

To trace back our genetic footprints

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Man was made out of clay and woman out of one of man's rib. No? Modern man arose from the Neanderthals. No? If truth be told, how far back can you retell your genealogy? Do you know where your grandmother grew up, or her mother? Theories about where modern human stem from have been drawn since early ages, but since the oldest historical records only date as far back as 5 - 6 thousand years ago (KYA, from kilo years ago) there has been no way to know with certainty the relation between modern human populations. With today's DNA technology, scientists are able to trace back human lineages as far a billion years. So where do we come from, really?

Out of Africa...

Today, there is a consensus among scientists about anatomically modern human's (AMH) origin in Africa. Already in the 19th century Charles Darwin drew the same conclusion based upon the presence of large apes on the continent. There has been other observations as well, leading to theories such as the Blitzkrieg hypothesis. These theories now have to face the test of genetic evidence.

Blitzkrieg

One observation that supports the theory of our origin in Africa is the lack of mega fauna (presence of larger animals such as elephants) on the other continents, which can be explained by the Blitzkrieg hypothesis. It explains that there have been mega faunas all over the world, but due to man's exit out of Africa and rapid expansion over the globe some 50 - 60 KYA the large animals became extinct. Scientists have found archaeological evidence of this kind of eradication in Australia. The hypothesis claims that the large animals on these continents had not experienced the growing threat from when the girl lay in the treetop-cradle to when she started hunting in groups, with spears. Because of this, they were taken by surprise when we arrived. Can man have moved so quickly that she managed to go beyond the speed of evolution?

Genetic evidence

Greater genetic diversity has consistently been found in the human populations of Africa than elsewhere in the world. Whereas there are several mitochondrial strains in Africa, only two are present in non-Africans. It is believed that there might have been as few as 1,000 individuals making the first successful trespassing out of Africa (Sahara had been a major obstacle to circumvent). This created what population geneticists refer to as a bottleneck. When few individuals out of an originally diverse population set out to found a new population, they bring only part of the genetic diversity. Thus, as we

look at global genomics, we can see that all people outside of Africa share their ancestry, and that it traces back to a few lineages that stem from Eastern Africa - and which have continued to evolve and diverge even there. L3 is a site in the mitochondrial DNA that all non-Africans share, which is sometimes referred to as Mitochondrial Eve. The ancestress with this mitochondrial marker is computed to have lived in north-eastern Africa some 50 - 60 KYA. There is also a marker on the Y-chromosome which is shared by all men outside of Africa, namely M168. This marker on the male chromosome is sometimes referred to as Eurasian Adam, since it is present in all Europeans and

What DNA?

There are two ways in which you can trace our genetic history. Either, you sample and analyse the genome from living individuals or, you retain DNA from dead individuals. With today's technologies, it is possible to retain DNA from remains 50,000 years, or even 100,000 years old.

Asians.

...but where to?

So we all agree that we stem from Africa, but how many populations actually moved away and which route they decided to explore first has been widely discussed.

The Southern Route

Scientists have found archaeological evidence of human activities near the north of Australia dating to 60 KYA. One asks how this can be possible when the oldest fossils found in Asia are dated to 40 KYA. One theory which proposes an explanation is the Southern Route model which claims that certain groups of humans have adapted to a life on the coast of Africa. Huge amounts of shells from clams have been found along the east coast of Africa, suggesting a diet rich in sea food.

Furthermore, archaeological findings of similar tools with shared dating ages along the whole or long stretches of the eastern coast suggests there might have been trading between the coast dwellers.

The problem with finding archaeological evidence is that the sea level was about 100 meters lower then than what is today (due to the ice blanket covering our northern hemisphere). This of course is a supposition for the theory to hold, since the distances between continents and island were shorter. Maybe there were even land routes between some of the oceanic islands? However, due to the rise in sea level, many hundred kilometres of land has sunk under water, possibly hiding archaeological evidence on what is now the ocean floor. With no archaeological evidence, can genetics lend a helping hand?

Genetic evidence

As stated above, all non-Africans share their mitochondrial L3 marker. However, there is a deep split in mitochondrial lineage of non-Africans. From L3 there is a divergence, with two separate markers, M and N. M seems to have almost the same age as L3. It can only be found in low frequencies in the Middle East, and not at all in Europe. However, 20 % of the Indian populations have the M-marker, and 100 % of the aboriginal Australians. This speaks for that there actually was an early migration to Australia. What is more, there is a similar pattern in the global pattern of the Y-chromosome. There is a marker called M130 which does not exist to the west of the Caspian sea,

but is shared by 60 % of aboriginal Australia men. The frequency of this marker gets lower in the Oceanian populations, and it exists in only low frequencies in India (about 5 % or less).

Mitochondria Schmitochondria, what about it?

When scientists first set out to compare human DNA, there were major benefits with using mitochondria. Firstly, there are about a thousand copies of mitochondrial DNA in each human cell, compared to two copies of the nuclear genome. Secondly, because the mitochondria has bacterial ancestry (the endosymbiont hypothesis) its' DNA is a circular molecule which does not recombine. Since recombination is the big reshuffle-er of the human genome, it is very much easier to trace the genetic lineage of the non-recombining mitochondrial DNA and Y-chromosome (remember the Y-chromosome exist in only one copy in each male cell, which prevents recombination during meiosis).

How can we explain that the mitochondrial lineage, supposedly taking the Southern Route, exist in higher frequency than the Y-chromosomal lineage following the same thoroughfare? Imagine for a second that there was a wave of migration, some thousand years later than the Southern Route, which entered from north of India. If they were to encounter the coast dwelling M-women and M130-men, what is likely to have happened? Well, what usually happens when two groups of people fight over territory; the men are killed and the

women are raped or taken as prisoners. By these means, the Y-chromosomal lineage is abruptly erased and the mitochondrial lineage continue to live on, although in lower frequency when mixed

with the invasive population.

On and upward!

The second daughter of mitochondrial Eve (L3), the N marker, as well as the second lineage on the Y-chromosome, M89, seemed to have expanded slowly from the near east northward. The majority of the Eurasian and Oceanian land masses were populated some 30 KYA. Since we observe all this in retrospect, we will never be able to know the actual incentive in our ancestresses which caused them to move and expand into new territory. One favoured approach though, is to view human migrations in the perspective of climatic change. As suggested above, the ice age during human's exit out of Africa supports the possibility of the Southern Route theory. Climatologists can give new approaches which may support or overthrow migration theories. For example, it is believed that major droughts can have made human game leave the near east. This may have been what caused our ancestress to migrate. In quite the same manner, geographical barriers seem to have separated the populations migrating into Asia some 45 KYA.

You are marked, but how?

Geneticists look after differences in the DNA of different individuals or populations. These differences, if sufficiently pronounced, are called genetic markers. There are several types, whereof some are listed below.

SNP – single nucleotide polymorphism, can be due to a base substitution (when one nitrogen base is exchanged for another) or an indel (an insertion or deletion of an extra nucleotide).

VNTR – variable number of tandem repeats, can be either due to the size of the repeating units, the number of units in the arrays or the level of variability.

The Hindu Kush

There are significant genetic differences between the people to the south and north of the great mountain range of Hindu Kush. South of the mountains lies India. A genetic marker called M20, stemming from 30 KYA, is shared by 50 % of the men in southern India. This lineage seems to have expanded to the far east. 30 % of Korean populations share a marker called M175, which originated about 35 KYA from the M20 lineage. The M175 marker does not exist at all in either Europe or Western Asia, but it appears in 60 – 90 % of the Y-chromosomes of East Asians (depending on the population sampled).

To the north of Hindu Kush lies Central Asia and Siberia. Men originating from this area share a genetic marker called M45. It seems that the populations migrating to the north of Hindu Kush spread over all of central Asia and eventually came to meet with the descendants of the M20 lineage who had expanded to the east south of the mountain range. This meeting has left genetic traces; the

northern Han groups are closer relatives to northern non-Han groups than they are to southern Han groups. Thus, despite a shared culture today, their DNA tells of different ancestries.

Your cells - ticking clocks

It is one thing to compare and contrast DNA segments, but how can you estimate the age of a genetic difference? The simplest explanation requires that mutations occur regularly. If you know that there is about one mutation each x generation, you can then count the differences between two DNA segments and derive how many generations ago they were separated.

Cold blooded

It is believed America was populated only 15 KYA. It is thought that there were Siberian populations that crossed the Bering Strait during the last ice age. This could only be possible if they were extremely well adapted to an arctic lifestyle. Probably, it was due to the harsh conditions of Central Asian steppes and the southern parts of Siberia that the populations had developed skills sufficient to trespass the Bering Strait. Probably, they then

migrated down the east of the Rocky Mountains down into the continent. However, the aboriginal Americans belong to two separate lineages. It is believed that there were two waves of migration into America. The first one left descendants all over America who are identified by the marker M3. It is shared by 90 % of South- and Central Americans, and 50 % of North Americans. The second wave of migration only left descendants in the north, who are identified by a marker M130. 25 % of the Na-Dene men share this marker, but it is absent in the men of South America.

A genetic melting pot

When it comes to Europe, the pattern is not too easily resolved. Because the migration to the west happened relatively recently, and by two or more independent waves of migration by populations that had much time to differentiate and mend on their own before they met in Europe, the genetic diversity is a puzzle.

Martha, right?

The exploration of the genomes of Europeans have indeed been rewarding. As other populations migrated away from the Arabian peninsula, there were also people staying in north eastern Africa. When a subgroup of this population went out of Africa and headed west, they came in close contact with some distant kin. The evidence now points to that AMH, our ancestresses, lived side by side with Neanderthals. In addition to the M89 marker which is shared by almost all Europeans, about 2 % of some Europeans' genome has Neanderthal ancestry. Thus, there obviously was more than just cultural exchange between the groups. However, this mixture happened on a short time scale. AMH entered Europe 35 KYA, and the Neanderthals were extinct at 25 KYA.

Over 70 % of men in southern England and 90 % of the men in Ireland and Spain have a polymorphism named M173, which stems from the M45 lineage. Thus, the men of western Europe are descendants from the Central Asian clan, the same lineage that conquered Southern Siberia and later on America. About 80 % of the European gene pool has this ancestry, and it is thus likely that Europe was colonized from Siberia downwards. However, 20 % of the European gene pool has a more recent origin, stemming from the Middle East. This new wave of migration may have brought more than genetic diversity to the area.

Old MacDonald had a farm...

The step from being hunter-gatherers to farmers, called the Neolithic or Agricultural Revolution, was indeed a major breakthrough for humanity. From having been slaves under our game, we

Models of human expansions

Linkage disequilibrium - based upon the theory that genes do not appear as separate entities. They are linked with other genes, and are replicated with other genes. Sometimes, through the act of recombination, the linked genes are separated. By finding the point when the difference in a specific segment of DNA between two individuals appeared, you can trace their most recent common ancestor.

Wright's island model - assumes that each population could be seen as living on a separate island, with all other populations representing a parent population with which the island population could exchange genetic diversity with by migration.

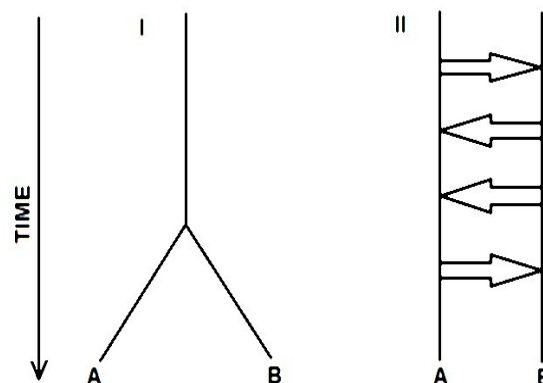


Figure I represents the Linkage disequilibrium model, with population A and B share genetic resemblance due to a common ancestor. **Figure II** represents Wright's island model, with arrows demonstrating regular migration between population A and B.

suddenly decided to seize control over our food. As we settled and started to till the soil the definition of ownership arose – this is my land, not yours. However, there is an ongoing dispute amongst historians as well as geneticists of how this trend expanded.

May I borrow your plough

The Neolithic Revolution happened at a very fast rate about 10 KYA, but how? Was agriculture spread as a cultural phenomenon, or was it the farmers who spread? The 20 % of European gene pool which comes from the second wave of migration from the Middle East seems to have Neolithic ancestry. This indicates the Neolithic age was brought to Europe by farmers who displaced the hunter-gatherers.

Son of a...

One believes that as a result of ownership over land, patriarchy evolved. It was necessary to make sure that what you owned would be passed on to your children, and the concept of inheritance arose. Genetics have confirmed the patriarch-locality of human groups. When studying the genetic disposition of different populations one thing is clear; the Y-chromosomal difference is much higher than mitochondrial differences. Remember mitochondria are transferred from the mother, and the Y-chromosome is passed from father to son. According to our genomes, men have stayed put whilst women have moved between different populations. What is more, one can see a great amount of homogeneity in the Y-chromosomal DNA in each population, that is, the Y-chromosome in each population goes way back. This means that there must have been only a few men in each population that were given the opportunity to reproduce, and once they had seized this power they made sure that the same privilege was given to their sons. In all aspects the prerogative to sow their seeds quite literally went from father to son.

Are your father American?

One approach to draw the picture of human origin and migration is to trace cultural developments and linguistic patterns. If you find very similar tools in two areas, you may come to the conclusion that there must have been a migration of men from the one point to the other. In the same manner, if you observe that all humans in the western part of a country speak one language and all humans in the eastern part speak another, you figure they may stem from two different lineages. However, if you stop to think about the origin of the tools, clothes and words you will use today you soon realize that cultural exchanges does not always accompany genetic exchange.

Final conquest

In the middle of the Pacific, surrounded by vast amounts of sea, there are some spots of land. They are the Polynesian islands. It is hard enough to imagine how people got there in the first place, and even harder to believe that they got there twice. One example is the Easter Island, which is inferred to have been populated some 1.5 KYA. Analysis of the genomes of Easter Island populations has shown that there is a genetic difference between the people living in the middle of the island and the people living on the coast. It seems like the descendants of the first migration were later pushed into the centre of the island as a new wave of immigrants arrived.

Curious to learn more?

Jobling MA, Hurles ME, Tyler-Smith C. 2004. Human Evolutionary Genetics – Origins, Peoples & Disease. Garland Publishing, New York.

Sandell L. 2013. Genetic Methods to Trace Anatomically Modern Human Migration Outside of Africa. Independent project in Biology, Uppsala University.

Wells S. 2003. The Journey of Man. A Genetic Odyssey. Penguin Group, London, England.