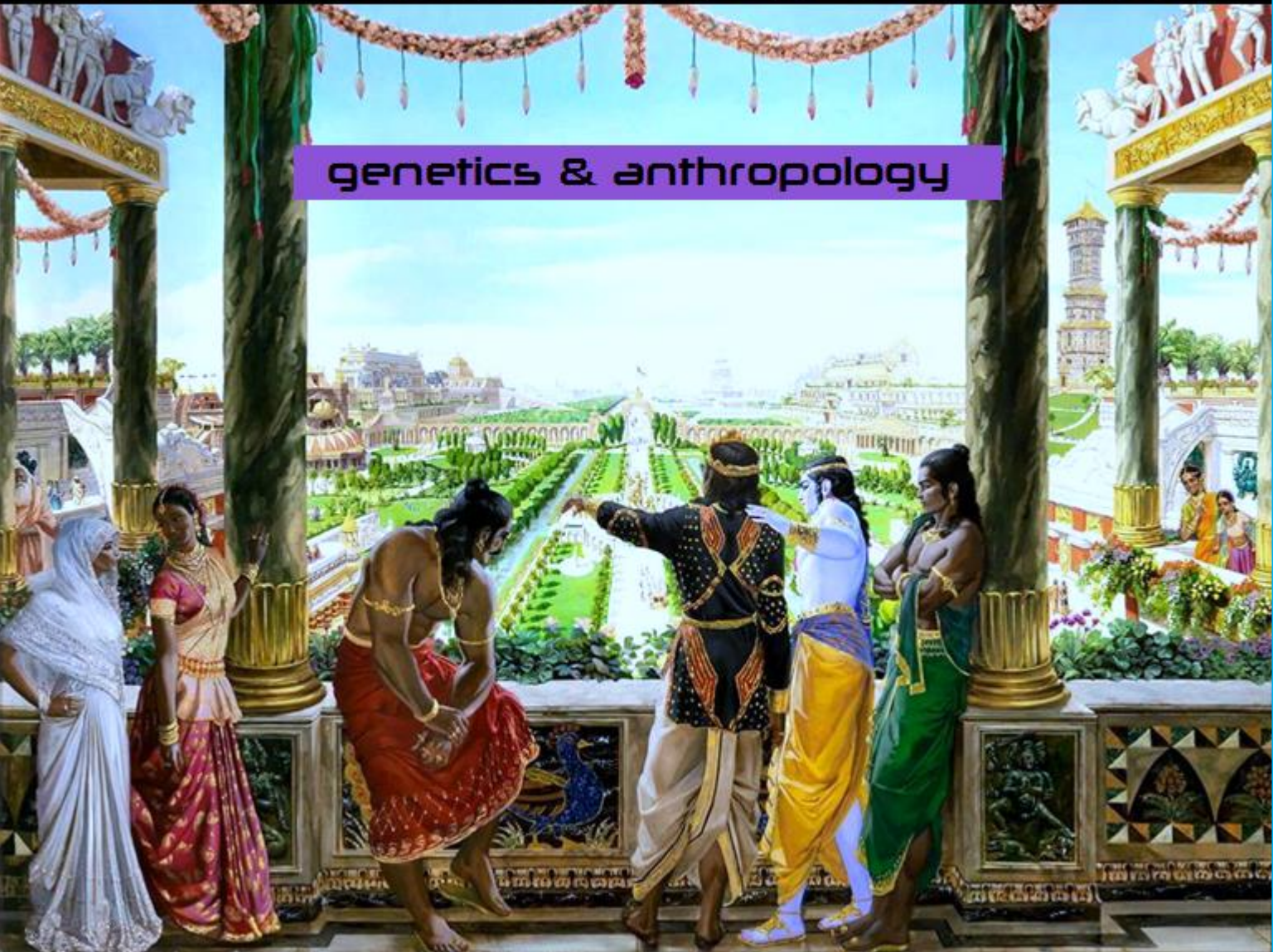
ARYAN INVASION DEBUNKING



Preface

Compiled. illustrated and written by

vedic civilization

Contact : vediccivilization58@gmail.com

INTRODUCTION

Aryan Invasion-Migration Theory states that 1500-1200 BCE white Europeans (Aryans) came into North India from steppes (grasslands) of central Asia and defeated and forced ethnic Dravidians to the south India and imposed their culture on them. Later Aryans got mixed with Dravidians to form prsent day Indians.

This theory was invented by Britishers and their agents in order to psychologically subvert Indians. Early Indologists wanted to convert Indians but later releasing that was impossible resorted to claim that their culture came from a foreign land. Despite having anamolies and evidence that points in opposite direction that Vedic culture influenced various civilizations. the white supremacists (zionist agents or misgided people) still propagate this theory.

Not only that in their arrogance they try to claim as orginators of all civilizations : Indus-Sarawati (Vedic) civilization. Sumerian civilization. Egyptian civilization. Chinese civilization. etc.

The so-called Aryanists are not the followers of any culture or religion of the civilizations they claim to be the part of and don't have the basic understanding of the civilizations they are talking about.

Hence their main attempt is to mix all other culture to Christianity (Jewsish religion).

Aryan Invasion-Migration Theory is nothing but a white man's quest for identity and certainly a misguided one.

What people don't understand civilization is not a part European culture they are tribals or nomads who practice Paganism (offshoot European version of Hinduism).

They consider genetics to be the backbone of this theory. So I will try to analyze the genetic claims.

BASICS OF GENETIC GENEALOGY

It is necessary for everyone to first learn get a basic knowledge of genetics in order to properly understand the arguments being discussed in this book.

Genetic Genealogy : Use of DNA testing and traditional genealogical methods (historical records etc.) to find relationships between individuals and their ancestory.

Genetics is the study of heredity - the expression of traits and how they are passed from generations to generations.

The factors that influence the expression of traits are Genes.

Each human has 20000-25000 genes and this collection is called Genome.

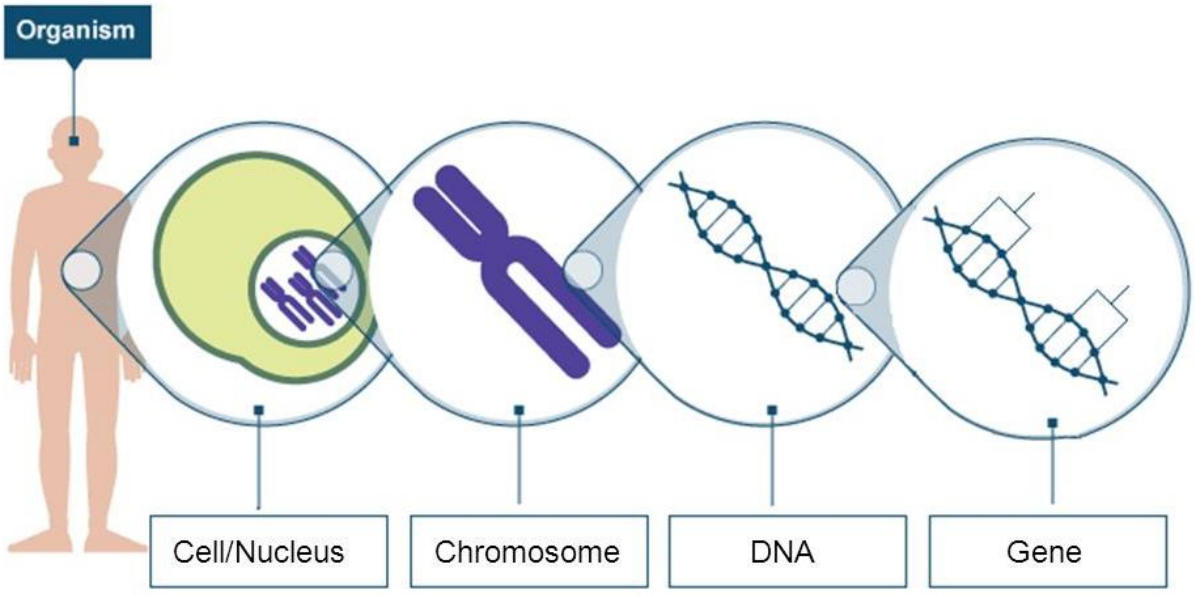
This determines a person's espression of traits on a cellular level.

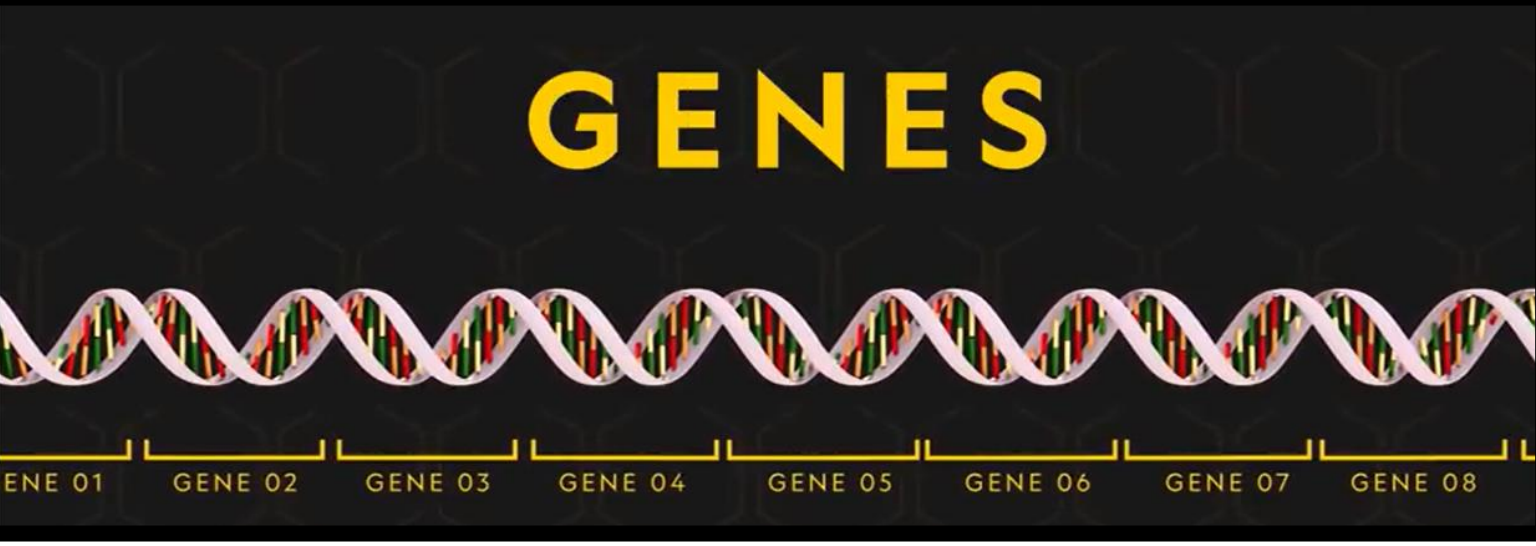
Genetic information is stored in a cell's nucleus.

The structures (inside nucleus) called chromosomes carry this information in the form of DNA (Deoxyribo Nucleic Acid).

DNA is a double helix of nucleotides (chemical compounds composed of sugar and phosphate molecules) along with 4 bases - A (Adenine) T (Thyamine) G (Guanine) and C (Cytosine).

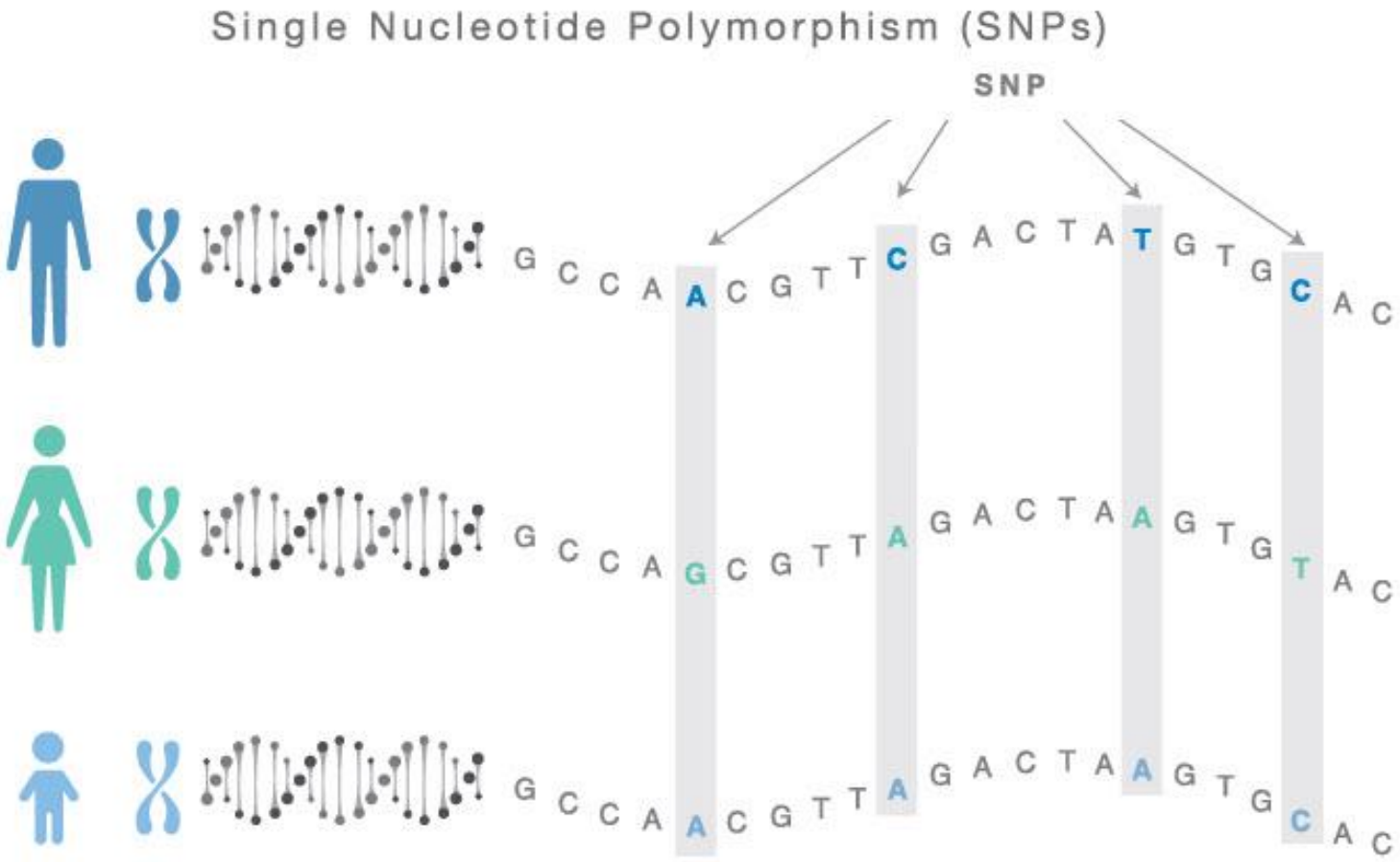
These segments of DNA are called Genes within which chemical compounds have all the coding required for a person's inherited traits.





Combination of any two bases out of 4 (ACTG) is called a base pair.

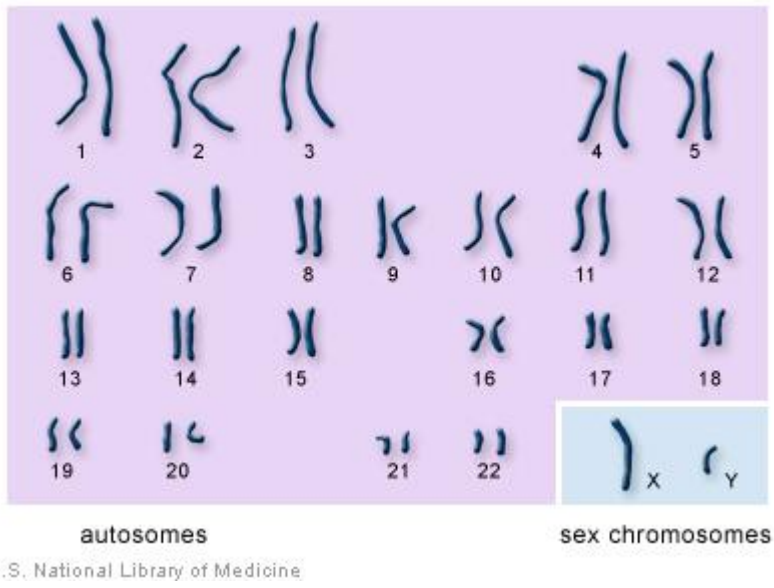
Single letter difference in base pairs in a DNA sequence leads to genetic variations is called SNP (Single Nucleotide Polymorphism).

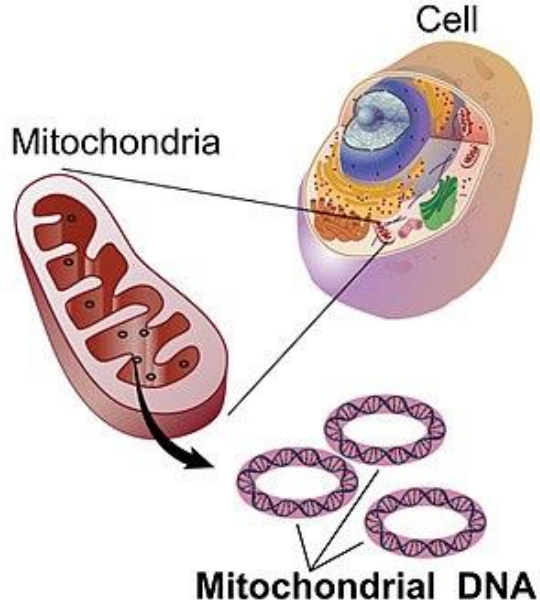


Each human has about 3 billion base pairs and 46 chromosomes (23 pairs). mtDNA is found in mitochondria.

Chromosome	Length (mm)	Base pairs	Chromosome	Length (mm)	Base pairs
1	85	249,250,621	14	36	107,349,540
2	83	243,199,373	15	35	102,531,392
3	67	198,022,430	16	31	90,354,753
4	65	191,154,276	17	28	81,195,210
5	62	180,915,260	18	27	78,077,248
6	58	171,115,067	19	20	59,128,983
7	54	159,138,663	20	21	63,025,520
8	50	146,364,022	21	16	48,129,895
9	48	141,213,431	22	17	51,304,566
10	46	135,534,747	X	53	155,270,560
11	46	135,006,516	Y	20	59,373,566
12	45	133,851,895	mtDNA	0.0054	16,569
13	39	115,169,878	total		3,095,693,981

22 pairs are similar and are called autosomes while 23rd pair is different (sex chromosomes). Females have 2 X chromosomes and males (1 Y and1 X chromosome)

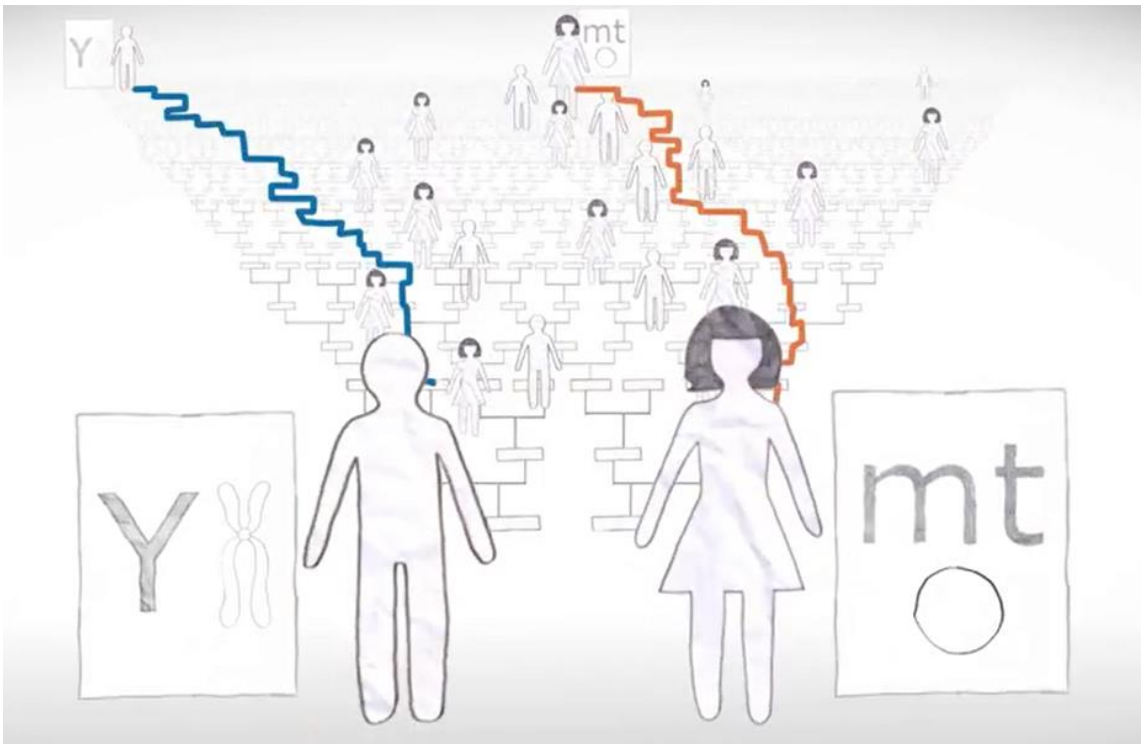




There are 2 main tests :

Y dna test which is passed down in males through Y chromosome (father to son)

X dna test & mtDNA test which passed down by females through mtDNA (mother to daughter). Also there is atDNA test which tries to find similarity of autosomes in both males and females.



The present day populations are combination of hundred of distinct groups of humans.

But later different mutations of DNA started to evolve due to a variety of factors like mating patterns (polygamy. monogamy. etc). geen-environment interaction. recombination process. racial endogamy. etc.

These mutations account for genetic (SNP) differences in humans of about 0.5 - 0.1 percent. All human are 99.5 - 99.9 percent genetically similar. However these minor differences do lead heavy aftereffects that are need to be studied.

Based on the above tests a haplogroup (a very specific new genetic mutation over time) is assigned to an individual.

If a haplogroup is born today it might only be detected hundreds or thousands of years from now when a significant portion of population is examined.

ETHNICITY FROM GENETICS
LIMITATONS OF DNA TESTING

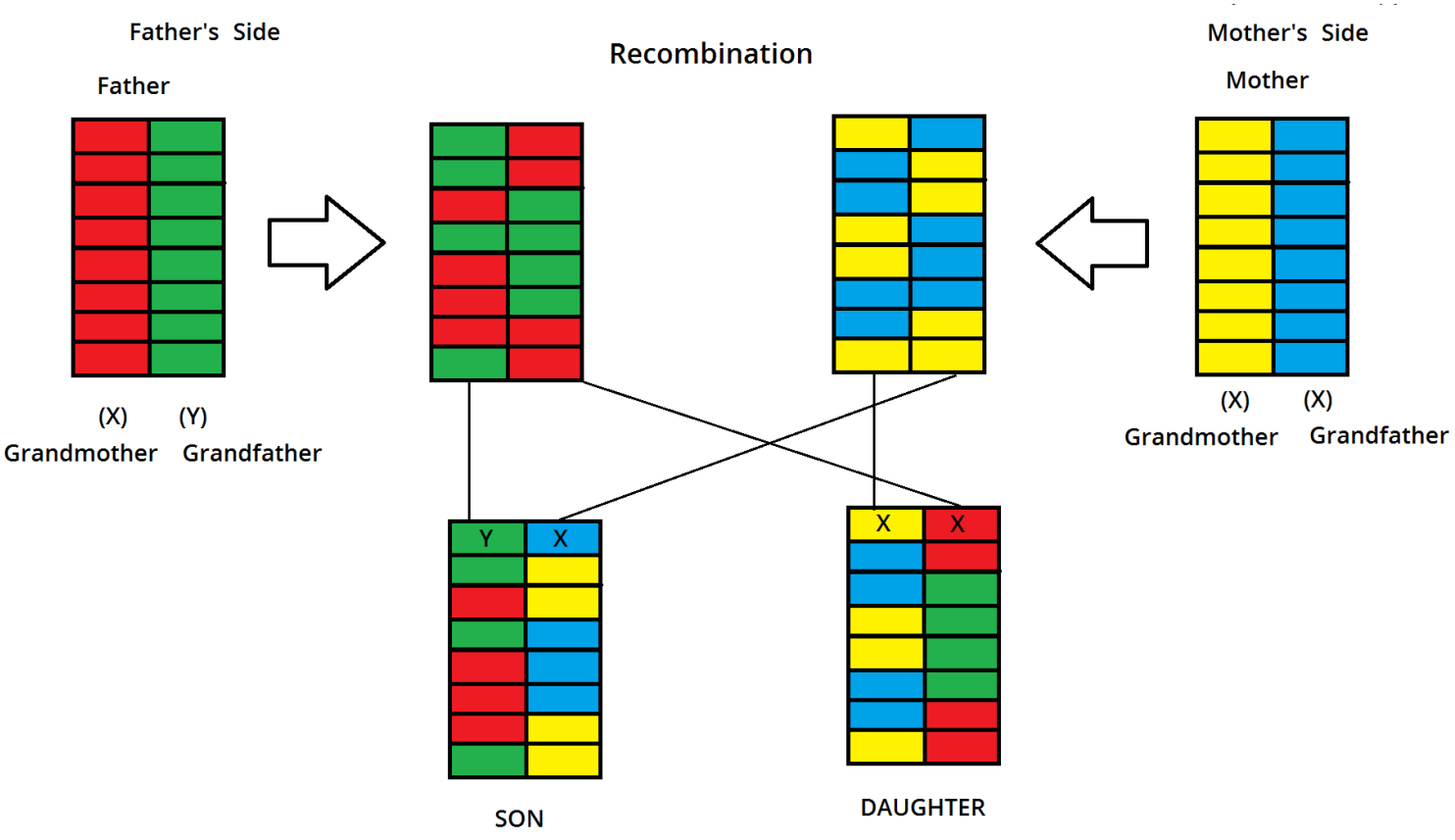
DNA DISAPPEARING

Through generations the DNA goes through a recombination process due to which chromosomes (from both mother and father) reshuffle (not chaotic) leading to new combination of acquired chromosomes.

Recombination process: Recombination of two chromosome sets acquired from parents (the amount of chromosomes from both mother and father remain equal).

e.g. If your Grandfather's second cousin DNA (parts of it) match with most of your Grandfather's DNA. it will match less with your father and even lesser with your DNA sequence and so on (given that your family is not inbreeding).

However similar parts of DNA may surface but it entirely dependent on probability. The genes that are hidden or having low probability to resurface are called recessive genes.



DOES NOT TELL ABOUT ORIGINS

You can be genealogically related to people but may not genetically-related. Our DNA is acquired from a very small subset of our ancestors. We can have many ancestors but we don't acquire their entire DNA but only a small fraction of it.

You didn't get all the DNA of your ancestors.

Theoretically.

Each person has two parents and those parents individually have two parents and so on. For generation n. you'll have 2^n ancestors (ancestor formula).

Limit 1 : We have 3 billion base pairs (800 years ago. 1200 years)

We cannot be related more than 3 billion people (in old times the population was even less). If we apply ancestor we will have about 4.2 billion ancestors (not possible).

Even if they were 3 billion we did not acquire entire DNA from each one of them. And given that 99.5 percent humans are indistinguishable genetically. We take out that part from 3 billion.

Limit 2 : We have 10 million SNP's. (600 years ago. 1400 A.D.)

10 million is 0.3 percent of DNA it falls within the limit that 0.5 percent is different and 99.5 is not.. But are we related to all of them (genetically).

Limit 3 : 25000 genes (400 years ago. 1600 A.D.)

A gene cannot be divided randomly but in codes. But

Limit 4 : Recombination Hotspots

When atDNA recombines and changes positions (hotspots). At these spots the probability of swapping (change of position) to occur is highest. And that limit is around 120.

Hence. in any given generation you'll have 120 ancestors (approximately) with whom you share DNA.

We may have more or less ancestors than that but it is definite that there must be a higher limit on the ancestors through which we acquire our DNA.

HALF RULE

Mathematically we share on average 50 percent of our DNA with our parent and 25 percent with Grandparents and by 9th generation your DNA share becomes 0.2 percent.

With each past generation our share of DNA is halved and the number of ancestors whom we don't share DNA starts increasing.

This also actually confuses people because humans do share 99.5 percent of similar DNA this may produce false matches (people with whom we are genetically related but not genealogically related). This range is about 7- 10 Centimorgan (length of genetic distance) and below this range false matches start to occur.

Centimorgan (cM) is the probability of recombination happening between two points on your DNA.

(Each company uses different cM for their calculations. Men have much lower genome than women.)

Generation	Genealogy ancestors	DNA Ancestors	% Related	Shared DNA %
1	2	2	100	50
2	4	4	100	25
3	8	8	100	12.5
4	16	16	100	6.25
5	32	32	94	3.25
6	64	64	81	1.62
7	128	120	69	0.78
8	256	120	48	0.39
9	512	120	20	0.19

Hence the longest (if not accurate) estimate for genetic genealogy to make is about 600 years.

SELECTION BIAS AND ETHNICITY ESTIMATE

To get your ethnicity results you are being compared to a reference database. To get a reference database people actually need to know where their grandparents are from.

DNA of a population in an area is measured and based on that DNA is assigned to a region. However. the problem is DNA results can vary if there are migrations in the past and DNA results (presently) can only account for a small time frame (say 600 years).

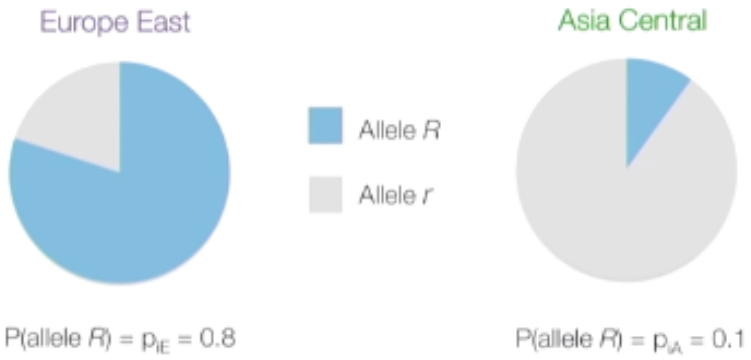
The greater the intermixing more will be the variation in DNA results. Europe is for example is highly intermixed (different DNA).

We actually have lack of data and no international database. Some of the data is taken from DNA studies.

DNA is broken into tiny segments using chips (based on algorithms). Each segment is compared to reference database. Then statistical smoothing or correction is done. Each segment is based on percentage of matching. After all this you get difference percentages of ancestry based on matching of your DNA to a reference database on regional basis.

Larger percentages are used as cues.

Some genetic markers (alleles) have different frequency of occurrence in different populations. DNA test measures your markers to these populations. (Courtesy: Ancestory.com)



For example. algorithm used by Ancestary.com

- This is an estimate, our best guess of the percentage for each population.

$$\mathcal{L}(Q,P|X) \propto \sum_{i=1}^{N}\sum_{j=1}^{G}\left[g_{ij}\ln\left(\sum_{k=1}^{K}q_{ik}p_{jk}\right)+(2-g_{ij})\ln\left(\sum_{k=1}^{K}q_{ik}(1-p_{jk})\right)\right]$$

Each company has different measuring standards and databases this causes a variation in percentages of your ethnicity from different tests. So if most data is from Europe and lesser from your area you are likely to get more percentage of European ethnicity. This is possible mathematically. [However your DNA is more likely to match with your regional population than other [far away] regional population. There is possibility of migration (but if it spans for 1000s of years. DNA results can't account for it).

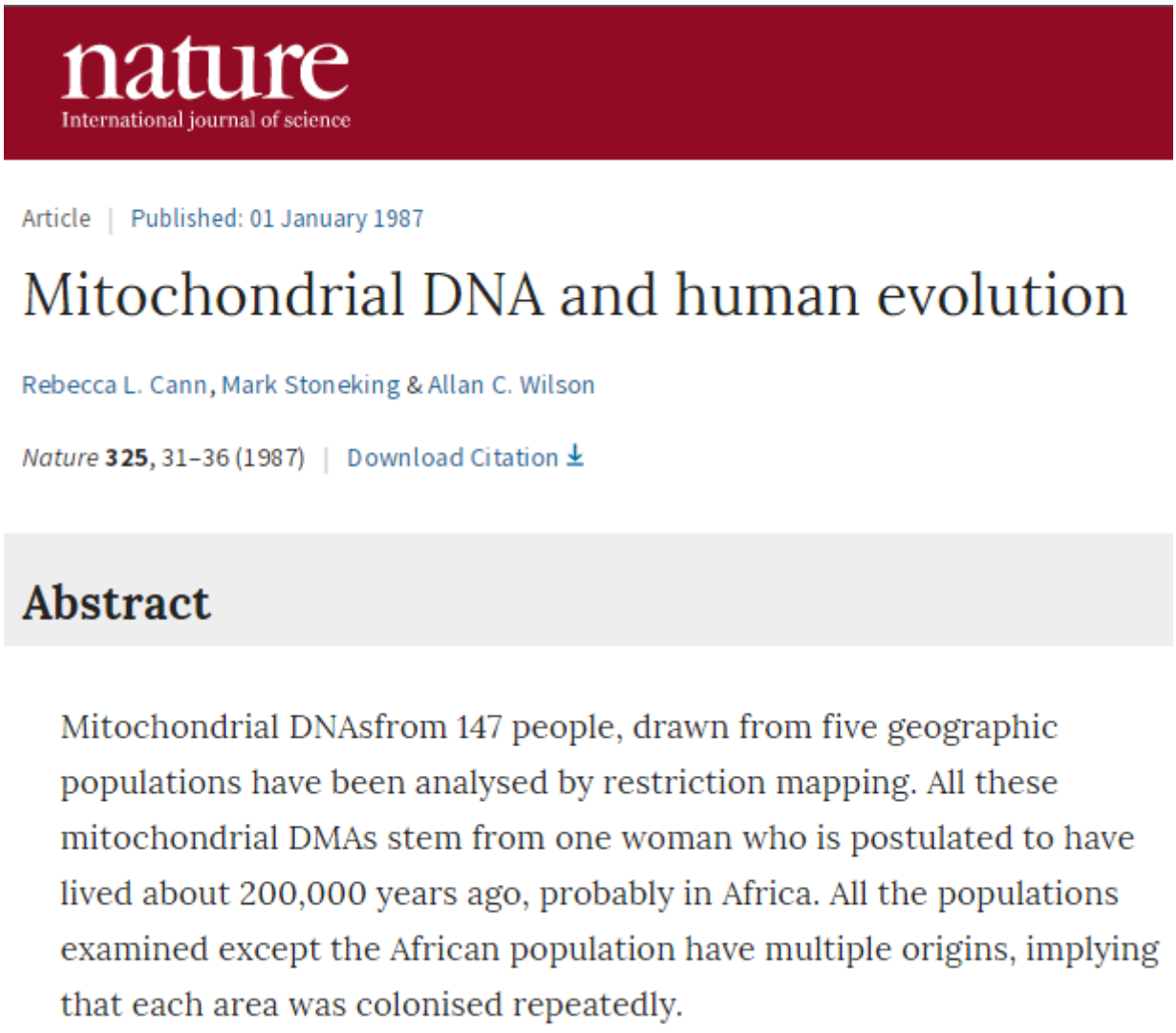
We find the place of origin (geography) of a haplogroup based on its concentration (at present) but we cannot determine the ethnicity. Hence DNA studies of present population are done and compared with DNA of skeletons in that region to find overlapping.

Given that you did not receive the entire DNA from your ancestors your results do not reflect all of your ancestry. There is also an overlap of physical features skin tones. eye colors. hair types. etc. around the world. Small percentages of ancestry from faraway places can be regarded genetic possibility (people not genealogically related but genetically related chances of that happening are very less).

In short DNA testing is volatile and inaccurate measure of genealogy. It does not even tell us about all of our ancestors and trying to establish history (that of genealogy) on it is like building castle on sand.

JOURNEY OF GENTIC STUDIES

The very first study that came into existence was done in 1987 on 147 people published in Nature. The reason it was done on so few people because of the expensive cost of conduction (lower processing computers. etc).



nature
International journal of science

Article | Published: 01 January 1987

Mitochondrial DNA and human evolution

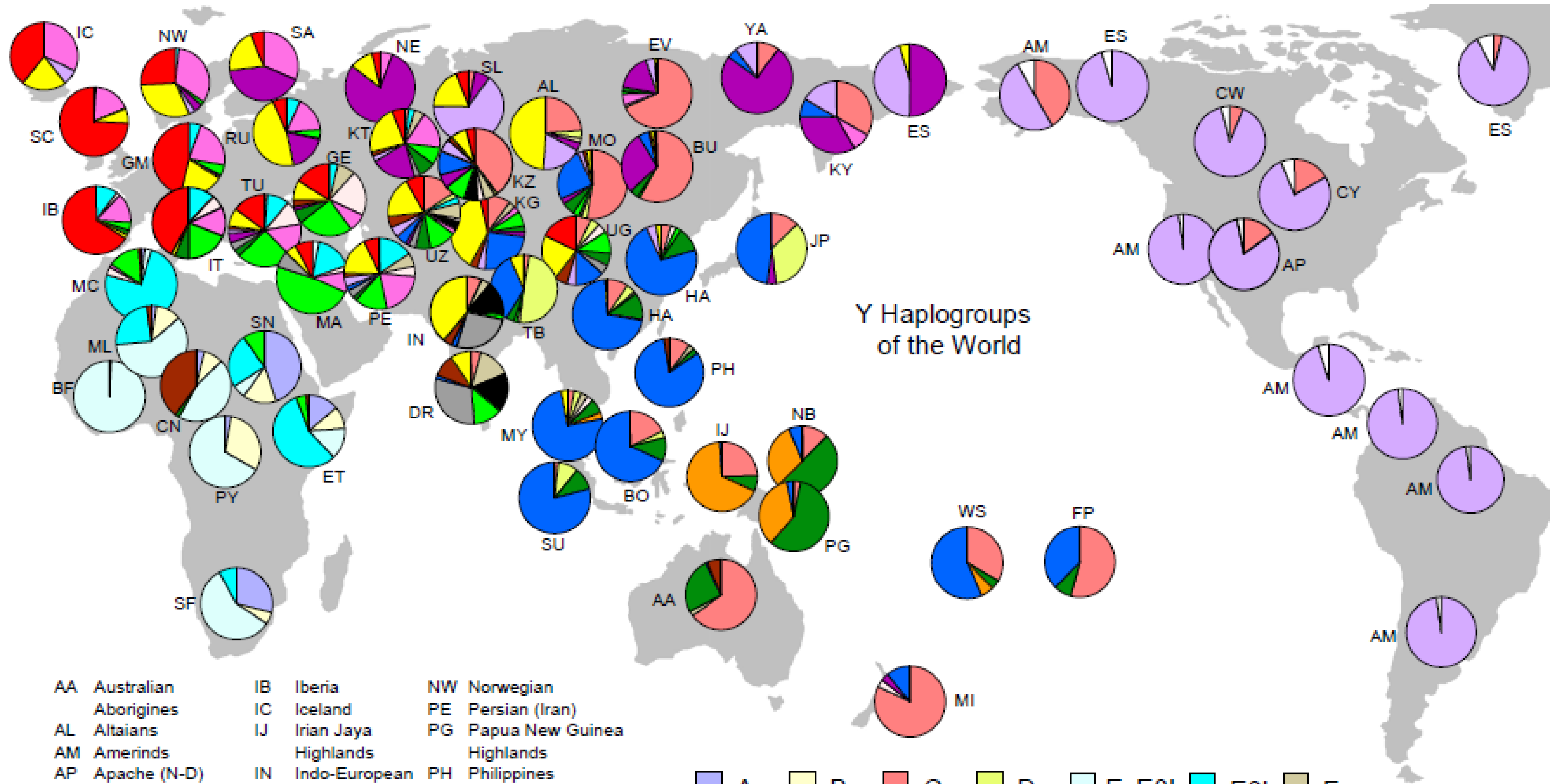
Rebecca L. Cann, Mark Stoneking & Allan C. Wilson

Nature **325**, 31–36 (1987) | Download Citation

Abstract

Mitochondrial DNAsfrom 147 people, drawn from five geographic populations have been analysed by restriction mapping. All these mitochondrial DMAs stem from one woman who is postulated to have lived about 200,000 years ago, probably in Africa. All the populations examined except the African population have multiple origins, implying that each area was colonised repeatedly.

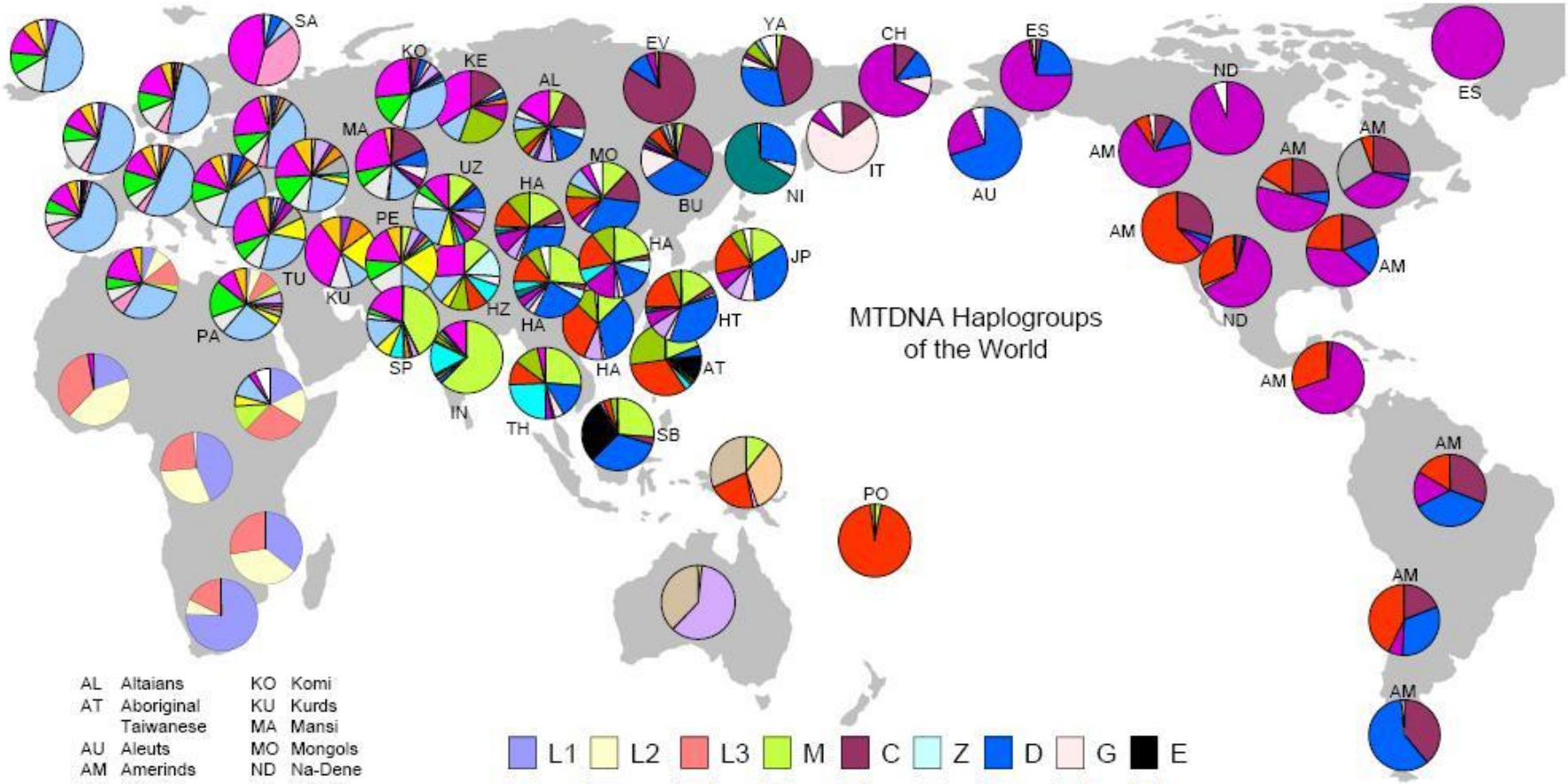
Later as technology progressed and DNA testing became easier we mapped out Y DNA and mtDNA on a global scale.



AA	Australian Aborigines	IB	Iberia	NW	Norwegian
AL	Altaians	IC	Iceland	PE	Persian (Iran)
AM	Amerinds	IJ	Irian Jaya Highlands	PG	Papua New Guinea Highlands
AP	Apache (N-D)	IN	Indo-European	PH	Philippines
BF	Burkina Faso	IT	Italy	PY	Pygmy
BO	Borneo	JP	Japan	RU	Russia
BU	Buryats	KG	Kyrgyzstan	SA	Saami
CN	Cameroon	KT	Kazan Tatar	SC	Scotland
CW	Chippeway (N-D)	KY	Koryaks	SL	Selkups
CY	Cheyenne	KZ	Kazakhstan	SF	South Africa
DR	Dravidian	MA	Mideast Arabs	SN	Sudan
ES	Eskimos	MC	Morocco	SU	Sumatra
ET	Ethiopia	MI	Maori	TB	Tibet
EV	Evenks	ML	Mali	TU	Turkish
FP	French Polynesia	MO	Mongols	UG	Uygurs
GE	Georgia-Armenia	MY	Malaysia	UZ	Uzbek
GM	Germany	NB	New Britain	WS	Western Samoa
HA	Han Chinese	NE	Nenets	YA	Yakuts

A B C D ExE3b E3b F
G H I J K L M
N O P Q RxR1 R1a R1b Other

The data in this map is supposed to represent the situation before the recent European expansion beginning about 1500 AD. In some cases such as some Native American tribes and the Maori this can be done reliably because STR typing was done. In other cases, especially in America, it is guesswork. The "Other" sectors in America indicate this. Native American groups are labeled by language group as Amerind, Na-Dene (N-D), and Eskimo. F, K, L, and P are in some cases "catchall" groups because some researchers did not use enough markers for a full haplotype determination.



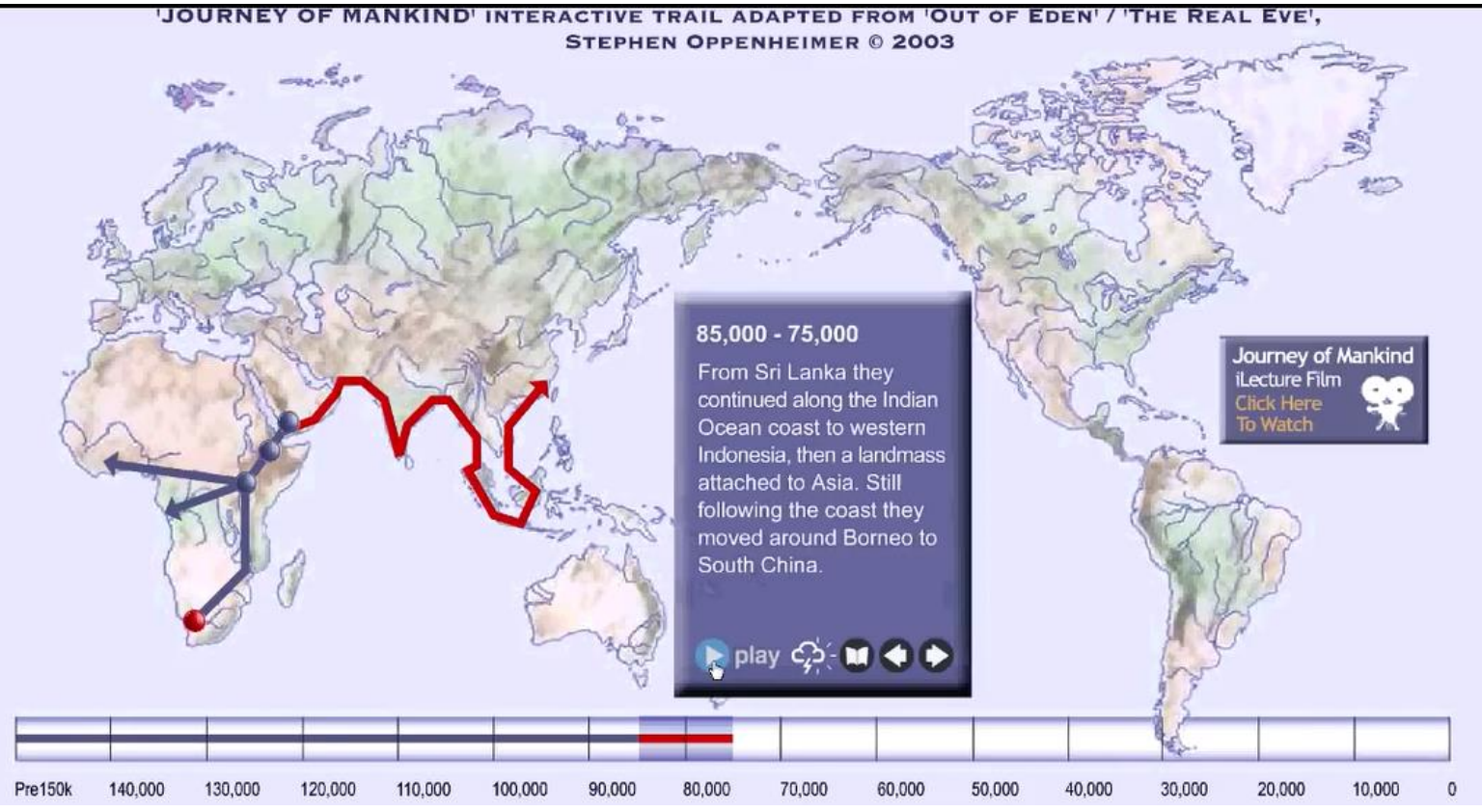
AL	Altaians	KO	Komi
AT	Aboriginal Taiwanese	KU	Kurds
		MA	Mansi
AU	Aleuts	MO	Mongols
AM	Amerinds	ND	Na-Dene
BU	Buryats	NI	Nivkhs
CH	Chukchi	PA	Palestine+Egypt
ES	Eskimo	PE	Persians (Iran)
EV	Evenks	PO	Polynesians
HA	Han Chinese	SA	Saami
HT	Han Taiwanese	SB	Sabah (Borneo)
HZ	Hazara	SP	South Pakistan
IN	India	TH	Thailand
IT	Itelmen	TU	Turks
JP	Japanese	UZ	Uzbeks
KE	Kets	YA	Yakuts

L1 L2 L3 M C Z D G E
Q N I W A X Y R B
F HV H V P J T U K Other

Specific tribes or locations are shown at left. Unlabelled pies are for general population in the area. African, American, and especially Polynesian areas are very large. The data in this chart is supposed to represent the situation before the recent European expansion beginning about 1500 AD. Assignments in Australia are somewhat iffy.

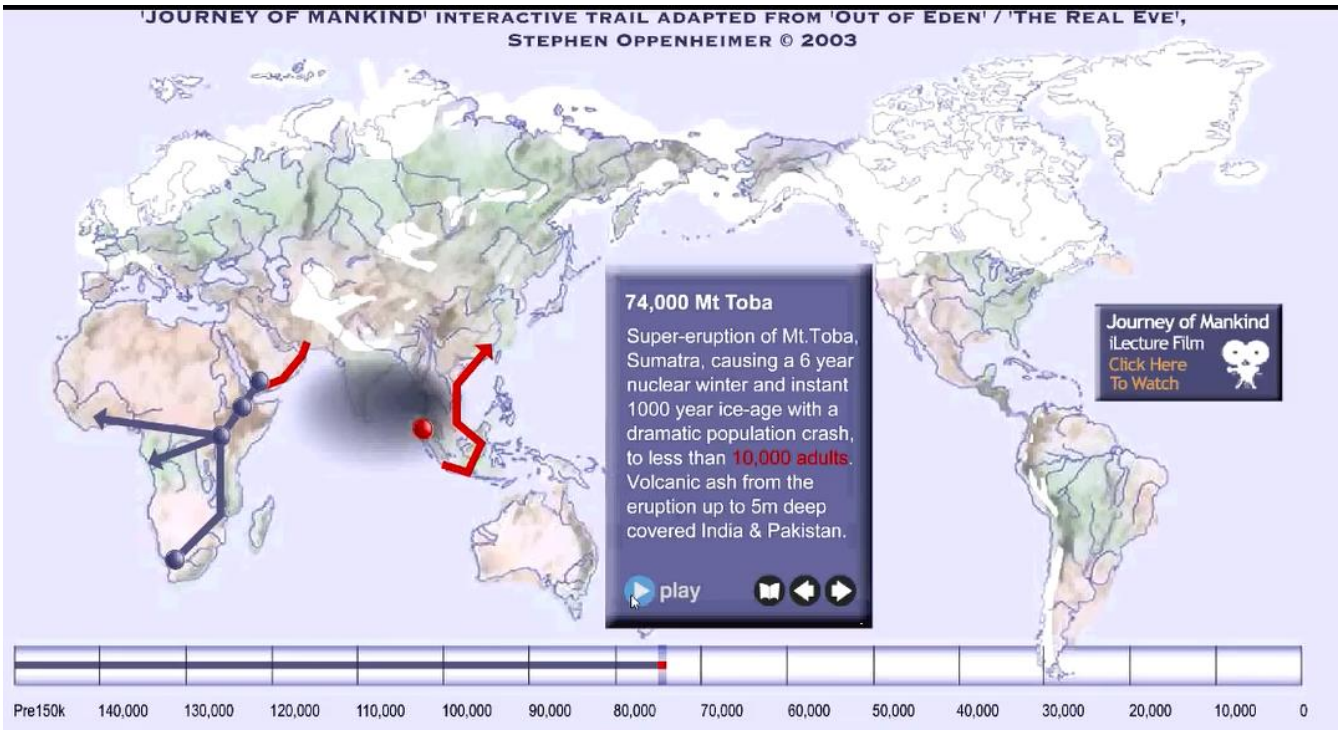
From these maps we can only conclude the distribution of haplogroups in the present day populations. We can't firmly conclude source or sink of these haplogroups but only their supposed path of distribution (more like an indication of flow).

mtDNA is used for deep ancestory and reliable human migrations. Makes sense because men used to go for invasions. wars. hunting or gathering not women. so for passing of mtDNA in a large population across an area you need large amount of females (as females mainly pass mtDNA). Hundreds of thousands of years ago men and women used to migrate together in tribes for better hunting grounds or survival friendly environment. Y DNA too show migration patterns. Only when we take both into consideration we get a glimpse of the entire story.

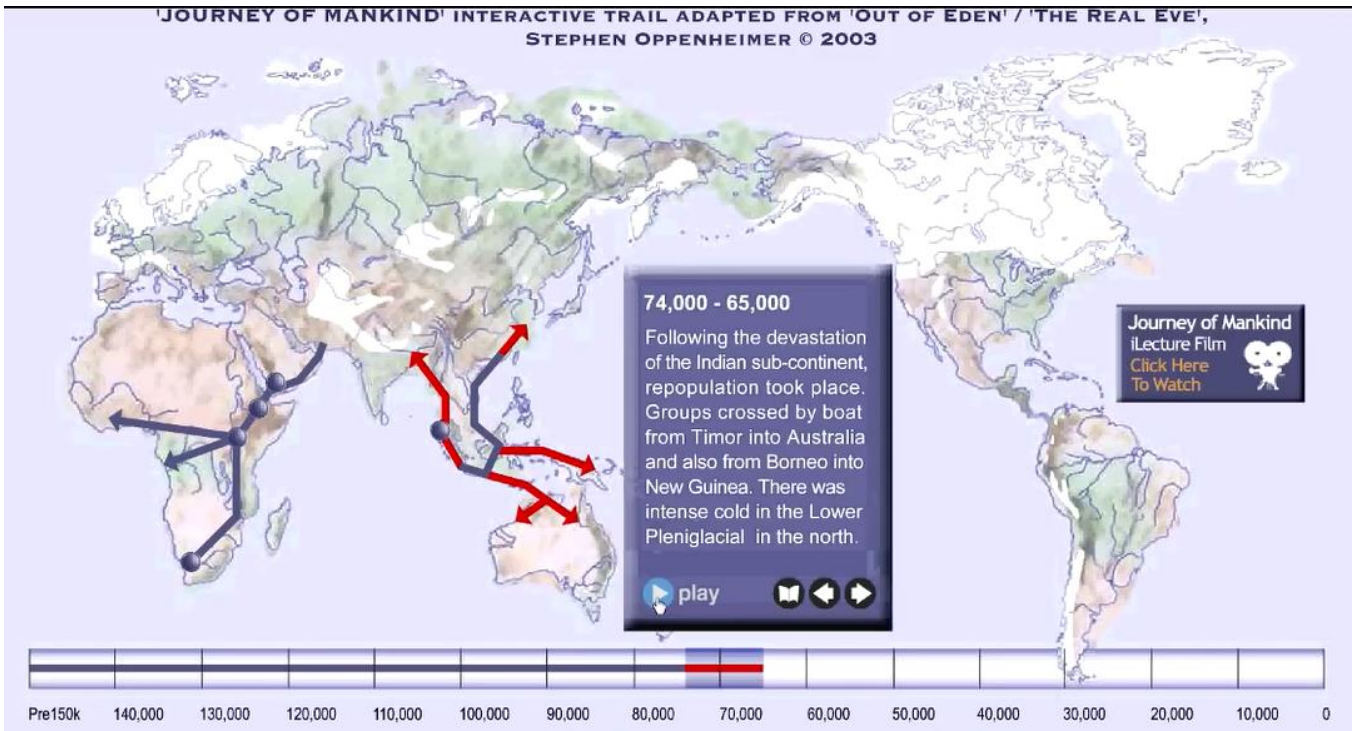


Humans took the path along costlines crossing Red sea and went along the coast of India it's very much possible that some of those (early Indians) settled along the rivers rest spread to South East and East Asia. Later an event of Mt. Tabo volcano

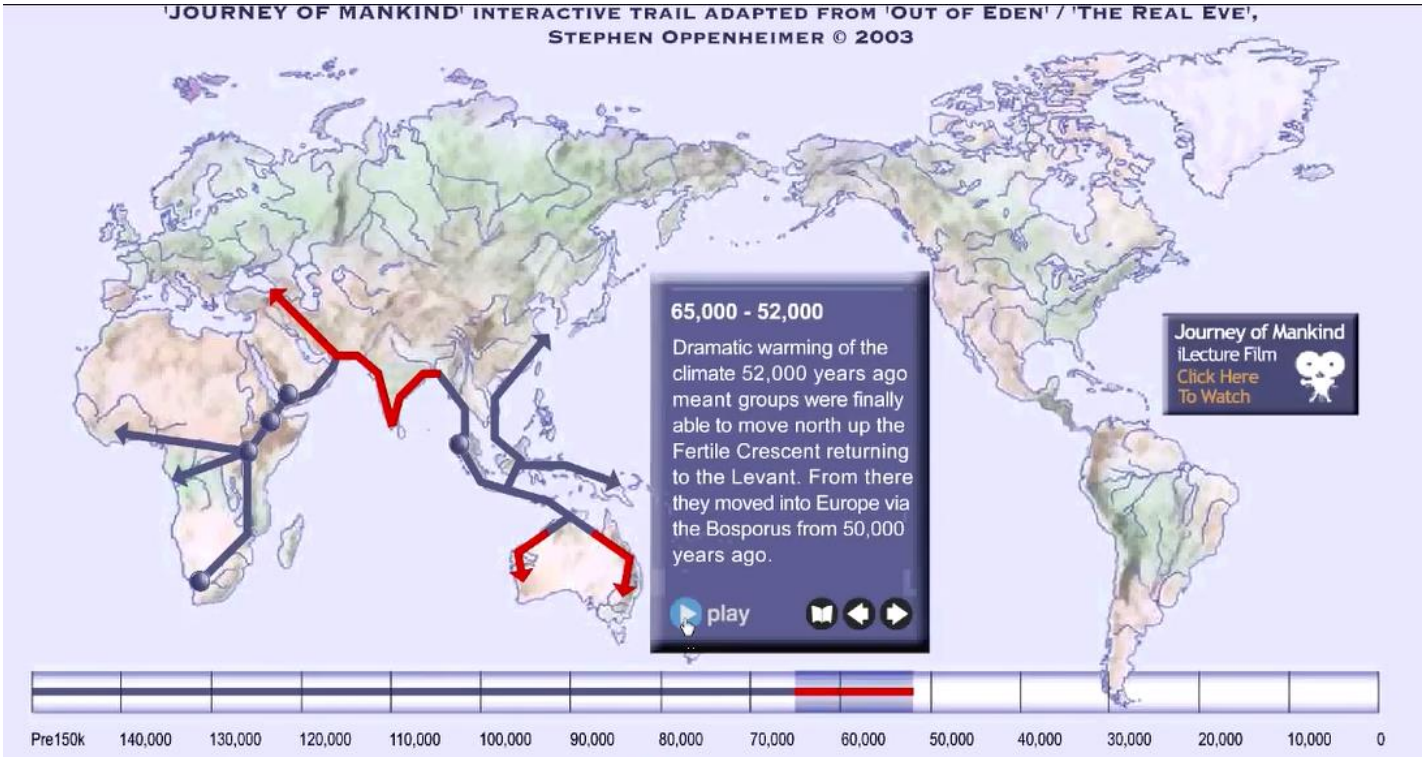
erupted caused nuclear winter and led to a huge population gap. Supposedly this caused ice age.

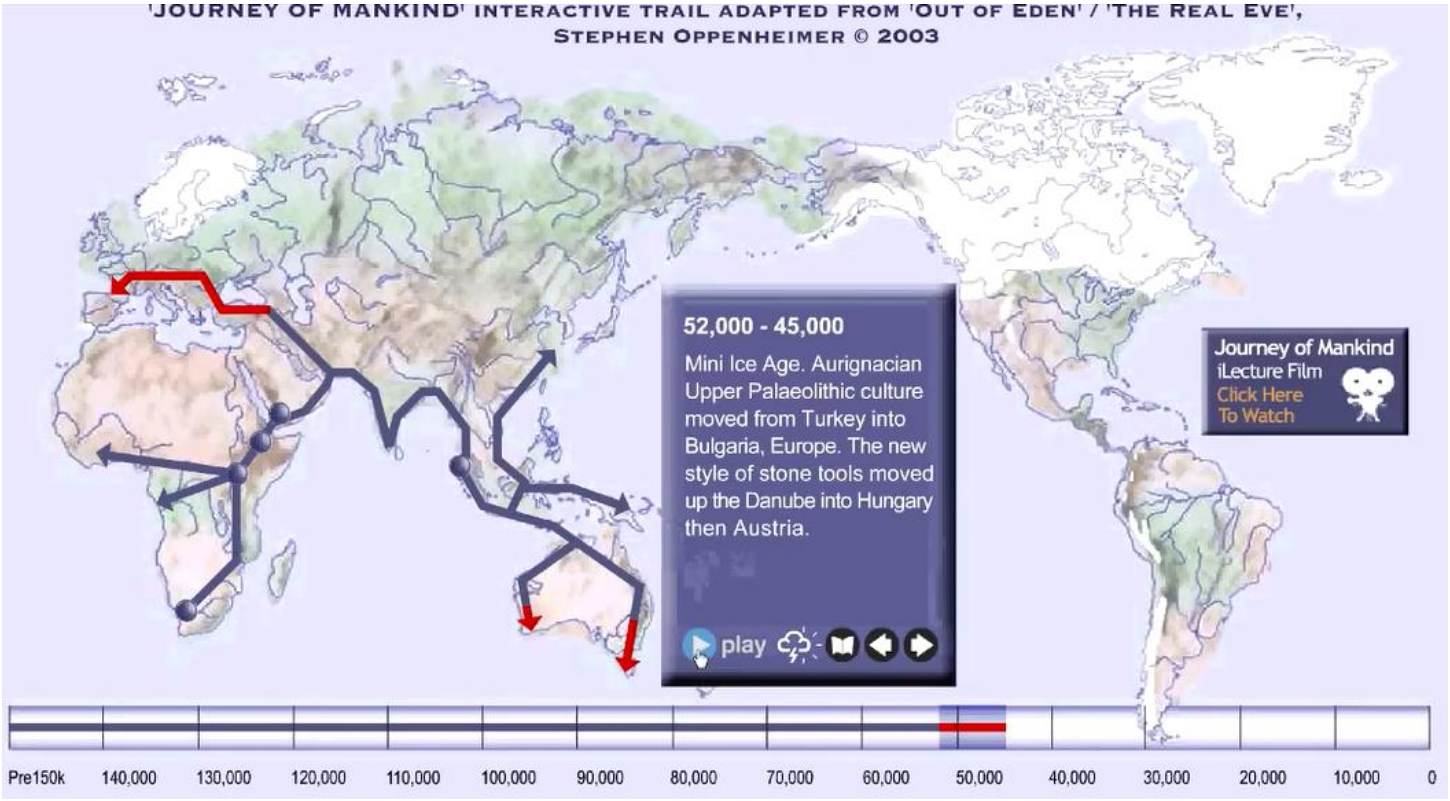


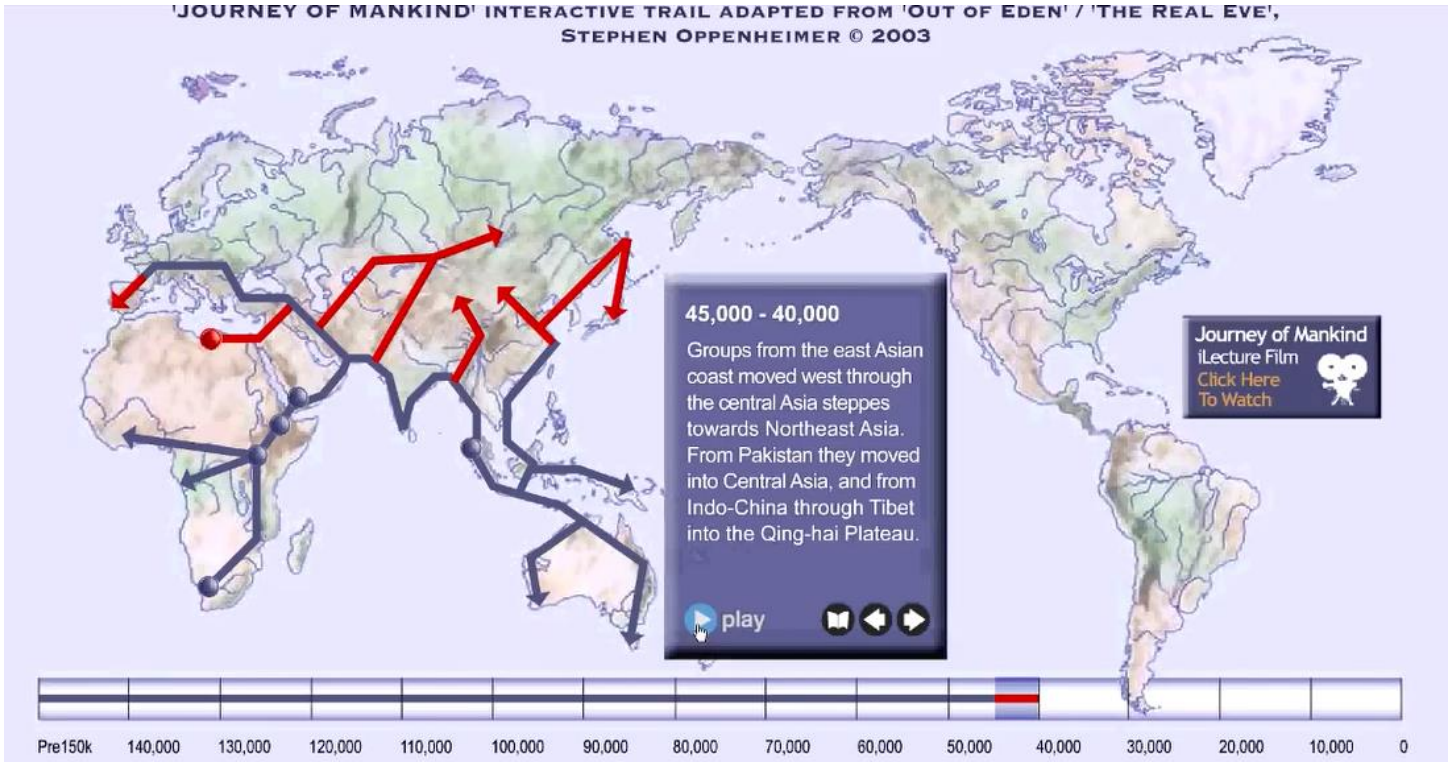
Afterwards people started to repopulate the Indian subcontinent from there they spreaded to Europe. Russia and to Americas.

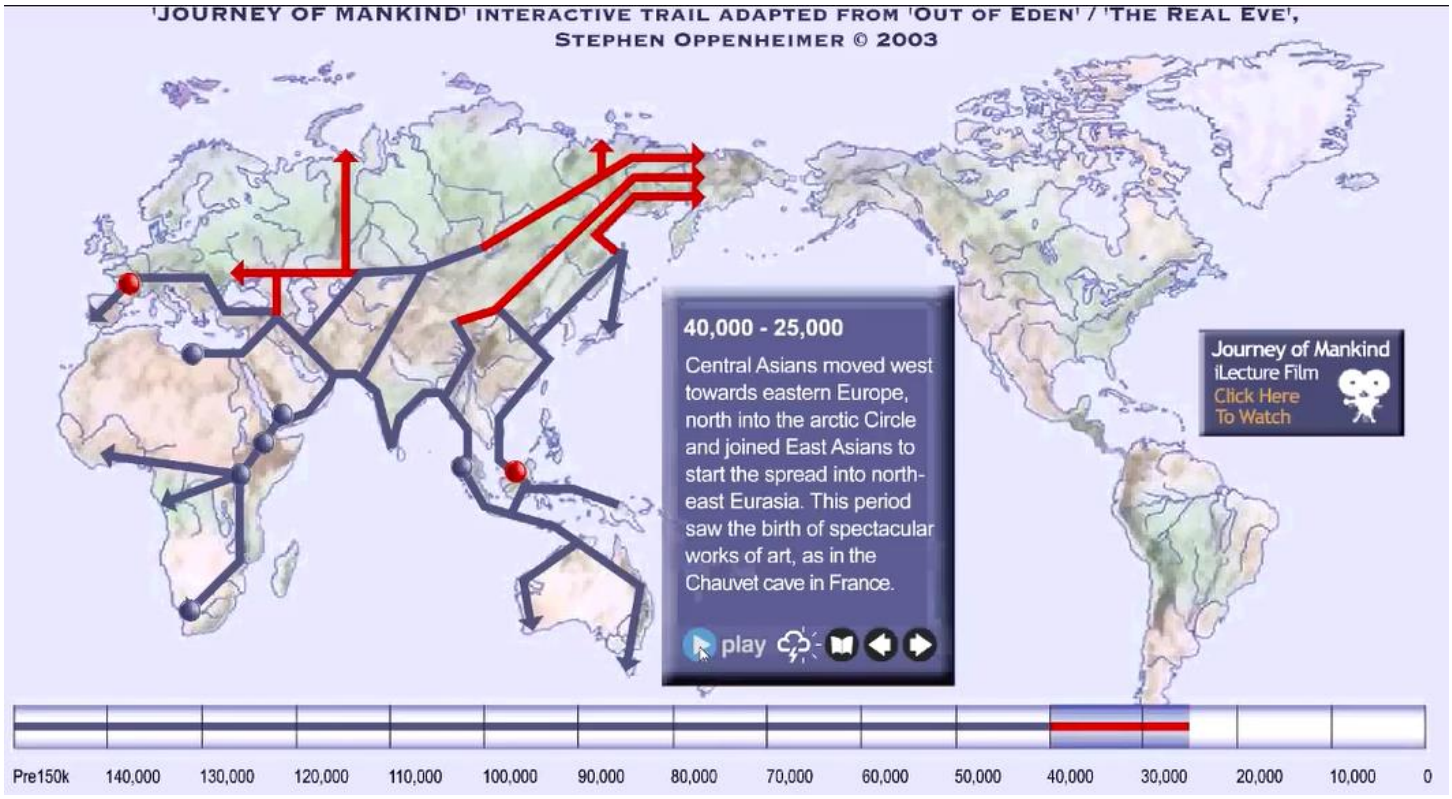


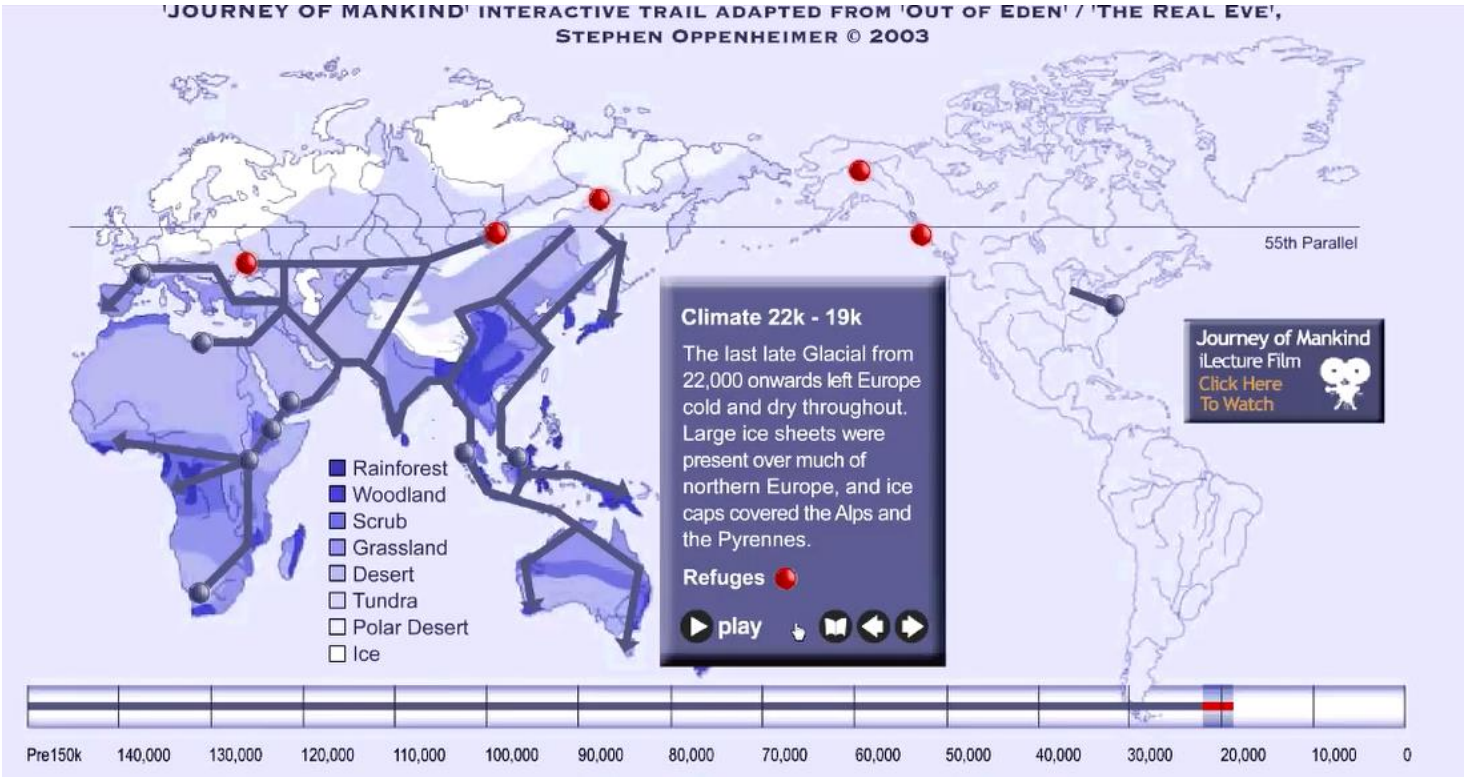
After moving to Europe mini ice age occurred as well followed by 4 warm periods.






'JOURNEY OF MANKIND' INTERACTIVE TRAIL ADAPTED FROM 'OUT OF EDEN' / 'THE REAL EVE',
STEPHEN OPPENHEIMER © 2003
45,000 - 40,000
Groups from the east Asian coast moved west through the central Asia steppes towards Northeast Asia. From Pakistan they moved into Central Asia, and from Indo-China through Tibet into the Qing-hai Plateau.
play
Journey of Mankind
iLecture Film
Click Here
To Watch
Pre150k 140,000 130,000 120,000 110,000 100,000 90,000 80,000 70,000 60,000 50,000 40,000 30,000 20,000 10,000 0


'JOURNEY OF MANKIND' INTERACTIVE TRAIL ADAPTED FROM 'OUT OF EDEN' / 'THE REAL EVE',
STEPHEN OPPENHEIMER © 2003
40,000 - 25,000
Central Asians moved west towards eastern Europe, north into the arctic Circle and joined East Asians to start the spread into north-east Eurasia. This period saw the birth of spectacular works of art, as in the Chauvet cave in France.
play
Journey of Mankind
iLecture Film
Click Here
To Watch
Pre150k 140,000 130,000 120,000 110,000 100,000 90,000 80,000 70,000 60,000 50,000 40,000 30,000 20,000 10,000 0



You can say **"**India is the center of human civilzation**"**

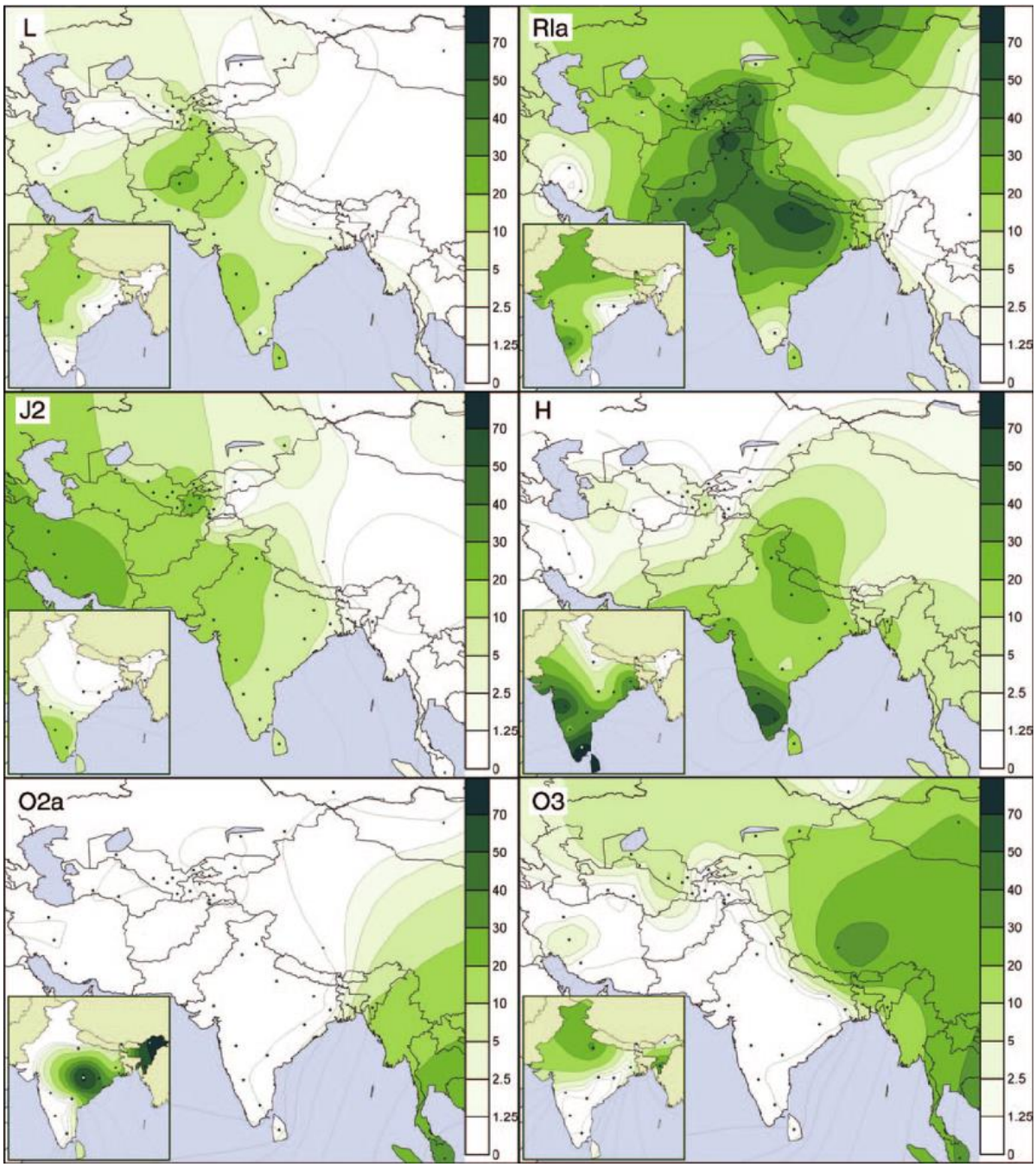
WHAT THE HELL IS R1A HAPLOGROUP ?

R1a haplogroup is the backbone of the Aryan Invasion Theory and genetical claim over our Vedic culture. I like to call it the **"**Jew's and white man's last straw of hope to colonize India**".**

When did the haplogroup R1a originated ?

About 77 percent Indian population comprises of 4 largest haplogroups - R. H. L. J

Let's look at Haplogroups individually.



Haplogroup	AGE (years ago)	Place of Origin
R (mt DNA) One of it's descendant is R1b which forms present day Europe	66,000	South Asia , South East Asia
R (Y DNA)	27,000	South Asia, Central Asia (or Serbia) Newer studies indicating it originated in India (North). The frequency distribution of R haplogroup is highest in India. Even if you consider this origination to be shaped by environment than Himalayas have same climatic conditions and geography like that of Europe and Central Asia
H (mt DNA)	20-25000	South-West Asia
H (Y DNA)	45,000	South Asia (India) or South East Asia
L (mt DNA)	150 - 230k	Eastern Africa
L M-20 (Y DNA)	Reliable study needed	South Asia (India), West Asia or Pamir Mountains
J (mt DNA)	45000	Levantine
J - M304 (Y DNA)	48000	West Asia

Front. Genet., 23 January 2018 | https://doi.org/10.3389/fgene.2018.00004

The Geographic Origins of Ethnic Groups in the Indian Subcontinent: Exploring Ancient Footprints with Y-DNA Haplogroups

 David G. Mahal[1,2*] and  Ianis G. Matsoukas[1]

[1]School of Sport and Biomedical Sciences, University of Bolton, Bolton, United Kingdom
[2]Extension Division, University of California, Los Angeles, Los Angeles, CA, United States

Major South Asian Y chromosomal lineage	H	J2	L	R1a	R2
Basu et. al. (2003)	–	–	–	Central Asia	–
Kivisild et. al. (2003)	India	West Asia	India	South or West Asia	South Asia
Cordaux et. al. (2004)	India	West-Central Asia	Middle East	Central Asia	South Asia
Sengupta et. al. (2006)	India	Middle East or Central Asia	South India	North India	North India
Thanseem et. al. (2006)	India	The Levant	Middle East	South or Central Asia	South or Central Asia
Sahoo et. al. (2006)	South Asia	Near East	South Asia	South or West Asia	South Asia
Mirabal et. al. (2009)	–	–	–	North west India or Central Asia	–
Zhao et. al. (2009)	India	Middle East	Middle East	Central or West Asia	Central Asia or West Eurasia
Sharma et. al. (2009)	–	–	–	South Asia	–
Thangaraj et. al.(2010)	–	Near East	Near East	South Asia	South Asia

Basu et al. https://genome.cshlp.org/content/13/10/2277.full.html#related-urls

Kivisild et. al. https://www.nature.com/articles/jhg2002

Cordaux et. al. https://www.sciencedirect.com/science/article/pii/S0960982204000405

Sengupta et. al. https://www.cell.com/ajhg/pdf/S0002-9297(07)62353-2.pdf

Thanseem et. al. https://bmcgenet.biomedcentral.com/track/pdf/10.1186/1471-2156-7-42

Sahoo et. al. https://www.pnas.org/content/pnas/103/4/843.full.pdf

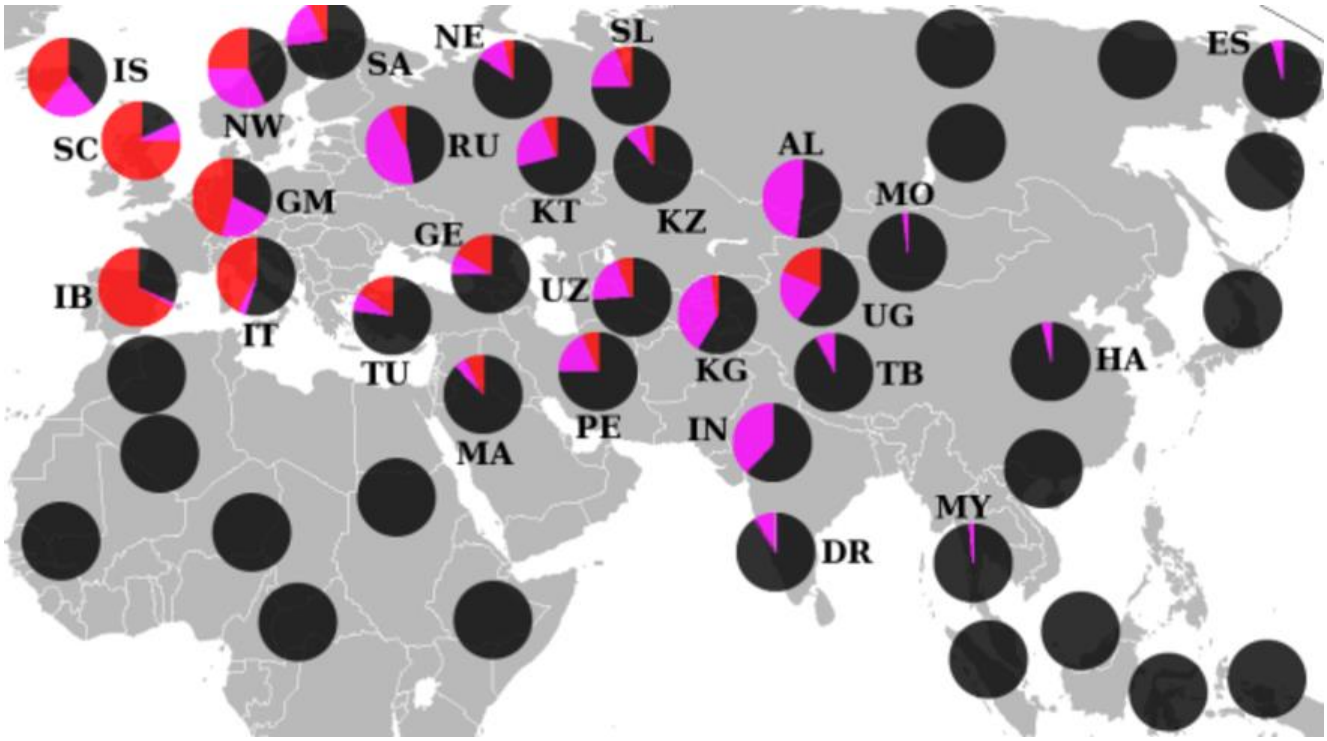
Mirabal et. al. https://www.researchgate.net/publication/24175266_Y-Chromosome_distribution_within_the_geo-linguistic_landscape_of_northwestern_Russia

Zhao et. al. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2755252/

Sharma et. al. http://web.vu.lt/rstc/a.pazeraite/files/2014/10/The-Indian-origin-of-paternal-haplogroup-R1a1-2002a1.pdf

Thangaraj et. al. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3004917/

India is not composed of a homogenous race but different ethnic groups. So the percentage of R haplogroup is more in North Indians and less in South Indians.



Red - R1b

Purple - R1a (not specified if it is for mtDNA or Y DNA (both are of Indian origin). It's likely they use a subclade of R1a which orginationated about 5800 years ago)

Black - Other haplogroup

Different studies show different results and places of origin. The percentage of R haplogroup is more in Indians (North) than Europeans :

https://en.wikipedia.org/wiki/List_of_R1a_frequency_by_population

Research on R1a1 and R1a1* haplogroup being from India Kivisild et. al. 2009. https://www.nature.com/articles/jhg200982

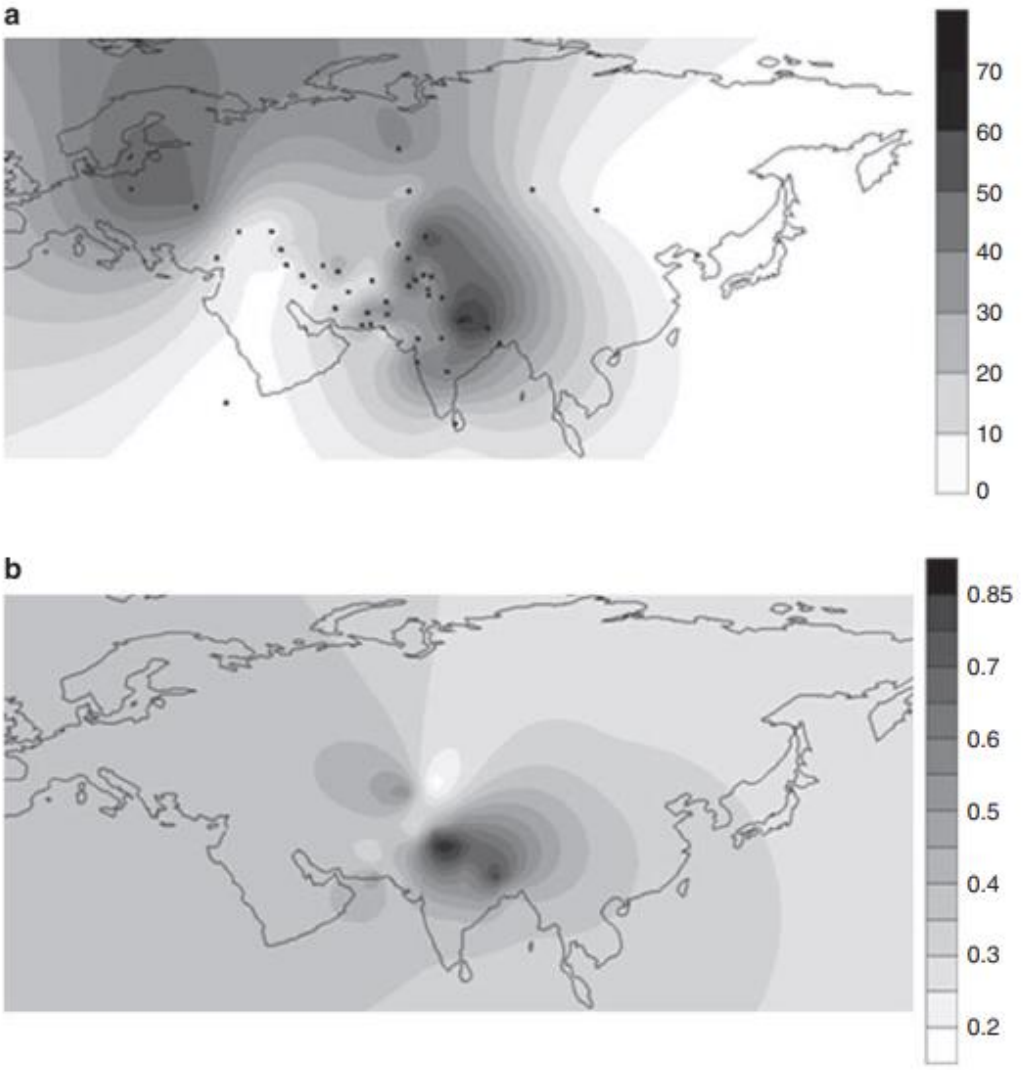
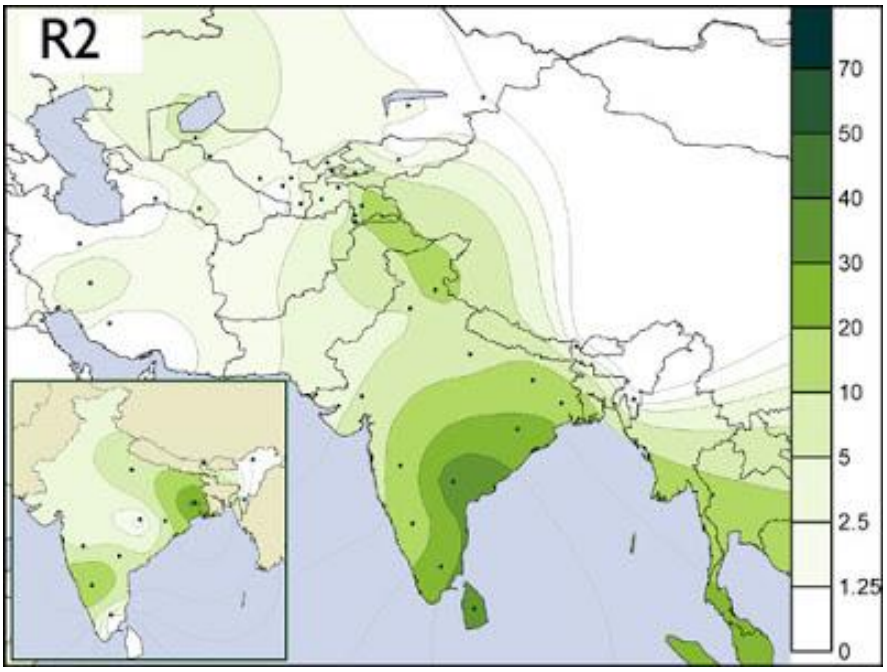


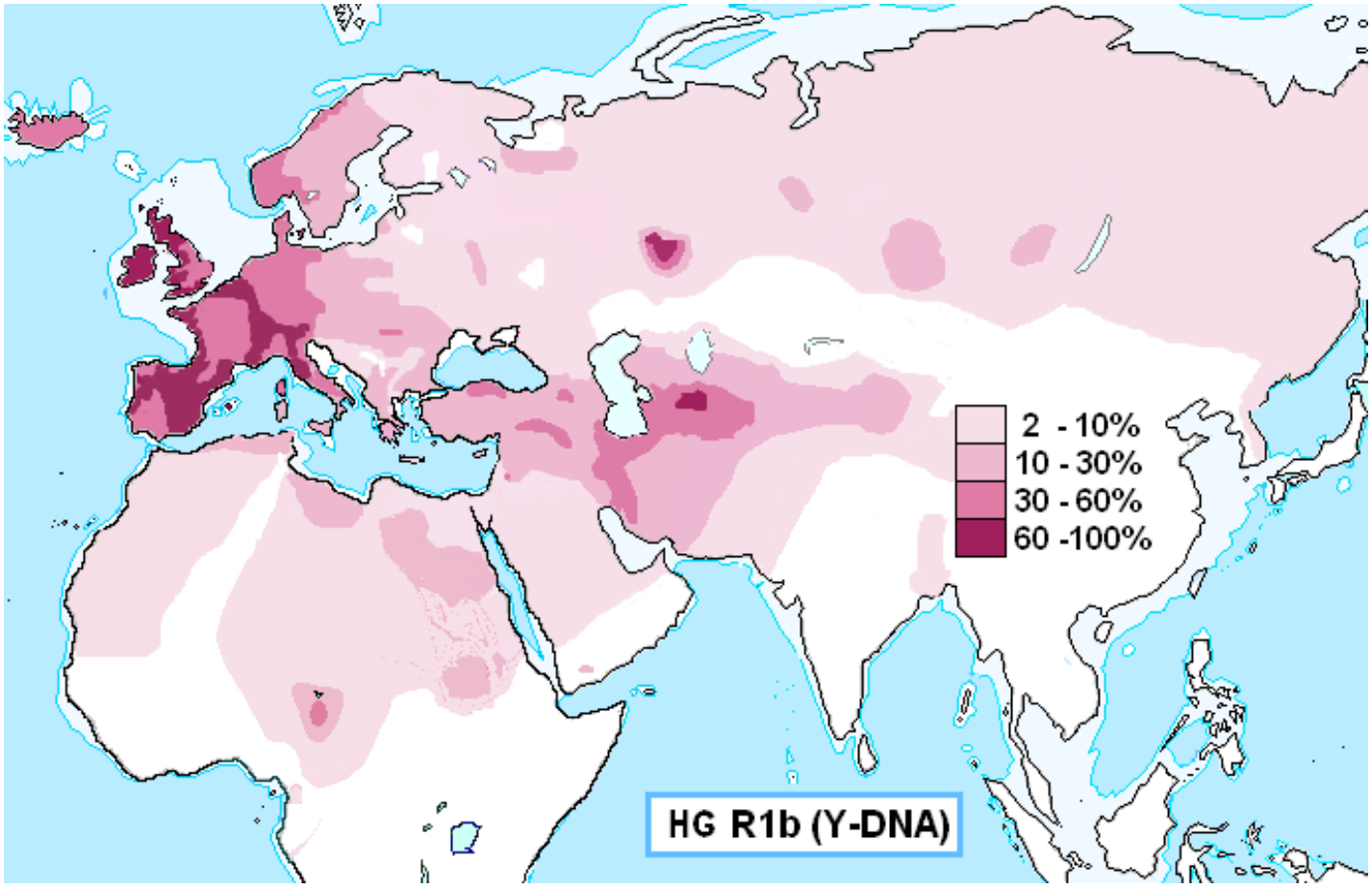
Figure 1 The spatial distribution maps of Y-haplogroup R1a1 generated by the Kriging procedure using SURFER version 8.0. **(a)** Spatial frequency distribution of Y-haplogroup R1a1* across Eurasia, Central Asia and the Indian subcontinent. **(b)** Spatial distribution of Y-haplogroup R1a1*-associated diversity based on microsatellite markers.

The concentration of both R1a1 and R1a1* haplogroup along with frequency distribution by population of R1a haplogroup suggest that gene flow didn't came from central asia to India but from India to central asia.

Also R2 haplogroup too originated in India.



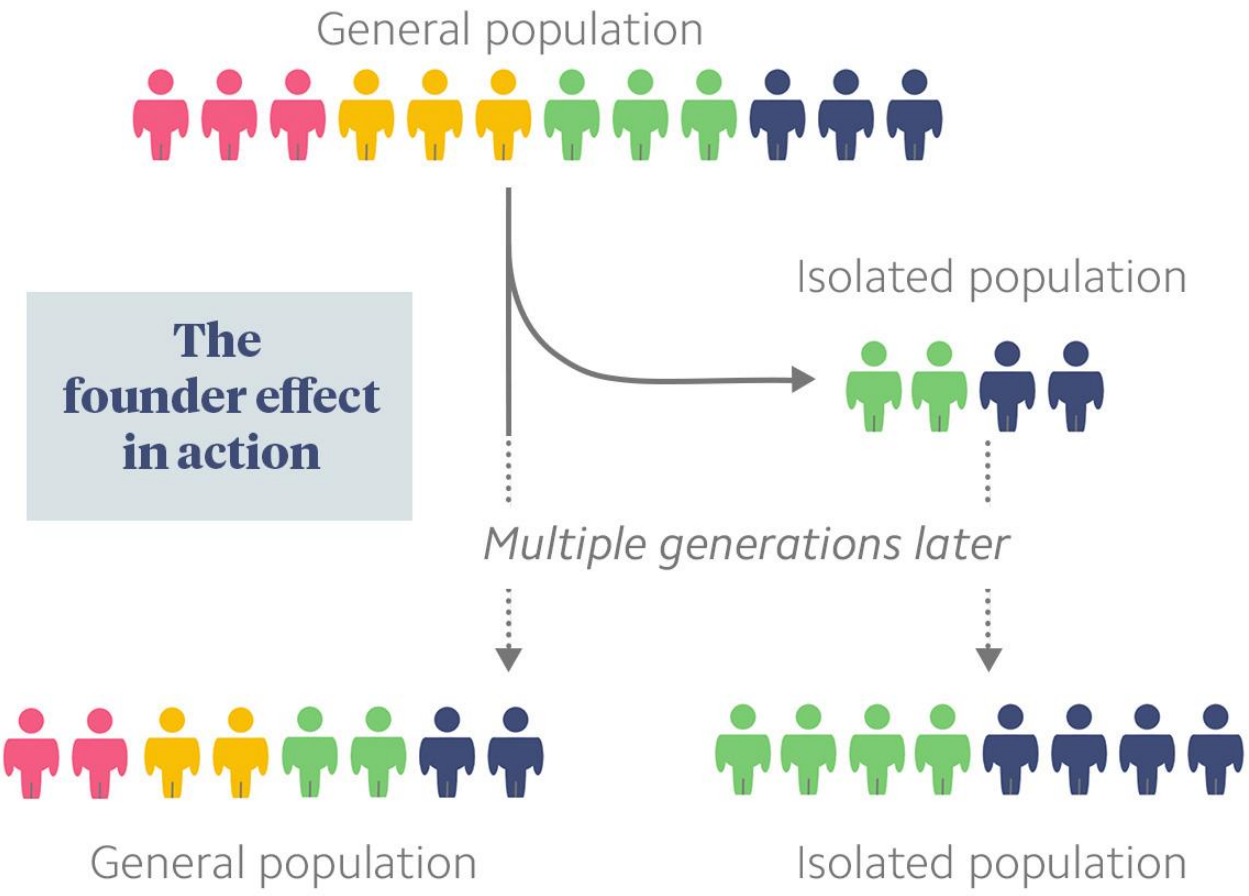
Europe has high concentration of R1b. But didn't R1b came from R1 branch which is from India.



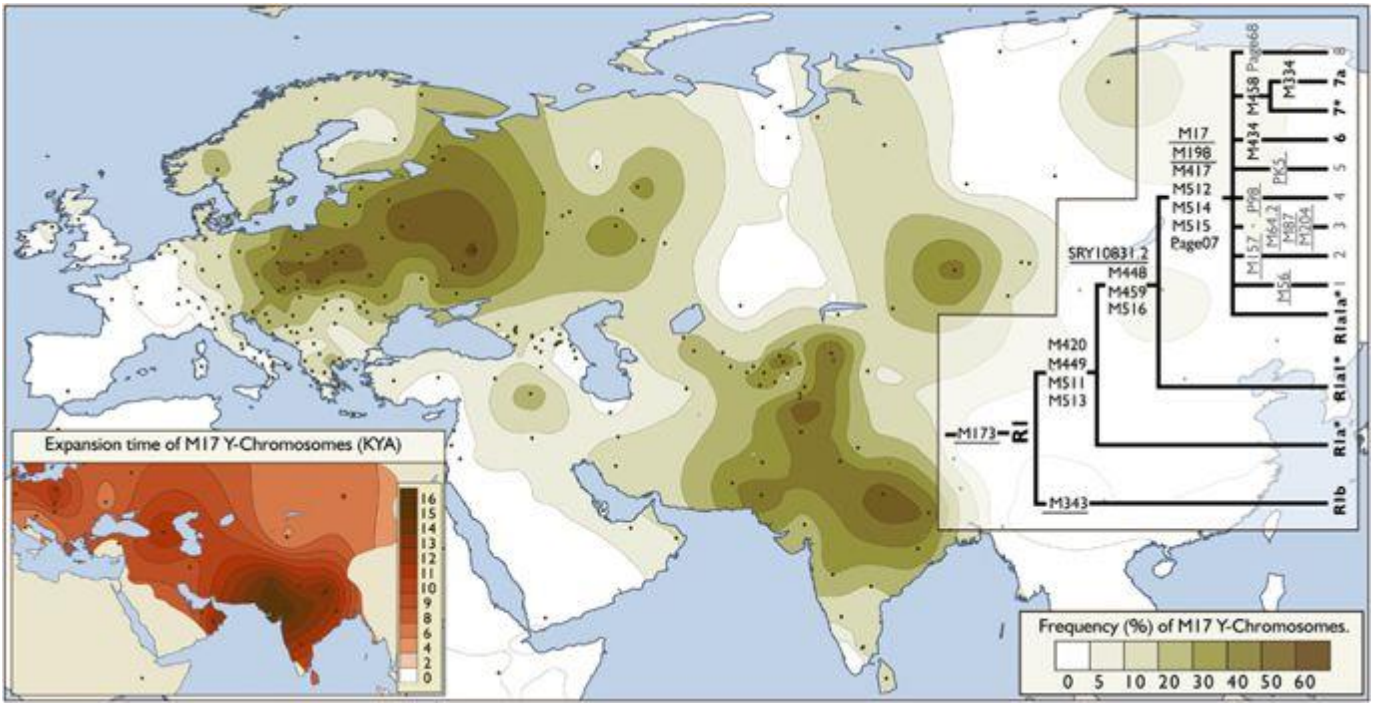
R1b originated about 4500 years ago (although I'm a bit skeptical on this one) and R1b chromosome carriers were the first movers to Europe.[https://www.nature.com/articles/s41598-017-07710-x.pdf]

The question is why Europeans have different skin tone. eye color. hair color than Indians. There can be many explanations.

Founder effect - loss of genetic variation that occurs when a new population is established by a very small number of individuals from a larger population.



M17 Y chromosome expansion.



In this study http://www.arslanmb.org/ArmenianDNAProject/PhylogeneticResolution-HG-R1a1.pdf they used Malaysian Indians(South Indians) not North Indians.

mtDNA and Y DNA originated in India and both migrated to Europe. This shows how much a serious blunder Aryan Invasion theory is.

ARYAN INVASION ON COMMON SENSE

According to Aryan Invasion Theory at around 1500 B.C. Aryans invaded India on "chriots". They knew haplogroups so they divided Indians on the basis of caste system. And in only few thousand years (about 3500 years) all white Aryans became brown from mixing with Dravidian (from Africa).

If two races intermix won't there be genetic defects and no people don't become brown from just mixing. That is not to say there was not any intermixing between selected groups. There wasn a caste system but that I will cover in a separate book.

Now to overwhelm the native Indian population genetically. the number of immigrants needed to be more than 4 times that of native population of Indus valley civilization.

(((David Reich))) [a jew] wrote a book called "Who we are and How we got here". From pages 148-153 he writes. Europeans are more closely related to Indians than to Chinese and Chinese are more closely related to Indians than Europeans.

It is clear Indians are the source or link between both groups but Reich purposedly choses Europeans as the center and regards Indians as a mix of all the different groups. But India is composed of distinct ethnic groups. He also promotes 3500 year old Aryan Invasion theory.

But to determine whether an ethnic group is native to a land or not. you need to measure it's populations' genetic stability e.g. https://www.longdom.org/open-access/the-major-ychromosome-haplotype-xi--haplogroup-r1a-in-eurasia-2161-1041-1000150.pdf

Hereditary Genetics

Lucotte, Hereditary Genet 2015, 4:2
DOI: 10.4172/2161-1041.1000150

Case Report Open Access

The Major Y-Chromosome Haplotype XI – Haplogroup R1a in Eurasia

Lucotte G*

Institute of Molecular Anthropology, Paris, France

Abstract

More than 6600 unrelated males from Eurasia were analysed by molecular hybridization experiments for the p49a, f *Taq* I polymorphisms. A total of 846 subjects (12.7%), belonging to haplotype XI/R1a haplogroup, were identified and further analysed for the two SNPs Z280 and Z93; these two SNPs define the European and Indian sub-haplogroups, respectively. Among Europe, approximate dating based on the study of a set of 12 STRs and subsequent TMRCA calculations are given for the Eastern, Central, Northern, Western and South-Eastern regions.

SNPs	Geographic regions	N	H	TMRCA
Z280	Northern Europe	41	0.961	6,940 ± 1,930
	Western Europe	61	0.995	9,220 ± 2,800
	Central Europe	49	0.992	11,500 ± 3,000
	South-Eastern Europe	52	0.985	11,170 ± 4,050
	Eastern Europe	53	0.992	12,516 ± 3,800
Z93	Pakistan-India	192	0.982	15,450 ± 2,900

Table 5: Approximate TMRCAs (in Kyears) of the two haplotypes Z280 (and into Z280) and Z93 of the five European regions.

He found for this sample the most recent common ancestor has to be around 25100 years (not 3500 years as claimed by Reich and gang) from present.

There is an abrupt geographic limit, located in West-Europe along the 15° meridian of longitude approximately [9], between the haplotypes XV and XI distributions (Figure 1). According to recent estimations based on whole Y-chromosome sequences and using a rate of one SNP per 122 years [22], it was estimated that the bifurcation of R1 into R1b and R1a had occurred ≈ 25,100 years ago. The global impression we have, based on dates we obtained, is that the waves of expansion during history of lineages bearing the haplotype XI toward West superpose areas of Western Europe previously occupied by populations bearing haplotype XV.

References

1. Lucotte G, Ngo NY (1985) p49f, A highly polymorphic probe, that detects Taq1 RFLPs on the human Y chromosome. Nucleic Acids Res 13: 8285.

s

CONFUSION EVERYWHERE

Story doesn't end here there are many other theories like Interregional evolution which differentiates humans as different parallel species.

Cromorgans (in Europe). Neanderthals (Europe and West Asia). Homo sapiens in Africa. Desinova (in Asia). Some fools still regard Indians as mixture of Desinova and neanderthals. But there are many more interregional human species (Ancient Indians) etc.

Later theories become logically possible but quite strange. For example it surfaces from close study of anthropology and mythology that humans are possibly descendants of aliens. There are many alien species both on earth and inside it (hollow earth theory which is valid). Humans are created by alien gods. Of course whites claim they are the most pure of all (coughs).

Aliens like Nordics. Reptilians. Greys. Gaints. Hyperboreans. Green skins. Tall whites. Blue skins. etc.

There are also different skulls and sketeletons of ancient humans from different parts with different skull sizes etc.

However above observations on haplogroups and human migrations are indeed true regardless but there is still much we don't know and left to discover.

Aryan Invasion Theory is a façade with main aim to get hijack our Vedic culture but whites are failing right into the trap of Jews and we must wait and prepare for war that is to come.

REFERENCES

NATIONAL GEORAPHIC

Genetics 101 : https://www.youtube.com/watch?v=v8tJGlicgp8

The Journey of your Past : https://www.youtube.com/watch?v=RGtaq3PiIoU

FAMILY HISTORY FANATICS

120 ancestors (part 1) - https://www.youtube.com/watch?v=9g-VwtRd8ks

120 ancestors (part 2)- https://www.youtube.com/watch?v=nlmK0X3I1Lo

DNA Ethnicity Results Accuracy 1 : https://www.youtube.com/watch?v=i70SZRW9t90

DNA Ethnicity Results Accuracy 2 : https://www.youtube.com/watch?v=u8lMfGqSrwg

Understanding Ethnicity 1 : https://www.youtube.com/watch?v=ScZtHuU78n4

Understanding Ethnicity 2: https://www.youtube.com/watch?v=1Cikj7FI6YM

Ethnicity to create genealogy cues : https://www.youtube.com/watch?v=xte6-34bJ_M

How DNA disappears : https://www.youtube.com/watch?v=rMBooDoB2Wk

Likelihood of a Genetic Connection with a Cousin : https://www.youtube.com/watch?v=4QhLzzIszIw

ANCESTARY.COM

Breaking Down the Science Behind Ethnicity : https://www.youtube.com/watch?v=o0mVUu2kRcs

OPPENHEIMER MODEL

Peopling of the world : https://www.youtube.com/watch?v=aCj7bFIOBKU

ARTICLES

http://www.biomedcentral.com/1471-2164/8/68

Beginners' guides to genetic genealogy : https://isogg.org/wiki/Beginners%27_guides_to_genetic_genealogy

REFERENCES FOR R1A DISTRIBUTION BY POPULATION

Adams: Bosch. Elena: Balaresque. Patricia L.: Ballereau. StēPhane J.: Lee. Andrew C.: Arroyo. Eduardo: Lōpez-Parra. Ana M.: Aler. Mercedes: Grifo. Marina S. Gisbert: Brion. Maria: Carracedo. Angel: Lavinha. João: Martīnez-Jarreta. Begoña: Quintana-Murci. Lluis: Picornell. Antōnia: Ramon. Misericordia: Skorecki. Karl: Behar. Doron M.: Calafell. Francesc: Jobling. Mark A. (2008). "The Genetic Legacy of Religious Diversity and Intolerance: Paternal Lineages of Christians. Jews. and Muslims in the Iberian Peninsula". American Journal of Human Genetics. 83 (6): 725-36.doi:10.1016/j.ajhg.2008.11.007. PMC 2668061. PMID 19061982

Al Zahery: Semino. O.: Benuzzi. G.: Magri. C.: Passarino. G.: Torroni. A.: Santachiara-Benerecetti. A.S. (2003). "Y-chromosome and mtDNA polymorphisms in Iraq. a crossroad of the early human dispersal and of post-Neolithic migrations" (PDF). Molecular Phylogenetics and Evolution. 28 (3): 458-472. doi:10.1016/S1055-7903(03)00039-3. PMID 12927131. archived from the original (PDF) on 2010-12-27. retrieved 2009-10-22

Balanovsky. Oleg: Rootsi. Siiri: Pshenichnov. Andrey: Kivisild. Toomas: Churnosov. Michail: Evseeva. Irina: Pocheshkhova. Elvira: Boldyreva. Margarita: et al. (2008). "Two Sources of the Russian Patrilineal Heritage in Their Eurasian Context". American Journal of Human Genetics. 82 (1): 236-250. doi:10.1016/j.ajhg.2007.09.019. PMC 2253976. PMID 18179905. archived from the original on 2008-08-10

Bamshad: Kivisild. T: Watkins. WS: Dixon. ME: Ricker. CE: Rao. BB: Naidu. JM: Prasad. BV: et al. (2001). "Genetic evidence on the origins of Indian caste populations". Genome Research. 11 (6). pp. 994-1004. doi:10.1101/gr.GR-1733RR. PMC 311057. PMID 11381027.

Barać. L: Perićić M: Klarić IM: et al. (July 2003). "Y chromosomal heritage of Croatian population and its island isolates" (PDF). European Journal of Human Genetics. 11 (7): 535-42. doi:10.1038/sj.ejhg.5200992. PMID 12825075.

Battaglia, V.; Fornarino, Simona; Al-Zahery, Nadia; Olivieri, Anna; Pala, Maria; Myres, Natalie M; King, Roy J; Rootsi, Siiri; et al. (2008). "Y-chromosomal evidence of the cultural diffusion of agriculture in southeast Europe". European Journal of Human Genetics. 17 (6): 820-830. doi:10.1038/ejhg.2008.249. PMC 2947100. PMID 19107149

Behar, Thomas, Mark G.; Skorecki, Karl; Hammer, Michael F.; Bulygina, Ekaterina; Rosengarten, Dror; Jones, Abigail L.; Held, Karen; et al. (2003). "Multiple Origins of Ashkenazi Levites: Y Chromosome Evidence for Both Near Eastern and European Ancestries". American Journal of Human Genetics. 73 (4). pp. 768-779. doi:10.1086/378506. PMC 1180600. PMID 13680527. archived from the original (- Scholar search) on 2012-12-11 . Also at http://www.ucl.ac.uk/tcga/tcgapdf/Behar-AJHG-03.pdf and https://web.archive.org/web/20090304100321/http://www.familytreedna.com/pdf/400971.pdf

Bowden, Balaresque, P.; King, T. E.; Hansen, Z.; Lee, A. C.; Pergl-Wilson, G.; Hurley, E.; Roberts, S. J.; et al. (2008). "Excavating Past Population Structures by Surname-Based Sampling: The Genetic Legacy of the Vikings in Northwest England". Molecular Biology and Evolution. 25 (2): 301-309. doi:10.1093/molbev/msm255. PMC 2628767. PMID 18032405

Capelli, Cristian; Redhead, Nicola; Abernethy, Julia K.; Gratrix, Fiona; Wilson, James F.; Moen, Torolf; Hervig, Tor; Richards, Martin; et al. (2003). "A Y Chromosome Census of the British Isles". Current Biology. 13 (11): 979-84. doi:10.1016/S0960-9822(03)00373-7. PMID 12781138. archived from the original on 2008-01-21 also at http://www.ucl.ac.uk/tcga/tcgapdf/capelli-CB-03.pdf

Cinnioğlu, Cengiz; King, Roy; Kivisild, Toomas; Kalfoglu, Ersi; Atasoy, Sevil; Cavalleri, Gianpiero L.; Lillie, Anita S.; Roseman, Charles C.; Lin, Alice A.; Prince, Kristina; Oefner, Peter J.; Shen, Peidong; Semino, Ornella; Cavalli-Sforza, L. Luca; Underhill, Peter A. (2004). "Excavating Y-chromosome haplotype strata in Anatolia" (PDF). Hum Genet. 114 (2): 127-48. doi:10.1007/s00439-003-1031-4. PMID 14586639

Cordaux, Aunger, Robert; Bentley, Gillian; Nasidze, Ivane; Sirajuddin, S.M.; Stoneking, Mark (2004). "Independent Origins of Indian Caste and Tribal Paternal

Lineages". Current Biology. 14 (3): 231-235. doi:10.1016/j.cub.2004.01.024. PMID 14761656

Dupuy: Stenersen. M: Lu. TT: Olaisen. B (2005). "Geographical heterogeneity of Y-chromosomal lineages in Norway" (PDF). Forensic Science International. 164 (1): 10-19. doi:10.1016/j.forsciint.2005.11.009. PMID 16337760

Ennafaa. Hajer: Fregel. Rosa: Khodjet-el-khil. Houssein: Gonzalez. Ana M: Mahmoudi. Hejer Abdallah El: Cabrera. Vicente M: Larruga. Josē M: Benammar-Elgaaïed. Amel (2011). "Mitochondrial DNA and Y-chromosome microstructure in Tunisia". Journal of Human Genetics. 56 (10): 734-41. doi:10.1038/jhg.2011.92. PMID 21833004

Firasat: Khaliq. Shagufta: Mohyuddin. Aisha: Papaioannou. Myrto: Tyler-Smith. Chris: Underhill. Peter A: Ayub. Qasim (2007). "Y-chromosomal evidence for a limited Greek contribution to the Pathan population of Pakistan". European Journal of Human Genetics. 15 (1): 121-126. doi:10.1038/sj.ejhg.5201726. PMC 2588664. PMID 17047675

Fornarino: Pala. Maria: Battaglia. Vincenza: Maranta. Ramona: Achilli. Alessandro: Modiano. Guido: Torroni. Antonio: Semino. Ornella: Santachiara-Benerecetti. Silvana A (2009). "Mitochondrial and Y-chromosome diversity of the Tharus (Nepal): a reservoir of genetic variation". BMC Evolutionary Biology. 9: 154. doi:10.1186/1471-2148-9-154. PMC 2720951. PMID 19573232

Helgason: Sigurðardōttir. Sigrūn: Nicholson. Jayne: Sykes. Bryan: Hill. Emmeline W.: Bradley. Daniel G.: Bosnes. Vidar: Gulcher. Jeffery R.: et al. (2000). "Estimating Scandinavian and Gaelic Ancestry in the Male Settlers of Iceland". American Journal of Human Genetics. 67 (3): 697-717. doi:10.1086/303046. PMC 1287529. PMID 10931763

Kasperaviciūte: Kučinskas. V.: Stoneking. M. (2005). "Y Chromosome and Mitochondrial DNA Variation in Lithuanians". Annals of Human Genetics. 68 (5): 438-452. doi:10.1046/j.1529-8817.2003.00119.x. PMID 15469421[dead link]

Kayser. Manfred: Lao. Oscar: Anslinger. Katja: Augustin. Christa: Bargel. Grazyna: Edelmann. Jeanett: Elias. Sahar: Heinrich. Marielle: et al. (2005). "Significant genetic differentiation between Poland and Germany follows present-day political borders. as revealed by Y-chromosome analysis". Human Genetics. 117 (5): 428-

443. doi:10.1007/s00439-005-1333-9. PMID 15959808 A copy can be found here https://web.archive.org/web/20090304100323/http://dirkschweitzer.net/E3b-papers/HG-05-428-Poland-Germany.pdf.

Kharkov, V. N.; Stepanov, V. A.; Borinskaya, S. A.; Kozhekbaeva, Zh. M.; Gusar, V. A.; Grechanina, E. Ya.; Puzyrev, V. P.; Khusnutdinova, E. K.; Yankovsky, N. K. (2004). "Gene Pool Structure of Eastern Ukrainians as Inferred from the Y-Chromosome Haplogroups". Russian Journal of Genetics. 40 (3): 326–331. doi:10.1023/B:RUGE.0000021635.80528.2f A copy can be found here [1].

Kharkov, V. N.; Stepanov, V. A.; Feshchenko, S. P.; Borinskaya, S. A.; Yankovsky, N. K.; Puzyrev, V. P. (2005). "Frequencies of Y Chromosome Binary Haplogroups in Belarusians". Russian Journal of Genetics. 41 (8): 928–931. doi:10.1007/s11177-005-0182-x A copy can be found here [2].

Kharkov; Stepanov, V. A.; Medvedeva, O. F.; Spiridonova, M. G.; Voevoda, M. I.; Tadinova, V. N.; Puzyrev, V. P. (2007). "Gene Pool Differences between Northern and Southern Altaians Inferred from the Data on Y-Chromosomal Haplogroups" (PDF). Russian Journal of Genetics. 43 (5): 551–562. doi:10.1134/S1022795407050110

King, R. J.; Özcan, S. S.; Carter, T.; Kalfoğlu, E.; Atasoy, S.; Triantaphyllidis, C.; Kouvatsi, A.; Lin, A. A.; et al. (2008). "Differential Y-chromosome Anatolian Influences on the Greek and Cretan Neolithic" (PDF). Annals of Human Genetics. 72 (2): 205–214. doi:10.1111/j.1469-1809.2007.00414.x. PMID 18269686. archived from the original (PDF) on 2009-03-05

Kivisild; Rootsi, S.; Metspalu, M.; Mastana, S.; Kaldma, K.; Parik, J.; Metspalu, E.; Adojaan, M.; Tolk, H.-V.; Stepanov, V.; Gölge, M.; Usanga, E.; Papiha, S.S.; Cinnioğlu, C.; King, R.; Cavalli-Sforza, L.; Underhill, P.A.; Villems, R. (2003). "The Genetic Heritage of the Earliest Settlers Persists Both in Indian Tribal and Caste Populations". AJHG. 72 (2). pp. 313–32. doi:10.1086/346068. PMC 379225. PMID 12536373.

Lell, Jeffrey T.; Sukernik, Rem I.; Starikovskaya, Yelena B.; Su, Bing; Jin, Li; Schurr, Theodore G.; Underhill, Peter A.; Wallace, Douglas C. (2002). "The Dual Origin and Siberian Affinities of Native American Y Chromosomes" (PDF). American Journal of

Human Genetics. 70 (1): 192-206. doi:10.1086/338457. PMC 384887. PMID 11731934. archived from the original (PDF) on 2008-05-09

Luca. F.; Di Giacomo. F.; Benincasa. T.; Popa. L.O.; Banyko. J.; Kracmarova. A.; Malaspina. P.; Novelletto. A.; Brdicka. R. (2006). "Y-Chromosomal Variation in the Czech Republic". American Journal of Physical Anthropology. 132 (1): 132-9. doi:10.1002/ajpa.20500. PMID 17078035

Malaspina; et al. (2003). Analysis of Y-chromosome variation in modern populations at the European-Asian border (PDF). pp. 309-313 in K. Boyle. C. Renfrew. and M. Levine. eds. Ancient interactions: east and west in Eurasia. McDonald Institute for Archaeological Research Monograph Series. Cambridge University Press. Cambridge

Marjanovic D. Fornarino S. Montagna S. et al. (November 2005). "The peopling of modern Bosnia-Herzegovina: Y-chromosome haplogroups in the three main ethnic groups". Annals of Human Genetics. 69 (Pt 6): 757-63. doi:10.1111/j.1529-8817.2005.00190.x. PMID 16266413.[dead link]

Mirabal; Regueiro. Maria; Cadenas. Alicia M; Cavalli-Sforza. L Luca; Underhill. Peter A; Verbenko. Dmitry A; Limborska. Svetlana A; Herrera. Rene J (2009). "Y-Chromosome distribution within the geo-linguistic landscape of northwestern Russia". European Journal of Human Genetics. 17 (10): 1260-1273. doi:10.1038/ejhg.2009.6. PMC 2986641. PMID 19259129

Mukherjee; Nebel. Almut; Oppenheim. Ariella; Majumder. Partha P. (2001). "High-resolution analysis of Y-chromosomal polymorphisms reveals signatures of population movements from central Asia and West Asia into India". Journal of Genetics (published December 2001). 80 (3). pp. 125-135. doi:10.1007/BF02717908. PMID 11988631.

Nasidze. I.; Ling. E. Y. S.; Quinque. D.; Dupanloup. I.; Cordaux. R.; Rychkov. S.; Naumova. O.; Zhukova. O.; et al. (2004). "Mitochondrial DNA and Y-Chromosome Variation in the Caucasus"(PDF). Annals of Human Genetics. 68 (3): 205-221. doi:10.1046/j.1529-8817.2004.00092.x. PMID 15180701. archived from the original (PDF) on 2011-06-08

Francalacci (2013). Low-Pass DNA Sequencing of 1200 Sardinians Reconstructs European Y-Chromosome Phylogeny Low-Pass DNA Sequencing of 1200 Sardinians Reconstructs European Y-Chromosome Phylogeny Check |url= value (help)

Nasidze, Quinque, Dominique, Ozturk, Murat, Bendukidze, Nina, Stoneking, Mark (2005). "MtDNA and Y-chromosome Variation in Kurdish Groups" (PDF). Annals of Human Genetics. 69 (4): 401-412. doi:10.1046/j.1529-8817.2005.00174.x. PMID 15996169. archived from the original (PDF) on 2009-08-23

Passarino, Semino, Ornella, Magri, Chiara, Al-Zahery, Nadia, Benuzzi, Giorgia, Quintana-Murci, Lluis, Andellnovic, Slmun, Bullc-Jakus, Floriana, Liu, Aiping, Arslan, Ahmet, Santachiara-Benerecetti, A.Silvana (2001). "The 49a.f haplotype 11 is a new marker of the EU19 lineage that traces migrations from northern regions of the black sea". Hum. Immunol.. 62 (9). pp. 922-932. doi:10.1016/S0198-8859(01)00291-9. PMID 11543894.

Passarino, Cavalleri, Gianpiero L, Lin, Alice A, Cavalli-Sforza, Luigi Luca, Børresen-Dale, Anne-Lise, Underhill, Peter A (2002). "Different genetic components in the Norwegian population revealed by the analysis of mtDNA and Y chromosome polymorphisms". European Journal of Human Genetics. 10 (9). pp. 521-9. doi:10.1038/sj.ejhg.5200834. PMID 12173029.

Pericic, Lauc, LB, Klarić, IM, Rootsi, S, Janićijevic, B, Rudan, I, Terzić, R, Colak, I, et al. (2005). "High-resolution phylogenetic analysis of southeastern Europe traces major episodes of paternal gene flow among Slavic populations". Mol. Biol. Evol.. 22 (10). pp. 1964-75. doi:10.1093/molbev/msi185. PMID 15944443.

Qamar, Ayub, Qasim, Mohyuddin, Aisha, Helgason, Agnar, Mazhar, Kehkashan, Mansoor, Atika, Zerjal, Tatiana, Tyler-Smith, Chris, Mehdi, S. Qasim (2002). "Y-Chromosomal DNA Variation in Pakistan". American Journal of Human Genetics. 70 (5): 1107-1124. doi:10.1086/339929. PMC 447589. PMID 11898125

Quintana-Murci, Krausz, C, Zerjal, T, Sayar, SH, Hammer, MF, Mehdi, SQ, Ayub, Q, Qamar, R, et al. (2001). "Y-chromosome lineages trace diffusion of people and languages in southwestern Asia". American Journal of Human Genetics. 68 (2): 537-542. doi:10.1086/318200. PMC 1235289. PMID 11133362

Regueiro, M.; Cadenas, A.M.; Gayden, T.; Underhill, P.A.; Herrera, R.J. (2006). "Iran: Tricontinental Nexus for Y-Chromosome Driven Migration" (PDF). Hum Hered. 61 (3): 132-143. doi:10.1159/000093774. PMID 16770078

Rosser, Z; Zerjal, T; Hurles, M; Adojaan, M; Alavantic, D; Amorim, A; Amos, W; Armenteros, M; et al. (2000). "Y-Chromosomal Diversity in Europe Is Clinal and Influenced Primarily by Geography, Rather than by Language". American Journal of Human Genetics. 67 (6): 1526-1543. doi:10.1086/316890. PMC 1287948. PMID 11078479. archived from the original on 2008-05-06

Saha, Sharma, Swarkar, Bhat, Audesh, Pandit, Awadesh, Bamezai, Ramesh (2005). "Genetic affinity among five different population groups in India reflecting a Y-chromosome gene flow". Journal of Human Genetics. 50 (1). pp. 49-51. doi:10.1007/s10038-004-0219-3. PMID 15611834.

Sahoo, S.; Singh, A; Himabindu, G; Banerjee, J; Sitalaximi, T; Gaikwad, S; Trivedi, R; Endicott, P; et al. (2006). "A prehistory of Indian Y chromosomes: Evaluating demic diffusion scenarios". Proceedings of the National Academy of Sciences. 103 (4): 843-848. Bibcode:2006PNAS..103..843S. doi:10.1073/pnas.0507714103. PMC 1347984. PMID 16415161

Sanchez, Børsting, C; Hallenberg, C; Buchard, A; Hernandez, A; Morling, N (2003). "Multiplex PCR and minisequencing of SNPs- a model with 35 Y chromosome SNPs". Forensic Sci Int. 137 (1): 74-84. doi:10.1016/S0379-0738(03)00299-8. PMID 14550618

Scozzari, Cruciani, F; Pangrazio, A; Santolamazza, P; Vona, G; Moral, P; Latini, V; Varesi, L; et al. (2001). "Human Y-Chromosome Variation in the Western Mediterranean Area: Implications for the Peopling of the Region" (PDF). Human Immunology. 62 (9): 871-884. CiteSeerX 10.1.1.408.4857. doi:10.1016/S0198-8859(01)00286-5. PMID 11543889

Semino, Passarino, G; Oefner, PJ; Lin, AA; Arbuzova, S; Beckman, LE; De Benedictis, G; Francalacci, P; et al. (2000). "The Genetic Legacy of Paleolithic Homo sapiens sapiens in Extant Europeans: A Y Chromosome Perspective" (PDF). Science. 290 (5494). pp. 1155-

59. Bibcode:2000Sci...290.1155S. doi:10.1126/science.290.5494.1155. PMID 11073453. archived from the original (PDF) on 2003-11-25.

Sengupta, Zhivotovsky, Lev A.; King, Roy; Mehdi, S.Q.; Edmonds, Christopher A.; Chow, Cheryl-Emiliane T.; Lin, Alice A.; Mitra, Mitashree; et al. (2005). "Polarity and Temporality of High-Resolution Y-Chromosome Distributions in India Identify Both Indigenous and Exogenous Expansions and Reveal Minor Genetic Influence of Central Asian Pastoralists". American Journal of Human Genetics. 78 (2). pp. 202-21. doi:10.1086/499411. PMC 1380230. PMID 16400607.

Sharma, et al. (2007). "The Autochthonous Origin and a Tribal Link of Indian Brahmins: Evaluation Through Molecular Genetic Markers" (PDF). THE AMERICAN SOCIETY OF HUMAN GENETICS 57th Annual Meeting

Sharma, Swarkar; Rai, Ekta; Sharma, Prithviraj; Jena, Mamata; Singh, Shweta; Darvishi, Katayoon; Bhat, Audesh K; Bhanwer, A J S; et al. (2009). "The Indian origin of paternal haplogroup R1a1(*)substantiates the autochthonous origin of Brahmins and the caste system". Journal of Human Genetics. 54 (1): 47-55. doi:10.1038/jhg.2008.2. PMID 19158816

Tambets, Kristiina; Rootsi, Siiri; Kivisild, Toomas; Help, Hela; Serk, Piia; Loogväli, Eva-Liis; Tolk, Helle-Viivi; Reidla, Maere; et al. (2004). "The Western and Eastern Roots of the Saami - the Story of Genetic 'Outliers' Told by Mitochondrial DNA and Y Chromosomes". American Journal of Human Genetics. 74 (4): 661-682. doi:10.1086/383203. PMC 1181943. PMID 15024688

Underhill, P.A.; Myres, Natalie M; Rootsi, Siiri; Metspalu, Mait; Zhivotovsky, Lev A; King, Roy J; Lin, Alice A; Chow, Cheryl-Emiliane T; et al. (2009). "Separating the post-Glacial coancestry of European and Asian Y chromosomes within haplogroup R1a". European Journal of Human Genetics. 18 (4): 479-484. doi:10.1038/ejhg.2009.194. PMC 2987245. PMID 19888303

Varzari, Alexander (2006). "Population History of the Dniester-Carpathians: Evidence from Alu Insertion and Y-Chromosome Polymorphisms" (PDF). Dissertation der Fakultät für Biologie der Ludwig-Maximilians-Universität München

Völgyi, Zalán, Andrea, Szvetnik, Enikő, Pamjav, Horolma (2008). "Hungarian population data for 11 Y-STR and 49 Y-SNP markers". Forensic Science International: Genetics. 3 (2): e27-e28. doi:10.1016/j.fsigen.2008.04.006. PMID 19215861

Wang (2003). "The origins and genetic structure of three co-resident Chinese Muslim populations: the Salar, Bo'an and Dongxiang". Human Genetics. 113 (3): 244-52. doi:10.1007/s00439-003-0948-y. PMID 12759817

Weale, Yepiskoposyan, Levon, Jager, Rolf, Hovhannisyan, Nelli, Khudoyan, Armine, Burbage-Hall, Oliver, Bradman, Neil, Thomas, Mark (2001). "Armenian Y chromosome haplotypes reveal strong regional structure within a single ethno-national group" (PDF). Hum Genet. 109 (6): 659-674. doi:10.1007/s00439-001-0627-9. PMID 11810279[permanent dead link]

Weale, Weiss, DA, Jager, RF, Bradman, N, Thomas, MG (2002). "Y Chromosome Evidence for Anglo-Saxon Mass Migration" (PDF). Mol. Biol. Evol., 19 (7), pp. 1008-1021. doi:10.1093/oxfordjournals.molbev.a004160. PMID 12082121.

Wells, Yuldasheva, N, Ruzibakiev, R, Underhill, PA, Evseeva, I, Blue-Smith, J, Jin, L, Su, B, et al. (2001). "The Eurasian Heartland: A continental perspective on Y-chromosome diversity". Proc. Natl. Acad. Sci. U.S.A., 98 (18), pp. 10244-9. Bibcode:2001PNAS...9810244W. doi:10.1073/pnas.171305098. PMC 56946. PMID 11526236. Also at http://www.pnas.org/cgi/reprint/98/18/10244.pdf

Wells, Spencer (2002). The Journey of Man: A Genetic Odyssey. Princeton University Press.

Wilson, Weiss, DA, Richards, M, Thomas, MG, Bradman, N, Goldstein, DB, et al. (2001). "Genetic evidence for different male and female roles during cultural transitions in the British Isles". Proc. Natl. Acad. Sci. U.S.A., 98 (9): 5078-5083. Bibcode:2001PNAS...98.5078W. doi:10.1073/pnas.071036898. PMC 33166. PMID 11287634

Zerjal, Beckman, L, Beckman, G, Mikelsaar, AV, Krumina, A, Kucinskas, V, Hurles, ME, Tyler-Smith, C, et al. (2001). "Geographical, linguistic, and cultural influences on genetic diversity: Y-chromosomal distribution in Northern European populations". Mol Biol Evol. 18 (6): 1077-1087. doi:10.1093/oxfordjournals.molbev.a003879. PMID 11371596

Zerjal, Tatiana; Wells, R. Spencer; Yuldasheva, Nadira; Ruzibakiev, Ruslan; Tyler-Smith, Chris; et al. (2002). "A Genetic Landscape Reshaped by Recent Events: Y-Chromosomal Insights into Central Asia". American Journal of Human Genetics. 71 (3): 466-482. doi:10.1086/342096. PMC 419996. PMID 12145751

Zhou, Ruixia; An, Lizhe; Wang, Xunling; Shao, Wei; Lin, Gonghua; Yu, Weiping; Yi, Lin; Xu, Shijian; Xu, Jiujin; Xie, Xiaodong (2007). "Testing the hypothesis of an ancient Roman soldier origin of the Liqian people in northwest China: a Y-chromosome perspective". Journal of Human Genetics. 52 (7): 584-91. doi:10.1007/s10038-007-0155-0. PMID 17579807
[1]

Zhao; Khan, Faisal; Borkar, Minal; Herrera, Rene; Agrawal, Suraksha (2009). "Presence of three different paternal lineages among North Indians: A study of 560 Y chromosomes". Annals of Human Biology. 36 (1): 1-14. doi:10.1080/03014460802558522. PMC 2755252. PMID 19058044

^ "The Genetics of Language and Farming Spread in India" (PDF).