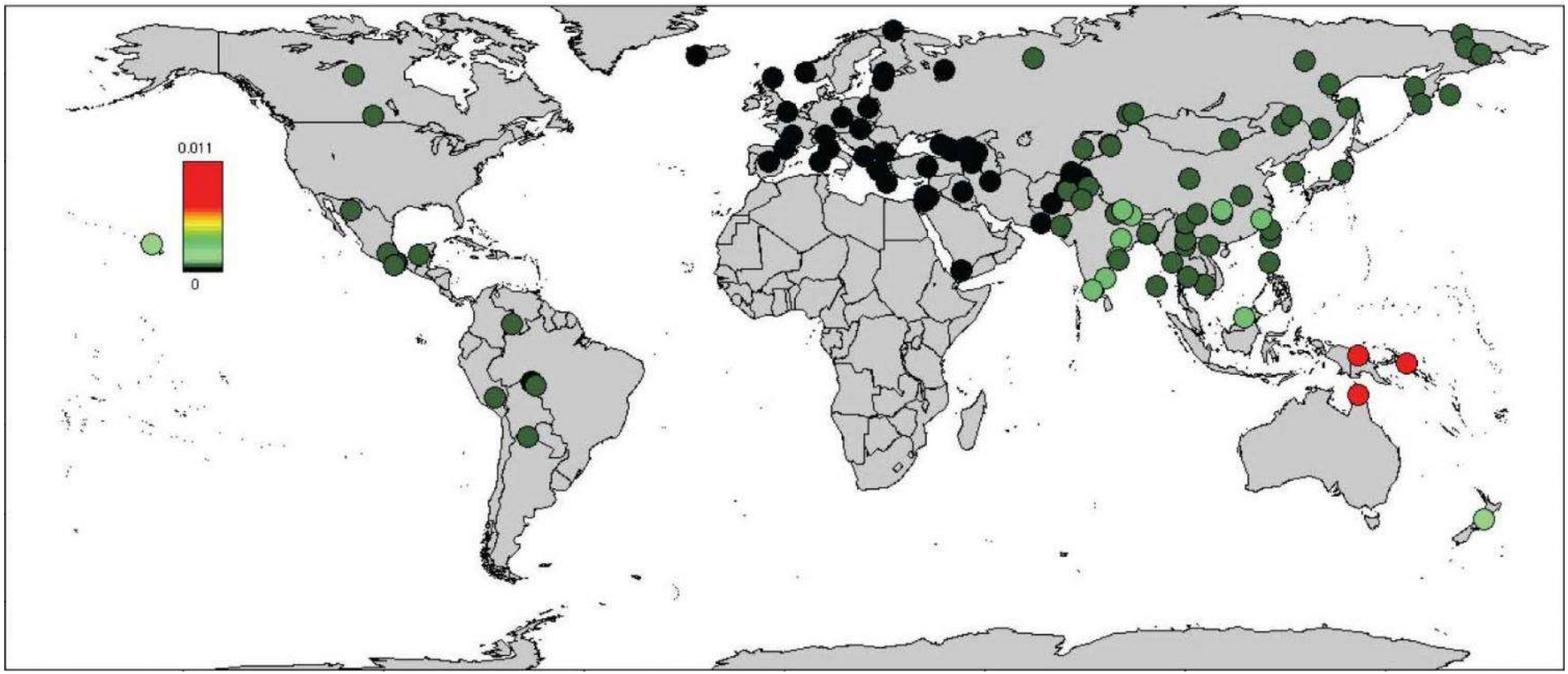
- More teeth and bones sequenced
- Some are Neanderthal on their DNA
- The Denisovans are very varied on their DNA – more than Neanderthals anywhere
- Denisovans and Neanderthal seem to have been users of the site over a long period - ? Alternate ? Or are we confused ?
- The individual Denisovan remains have been put onto a family tree by their DNA
- Now some time depth is apparent on the Denisovan DNA
- Tom Higham has now dated the site using C14.
- The layer the ‘pinkie girl’ is from is now known to be beyond the ~50K years ago limit of C14 – perhaps only just
- Two older Denisovans estimated at between 110K and 170K years ago

Denisova Cave

2016 Announcement:

- The Neanderthal female from the cave has an admixture of modern human DNA

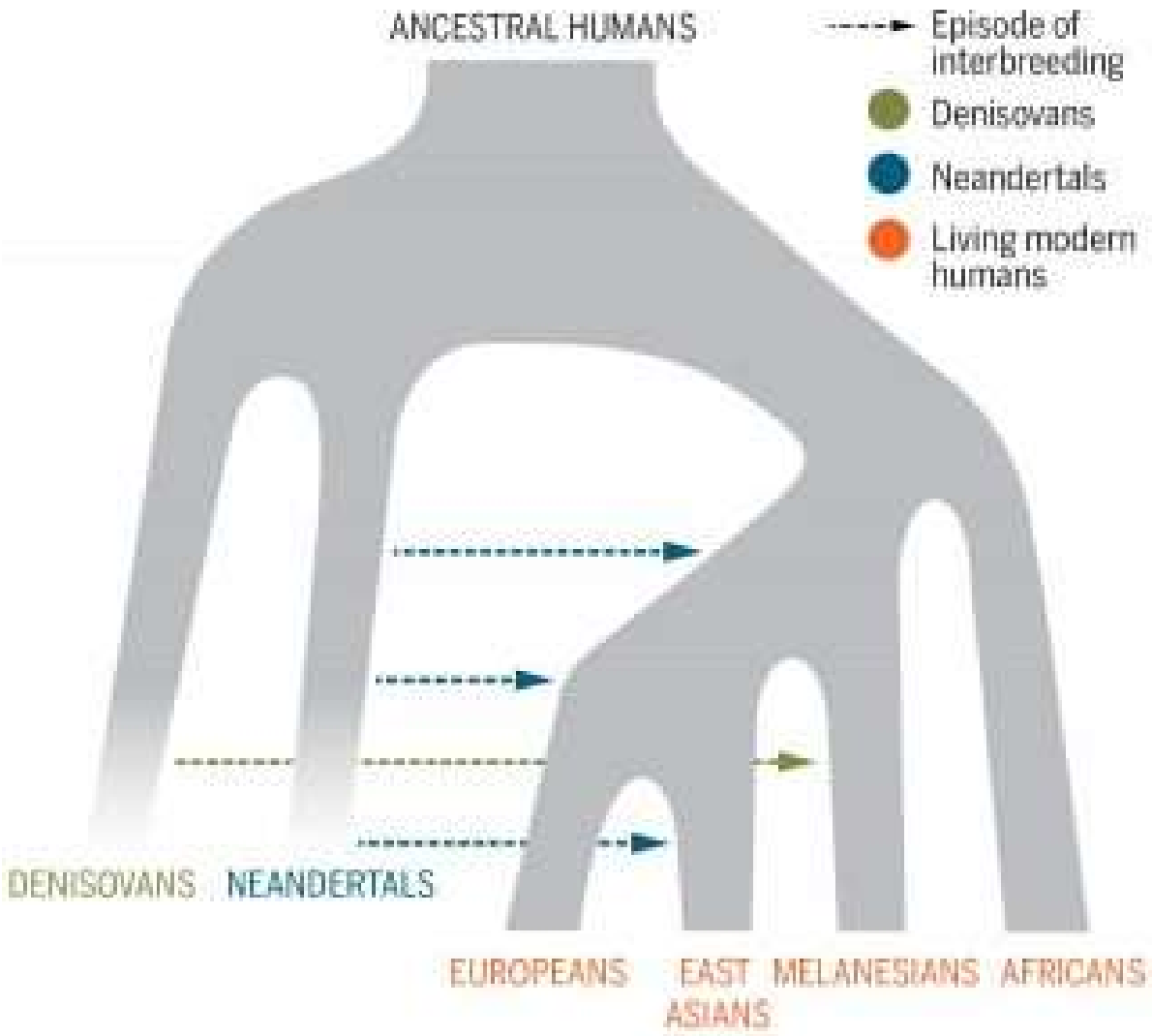
- Incorporating the Denisovan example in a history is particularly problematic
- We cannot relate its physical form to other fossil or modern man because it is unknown – It is a genotype without a phenotype.
- Denisovans are most closely related to Neanderthals but the divergence is ancient, close to the *H. sapiens* – Neanderthal divergence



Proportion of Denisovan Inheritance in current indigenous populations

Mixing it up in the Pleistocene

After the ancestral population of humans divided, modern and archaic people mated several times (arrows), likely on different continents. Three encounters with Neandertals left DNA in living people, and Denisovans mated with the ancestors of today's Melanesians.



2016 Update

Notes:

- On nuclear DNA
- No diagram date scale, text says ~60,000 years to oldest mating
- Relative date order OK but any date absolutes are estimates
- East Asians, Melanesians and Africans comparators are all modern DNA
- Where is unknown
- No certainty that Denisovans and Neandethals are the only extinct human lines

What is Known

	Neanderthal	Denisovan	Modern
Geographic Range	Known - but	Little Known	Known
Time Range	Known	Little Known	Patchy
Phenotype	Known	Totally unknown	Known
Genetic Diversity	Little known	Very little known	Known
Genome Completeness	Substantial for late individuals	Nearing full for individual bone fragments	Full – an expanding range of individuals
Phenotype – Genotype link	Yes – but The Pit of Bones old individual suggests it is problematic	Not known	Yes at general level – expanding quickly in detail
Phenotype – Material culture link	Yes	Not known	Patchy-

Introgression

First generation is a 50/50 mix on autosomal DNA

Is a genetic marker permanent once it happens?

No:

- If the 50/50 individuals are in a larger breeding population the intruding DNA contribution will quickly get diluted
- In small populations random loss can remove some DNA sequences
- Disadvantageous genes can be selected against – to the point of loss (also the reverse)

Individually non-Africans may only have a couple of percent (1-4%) but collectively 20% of the Neanderthal genome survives in non-Africans.

The early Romanian modern individual with higher Neanderthal content shows the reduction in process.

Surprising absences: 1?

Neanderthal DNA

- **No modern male has yet been found to have a Neanderthal derived Y chromosome** – if the introgression to *sapiens* came from male Neanderthals their all male line appears to be extinct – they has only female descendants. Hybrid male infertility is likely given the long species separation
- **No modern person has yet been found with Neanderthal derived mtDNA** – if the introgression into *sapiens* came from female Neanderthals then their all female line appears to be extinct. Perhaps their mtDNA was selected against.
- Don't know which introgression applied - ?or maybe both.
- Accidental loss of Y and mtDNA is quite likely if they are at a low frequency in small populations, unless there is very high population growth.
- **Modern X chromosomes have no Neanderthal content -** it appears to have been strongly selected against.

Surprising absences: 2?

Denisovan DNA

- No reports of Denisovan derived mtDNA in moderns
- Don't yet have any Denisovan Y so can't tell if that survives Hybrid male infertility is likely to be a factor here too.

Denisovan / Neanderthal Interbreeding?

- Not enough examples of Denisovans yet
- Shared Eurasia for a long time and certainly overlapped in space within it
- While the Denisovans were distinct at the point of time where we have found them - gene flow between the two is possible even likely over much of the time of their shared occupation of Eurasia

Unknown Others that might have been Inter-fertile

- There may be other varieties of hominin in Eurasia we have not yet identified e.g. the ancestors of the Homo florensis

Now that modern human autosomal DNA has been found in Neanderthals we can also anticipate looking for:

- Modern human Y chromosome in Neanderthals
- Modern human mtDNA in Neanderthals

But the same high likelihood of loss also applies here.

"They're really terrible-quality genomes", chock-full of gaps and errors and sections in which short stretches of DNA sequence have been put in the wrong place, ..."

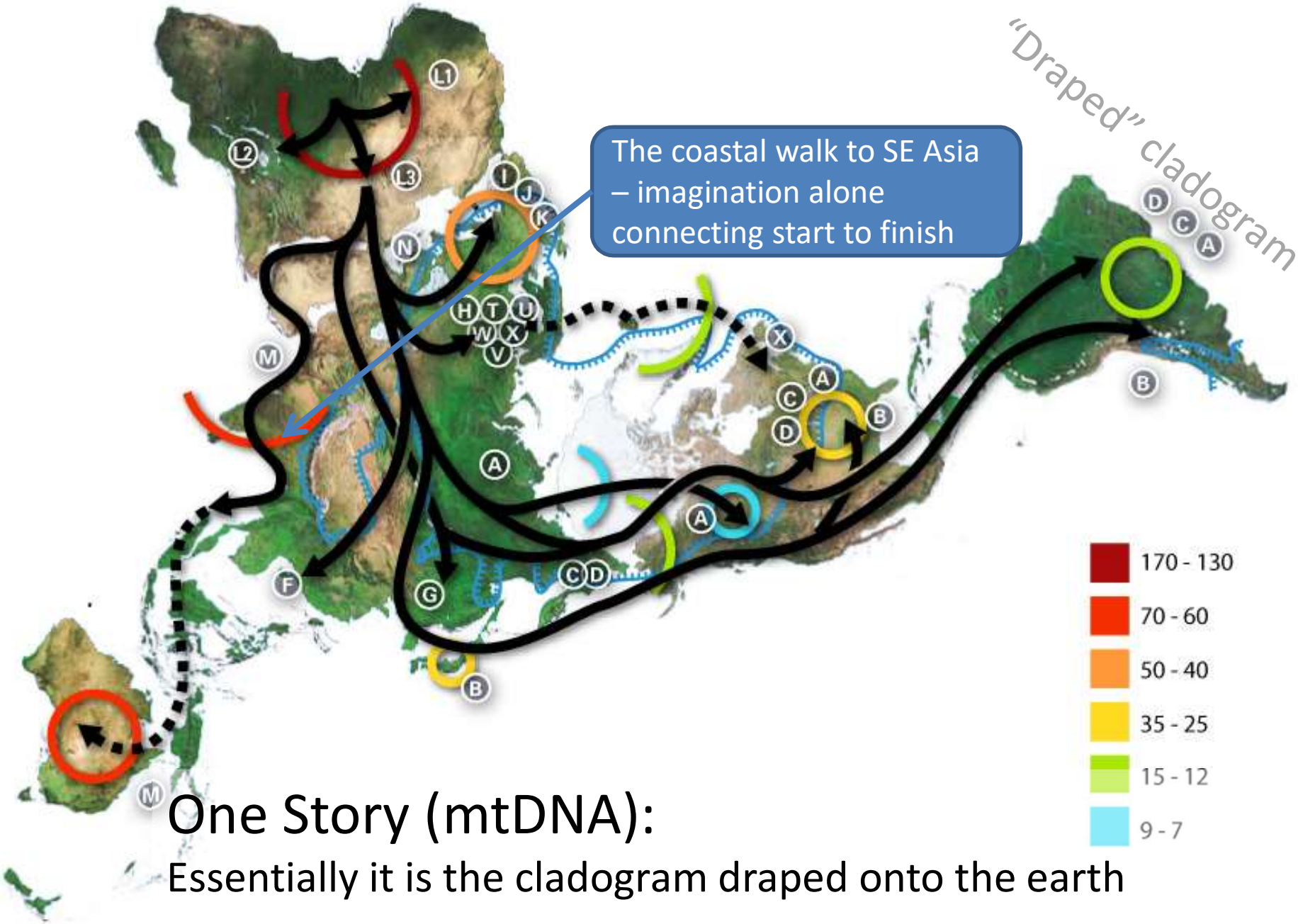
David Reich, principal author of *Genetic history of an archaic hominin group from Denisova Cave in Siberia*, Nature.

Is this a fragile basis on which to write history?

Back to Kuhnian ideas

- Normal science – between paradigm shifts – science is making small steps around confirming the current paradigm
- During shifts – crisis and chaotic change of ideas

We certainly seem to be experiencing the latter



One Story (mtDNA):

Essentially it is the cladogram draped onto the earth

True?

According to this:

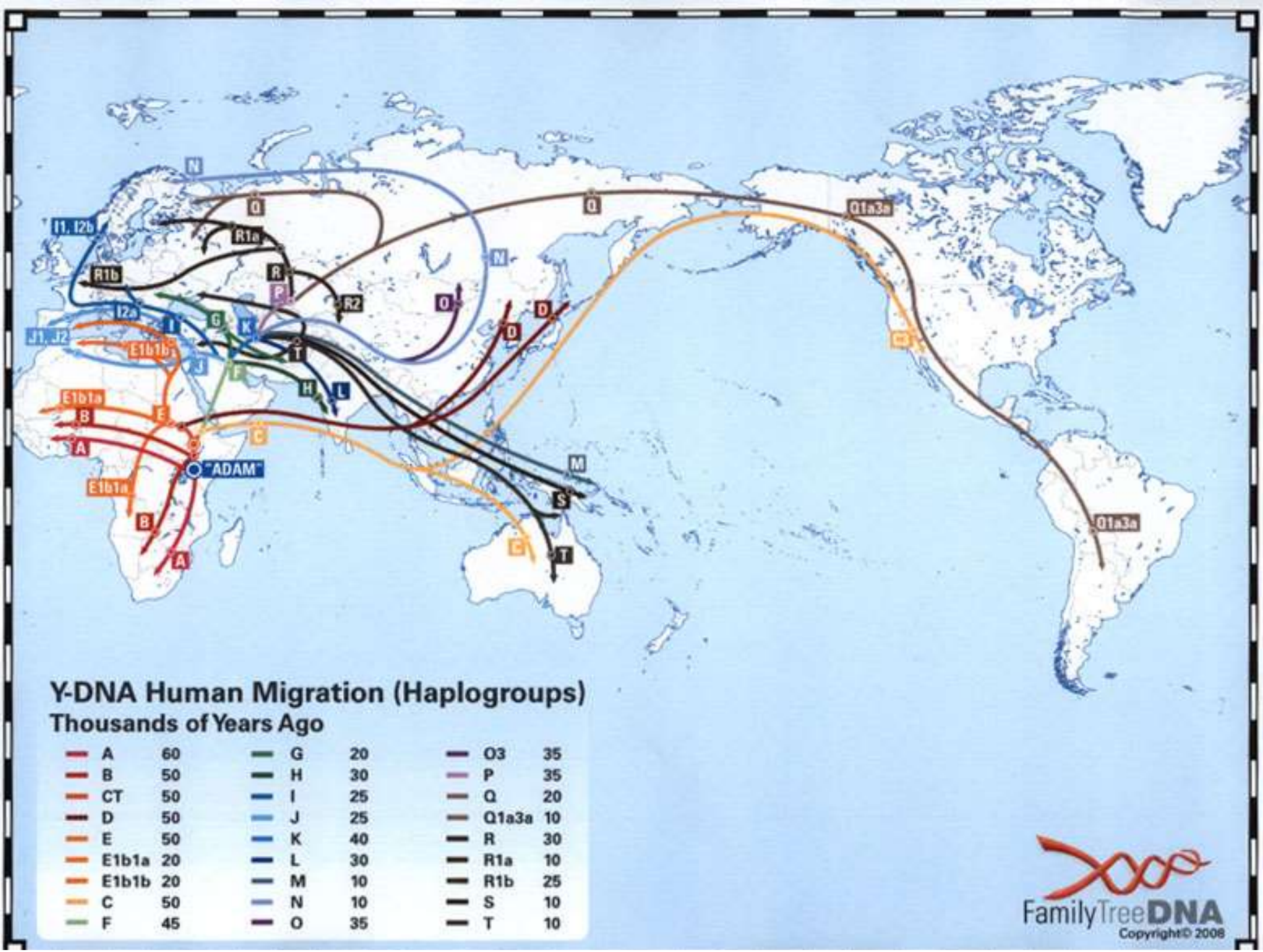
- Hapologroup M went on a trip to Asia
- Haplogroup N went to Europe

- Now know from aDNA that up to 14,500 BP hoplogroup was the dominant mtDNA in modern looking European fossils.
- Replaced after that by haplogroup N

So aDNA has shown the draped cladograms may be quite wrong.

Maps of Migrations

- In the absence of ancient DNA these can only be from the cladograms of haplotypes that survived.
- Ages have been attributed to the branches but they have been changing as better methods have been developed
- Some mtDNA and Y innovations have been assigned ancestral names
- Some can't resist turning these into migration maps
- They are often presented as incontrovertible
- Yet there is considerable diversity in what is concluded



Y-DNA Human Migration (Haplogroups)

Thousands of Years Ago

A	60	G	20	O3	35
B	50	H	30	P	35
CT	50	I	25	Q	20
D	50	J	25	Q1a3a	10
E	50	K	40	R	30
E1b1a	20	L	30	R1a	10
E1b1b	20	M	10	R1b	25
C	50	N	10	S	10
F	45	O	35	T	10

FamilyTreeDNA

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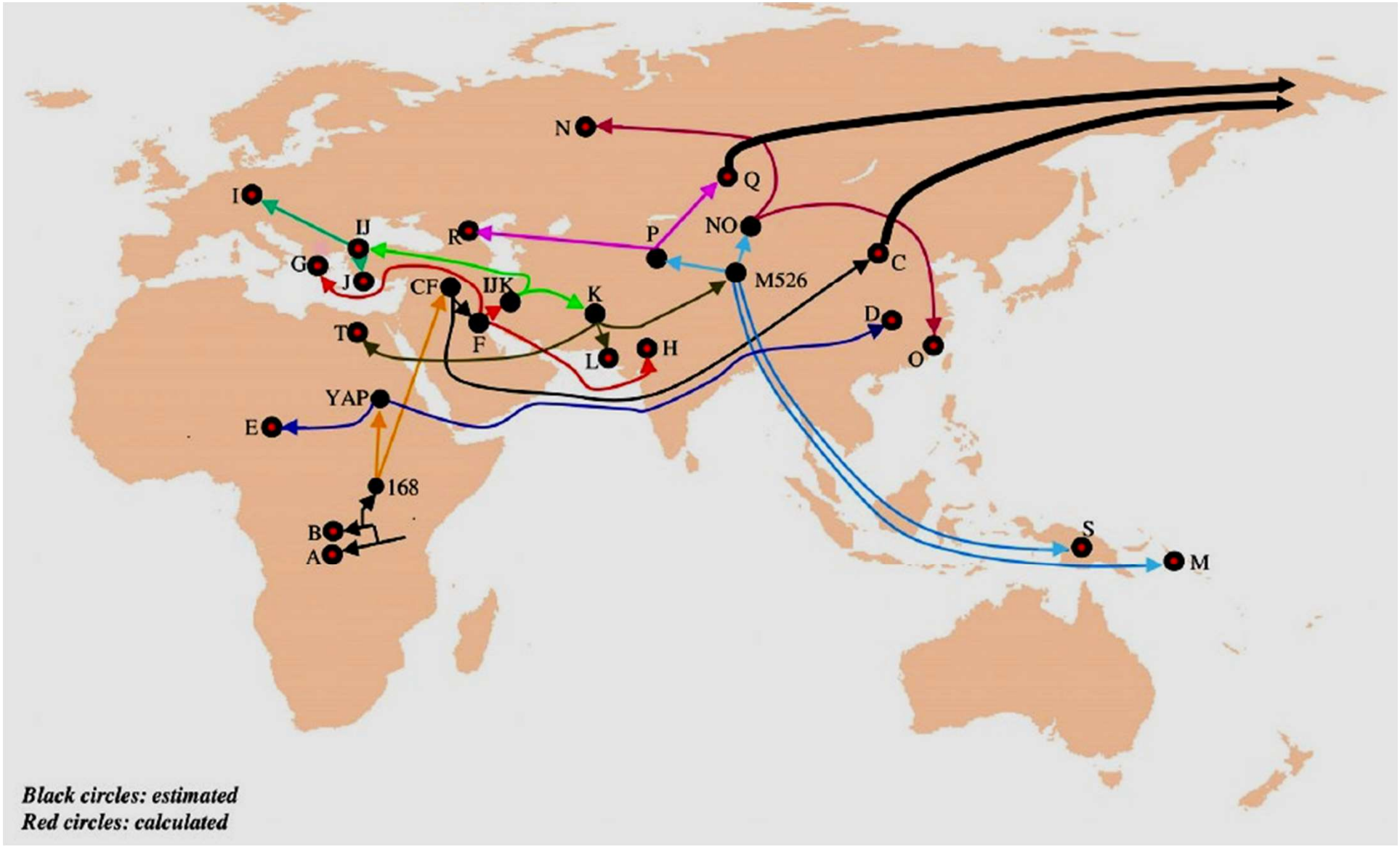
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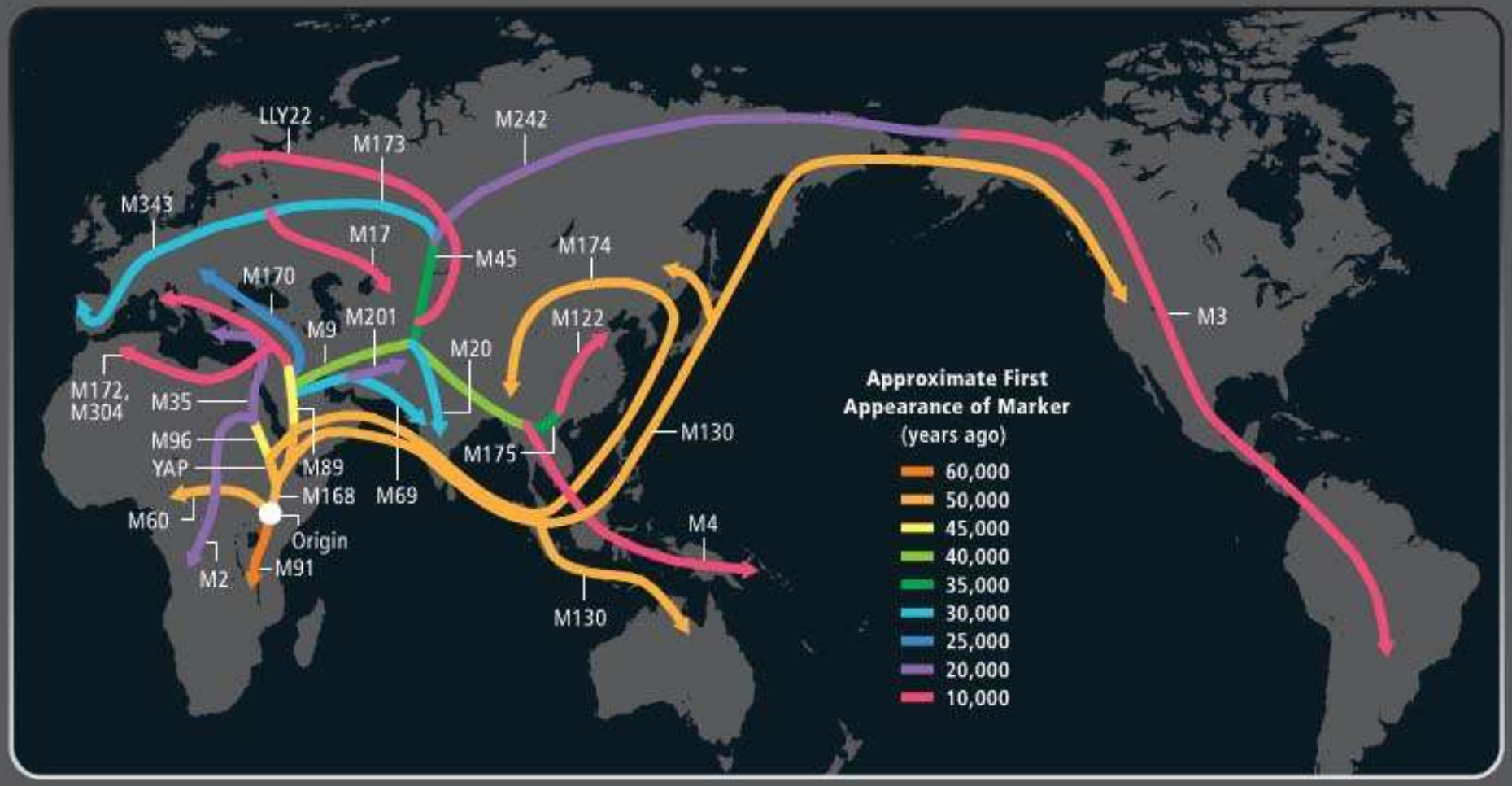
Black circles: estimated
Red circles: calculated

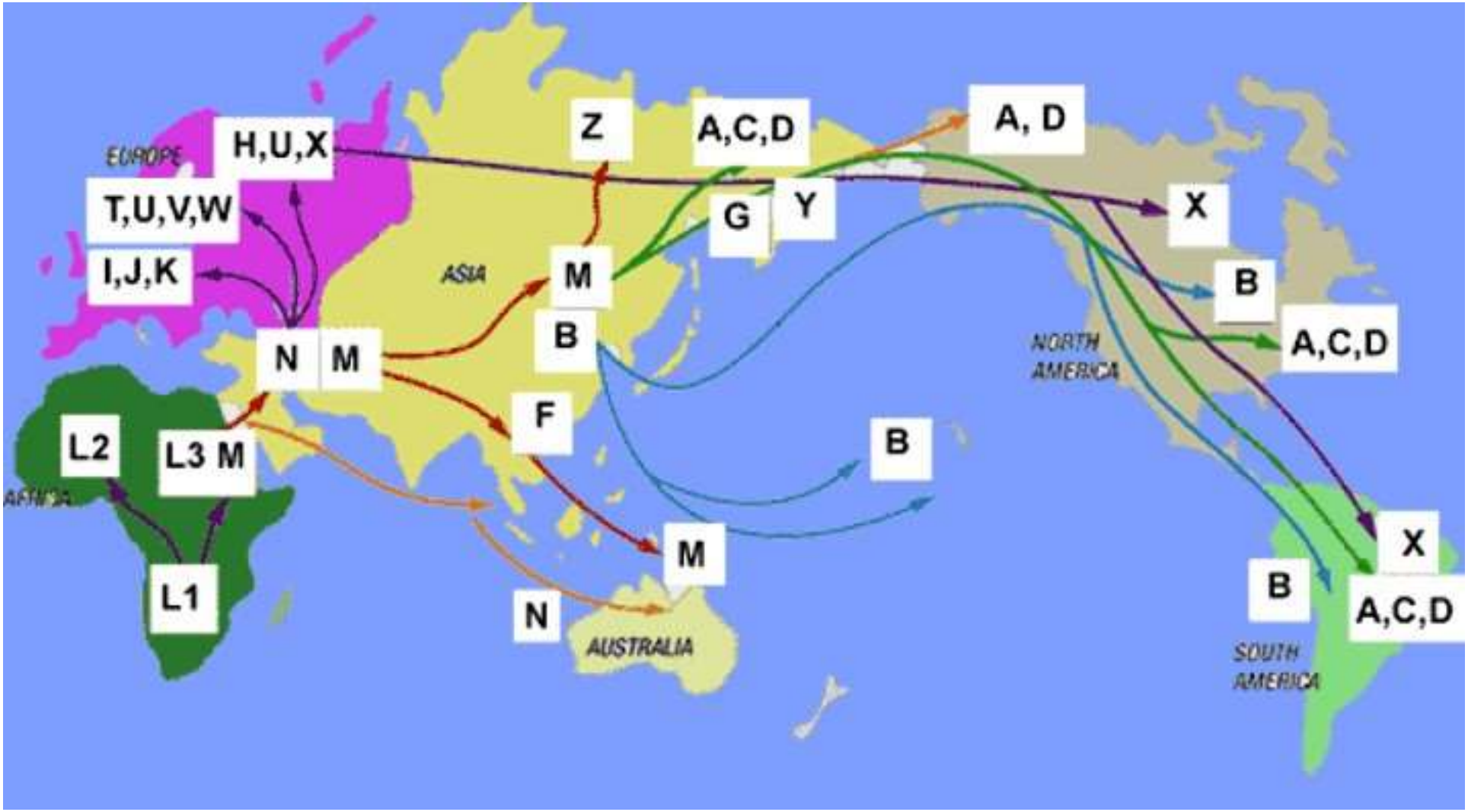
Y - DNA

TRACKING Y CHROMOSOMES THROUGH TIME

Geneticists can track the path of ancient migrations by examining genetic markers in Y chromosomes from men who hail from different parts of the world. Each marker, such as M168 or M89, identifies a lineage of men and where the lineage originated. By building an evolutionary tree based on observing many living people with the markers, investigators can determine the approximate ages of the lineages.

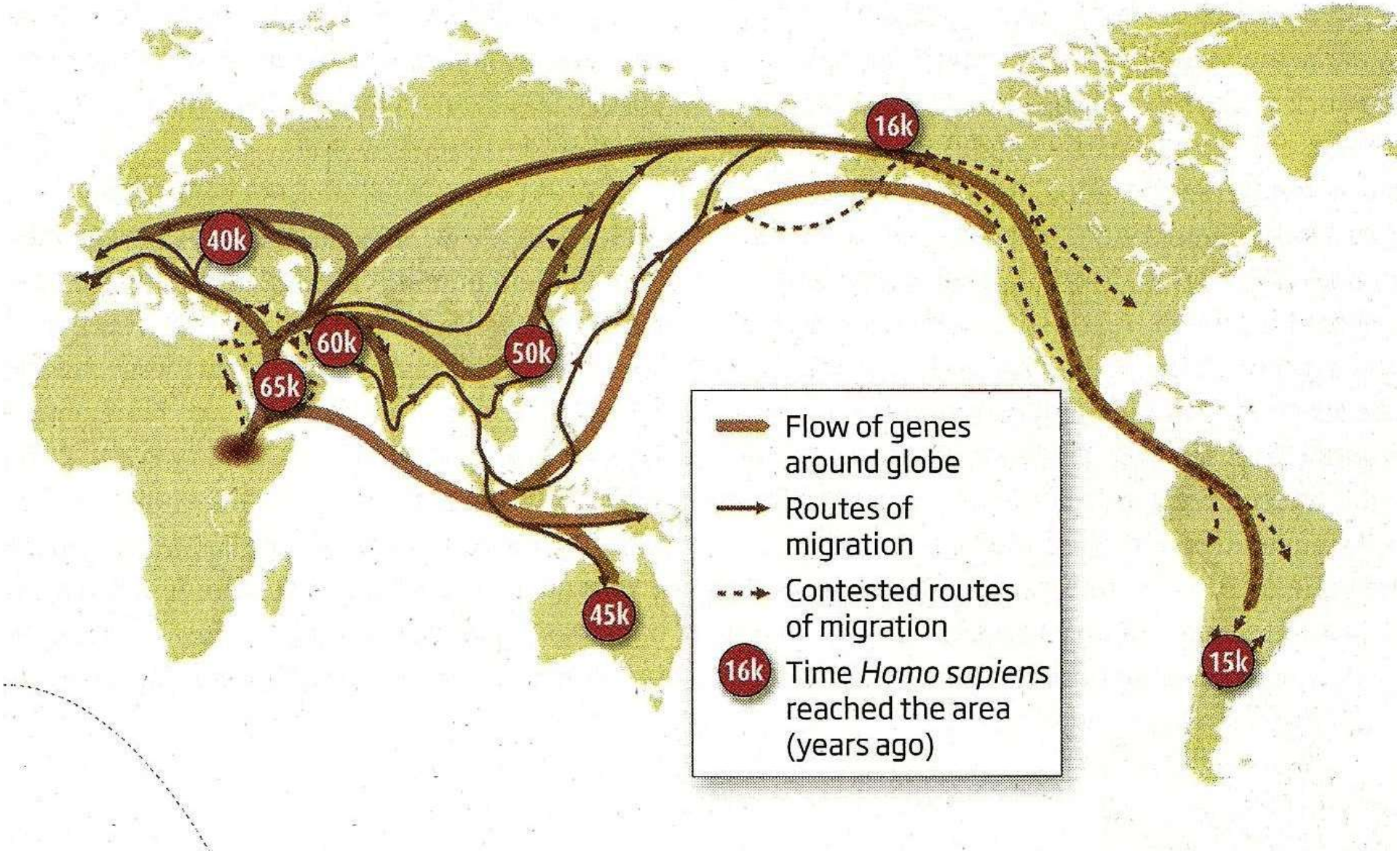


By replacement markers



Y - DNA

Credit this one with showing that some moved together.



Genes moving other than with migrants?

- The maps show the supposed travels of individual Y chromosome / mtDNA forms.
- But pre-modern populations were haplo-diverse.
- There is no reason to believe most ancient populations were not haplo-diverse to at least some extent.
- The migrations are almost exclusively uni-directional, often “shortest route” and sometimes favour some other hypothesis.

- Populations settled the earth, not chemical fragments alone.

  e.g. The Smiths and the Jones got to NZ from Britain fundamentally as part of a colonising movement, not as a migration of all the Smiths and a separate migration of all the Jones.
- Mostly unidirectional whereas modern history says not
- Mostly no basis in Ancient DNA to establish when and where

- Maps showing migrations of individual bits of DNA have to be very suspect.

What we are presented with as maps of movement of people comprehensively lack *place* reference points.

and often work on relative rather than absolute *time* reference points.

Remember the base geographic data of modern populations is not incontrovertible.

Your DNA - How many ancestors?

generations ago	1	10	20	30	40
years ago	25	250	500	750	1000
Ancestors (max)	2	1,024	1,048,576	1,073,741,824	1,099,511,627,776
Europe Population			120,000,000	70,000,000	34,000,000
ratio “ancestors” to population 1 to			**0.009**	**15**	**32,000**

Genealogist quote – ‘probably everyone in western Europe is a descendant of William the Conqueror’

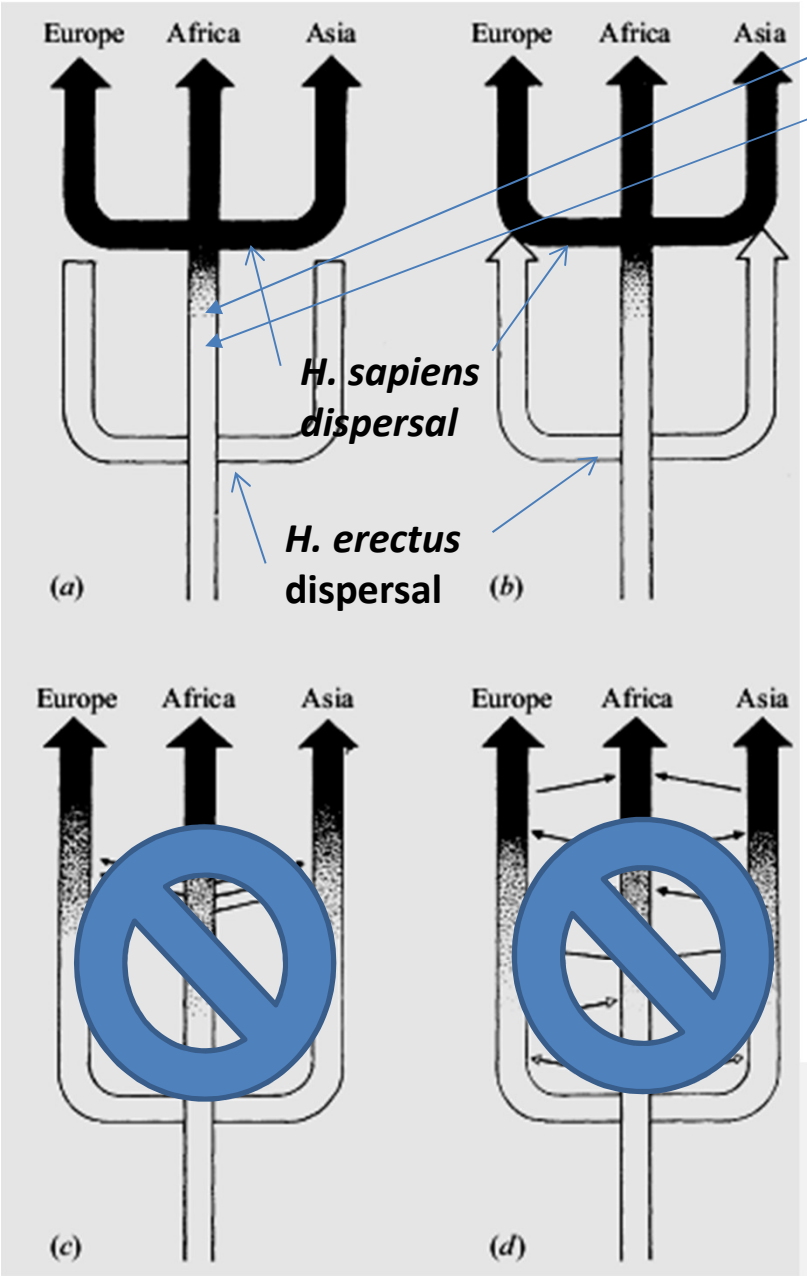
For that matter they are all likely to be descendants of everyone alive at that point in time, that is those who have descendants.

What value are individual DNA determinations?

- To you genealogically - on Y-DNA and mtDNA very little value – tells you about an infinitesimal part of your genetic inheritance
- To you - on tested markers on autosomal DNA – may give info on your propensity to disease
- To paleoanthropologists - if you can be included in a geographic population of some historical integrity – of considerable historical interest
- To the firm that provides the service – the potential to sell information to parties interested in the health of you and your close relatives.

Not all modern humans from migration from Africa?

- The fossil based view of human history retained a school that thought modern humans had some ancestral relationships to regional fossil pre-*sapiens* forms, but acknowledged gene flow as central or important.
- Post “Eve” they were dismissed by some geneticists as not only wrong, but racist.
- Suddenly with the new cross-breeding idea it is all alive again?



mtDNA "Eve"

Y Chromosome "Adam"

An early result from DNA analysis of modern people was that we all share common ancestors of quite recent origin 100K – 200K years.

This excludes (c) and (d) as alternatives.

Figure 2. Evolutionary models of modern human origins (modified from Aiello 1993). (*a*) Recent African Origin; (*b*) (African) Hybridization and Replacement Model; (*c*) Assimilation Model; (*d*) Multiregional Evolution.

Stringer 2002

Some Geneticist Quotes:

- “The journey of modern humans started when our ancestors left Africa”
- “Interbreeding (outside Africa with non-*sapiens* - GL) endowed humans with a 'hybrid vigour' that helped them colonize the world”

Put on an African hat and consider these – who’s racist now?

Is the new evidence of diversity with apparent time depth (the cross-breeding stories within and beyond Africa) fully reconcilable with "Eve"?

How is it the story is changing so rapidly?

The simple answer must be the story is not settled.

Paleo-anthropology is in the throes of a revolution brought on by DNA

- There have been some stunning and significant developments using DNA – but they are surely not finished
- The ancestry industry is selling their stories as certainty - where the reality is they are not
- The scientific news stories often simplify, don’t report uncertainty and sometimes misunderstand

END