

We Are Caucasians

Analysis of Our Genomic Ancestry

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Foreword

Until the advent of affordable DNA analysis was made commercially available for public research, the options for genealogical family history research included document searches, utilizing the experiences of genealogical societies and hiring a professional genealogist to explore libraries and archives. Then access to overseas records became available, either by hiring a professional or by taking expensive trips to look directly at the records. The LDS History Library was open to the public. Everyone was invited to use the extraordinary facilities, whether one was Mormon or a guest. The Church digitized its records and made access freely available to the public. One could do the research from home or office.

Having researched our family history by interviews and scanning relevant vital records, I seized upon the opportunity to obtain direct DNA evidence as another scientific resource that was uniquely positioned to reveal the links of our family history by utilizing the evidence revealed in the direct inheritance of our parental DNA

Over the past 15 years (since 2002), publications about DNA research have revealed details about our inheritance that were not anticipated. I am speaking of the confirmation of both the mutations of single nucleotides binding the double helix contained in the 23 pairs in our inherited chromosomes, as well as the multi-repeated sequences of runs of the nucleotides. Genetic field studies of indigenous populations, by such scientists as Spencer Wells, provided invaluable details about the regionalization of genetic haplotypes, thus permitting better understanding of the genomic migration of our ancestors. Mutation rates were refined and that calculus permitted better dating of ancient mutations. The database derived from the discovered mutations has grown globally, which has increased the scientific confidence in the findings.

I decided to publish my research findings for our family members and to share the techniques embodied in the detailed investigations that have been required. The data revealed that our modern human ancestors appeared in Africa, probably the Northeast region, about 300,000 years ago. They were dark-skinned and very few in number. In 2016, there were 18 skeletons discovered in a grave in Morocco. Scientific research

confirmed that the bones were human and 300,000 years old. Calculations of the DNA from 5 other Africans revealed their DNA was about 348,000 years old. Our ancestors were alive and well a very long time ago. The calendar of modern human existence was moved back by 250,000 years.

More recent ancestors lived in the Kura Araxes Valley of Georgia, Caucasus, about 15,000 years ago. We are Georgians – hence the title of this manuscript became, “We Are Caucasians.” Our paternal male ancestors were part of the Kura Araxes culture during the early Neolithic period, which expanded to Eastern Anatolia about 6,000 years ago and then to Antioch, Syria (now Turkey) and the Levant about 2,800 years ago. Finally, the Kura culture was discovered at Tel Bet Yerah located along the Southwestern edge of the Sea of Galilee, where the Jordan River emerges in the Jordan Valley of Palestine. Evidence suggests that our ancestors were members of the Hebrew Tribe of Naphtali. Lastly, DNA evidence indicates that we are “Ashkenazim,” and appear to have migrated to Europe in the 8th century C.E.

Our maternal Solomon family from Romania revealed Y-DNA from another African group, haplotype “E1b1b1b.” Those ancestors appeared in the Northwestern region, possibly the Horn of Africa, about 40,000 years ago. They remained for millennia in Africa. By about 15,000 years ago, mutations coded as E-34 appeared among our ancestors. By 20,000 years ago, it has been estimated the proto-Afroasiatic language appeared in Africa. This was the estimated forerunner of the Semitic family of languages/dialects.

Our E-M34 ancestors appeared in Morocco from where they migrated to Iberia about 18,000-15,000 years ago. Members of that haplogroup migrated further to Sardinia, Italy and Greece about 12,000 years ago. Their DNA split into several subclades (subgroups) and our direct ancestors then migrated to Eastern Anatolia about 3,000 years ago. WOW!!! THE ANCIENT MALE ANCESTORS FROM BOTH OUR PATERNAL AND MATERNAL FAMILIES MIGRATED TO THE SAME REGION OF ANATOLIA AND ARRIVED AT THE SAME PREHISTORIC TIME.

In 1964, I became a Capt. In the United States Air Force, serving as a flight surgeon at the NATO airbase in Incirlik, Turkey (7-miles south of Adana, Turkey). It was a fascinating assignment that provided innumerable medical responsibilities:

administrative, direct care of the flying personnel and often their dependants, public hygiene, water safety, food contamination issues, sewage control and immunizations. My wife, Marlene, and I travelled locally and throughout both Turkey and nearby Middle Eastern countries, such as Syria, Iran, Jordan, Egypt and Israel. On military duties I was deployed to Anatolia, Ankara, Istanbul, Trabzon, Varto (Kurdish rural town located in the lee of Mt. Ararat, Antioch, etc. I had no concept that I had been living and working in the footsteps of the lands that my genomic ancestors from 15,000 – 3,000 years ago. This topic is more fully presented in the manuscript.

I have high confidence in the analyses of both the genomic data, as well as the published facts from the scientific disciplines of archeology, anthropology, geography, linguistics and religious history. With the addition of the genomic data, the cross-referenced facts appear to re-enforce my conclusions.

It is hoped that each of you readers will take this journey of discovery with me. I urge you to think about the fact that I have only discovered the names of our ancestors since written documents were discovered. The documents account for only 200 or so years of our family history. What about the ancient history that began 300,000 years ago? I can only offer their genetic identity as Mr. AA0 or Mr. J2a/M410. Will anyone in the future think of them or remember them? They had real lives, families and descendants. In the beginning of the modern human era in Africa, our ancestors had dark skins, different voices and language of some rudimentary type. We exist today because of their successful lives. Let us think of them most kindly as we tour Western Asia, the Caucasus, Kura Araxes Valley, Anatolia and the Levant.

Only after the 18th century are we able to identify their given names; in the 19th century we had the first glimpse of legal surnames from Poland, Romania and Russia. A mere 12,000 years ago, we had the great fortune of ancestors, who thrived in Neolithic times in the Fertile Crescent region of the Middle East. It will be very evident that our ancestors had culture and an ancient spirituality. They migrated and expanded to the Levant, where they became part of the Hebrew Tribe of Naphtali located at the shores of the Sea of Galilee. Read with enjoyment and the pleasure of finally knowing our particular ancient family history. Genetic science has preserved our history; there are no other memorials. Let us be very thankful for the blessing of learning who our ancient

ancestors were and where they thrived. I have published this work as my personal family legacy.

With love, and best wishes for your personal successes and good health,

Robert

Robert S. Sherins, MD

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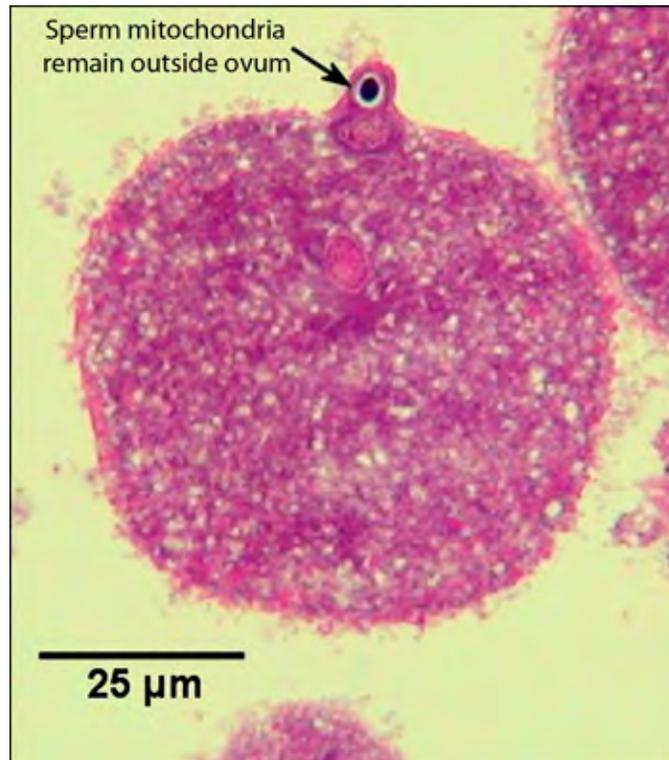
Our Ancestral Genomic Journey

Modern humans appeared in Africa about 348,000 years ago. Dr. Michael Hammer, University of Arizona, and founder of the Family Tree DNA Company first estimated this calculation. In 2017, a team of archeologists discovered 18 skeletons that were buried in a common Moroccan grave. DNA was obtained from several of the skeletons that were dated 300,000 years ago. It appears that every modern human living today evolved from humans who lived in Africa at that time.

Mating consequences involve merging of genetic materials in the conceptus. The image below was taken during fertilization of a human ovum. Of importance is the fact that both the ovum and the sperm are haploid, which means that each gamete contained only half of the genetic DNA. When combined during fertilization, the conceptus gains the full compliment of genetic material to grow into a human offspring.

Only the nucleus of the sperm enters the ovum to be inserted into the egg nucleus. The image below demonstrates that the sperm mitochondria located in the tail remains outside the ovum and is not directly transferred to the conceptus. Therefore, the maternal mitochondrial DNA (mtDNA) in the ovum must produce both the maternal and paternal components of the pairs of mitochondrial DNA in the offspring. This knowledge is fundamental in understanding the results of DNA testing.

DNA testing scans for the sequences of single mutations on the male Y-Chromosome and the X-Chromosome in either the male or female. The 22 other autosomal chromosomes are not yet tested. There are over human 20,000 genes located on the 23-pairs of chromosomes. The Y-Chromosome has only about 1,6100 genes. So far, most of the DNA studies for genealogical purposes have been restricted to that 23rd chromosome. However, as the technology and algorithms improve in the future, we may expect even more precise and affordable analyses will become available to the public.



Fertilized Conceptus with Mitochondria of the Sperm Outside the Ovum

DNXA testing is may be easily performed on an oral specimen obtained by swabbing inside cheek tissue or saliva. Chemical amplification of the DNA in the specimen provides an adequate amount of genetic material for testing.

The advent of the scientific investigations under the auspices of the Human Genomic Project made possible relatively inexpensive genetic testing, which was readily available to the public.¹ Several laboratories offer the services. The Family Tree DNA company was selected by the author to process his specimens, which were performed at the molecular biology laboratory under the direction of Professor, Dr. Michael Hammer at the University of Arizona. Dr. Hammer's laboratory has accumulated a genomic database of about 750,000 samples worldwide, which is currently the largest and foremost genomic testing laboratory for this purpose. The data are secured and indexed so that only the owner of the individual specimen can obtain his or her data by

¹ *The "Human Genome Project" was organized and coordinated by the U.S. Department of Energy and the National Institutes of Health. The program was launched in 1990 in order to identify the approximately 20,000-25,000 genes in human DNA and to determine the sequences of the 3 billion chemical base pairs (nucleotides) that make up human DNA. By 2003, the results of the research investigations were released to the private sector.*

knowing both the sample number and password. As future new information is learned, the laboratory at no extra charge will provide updates to its participants. Additionally, Dr. Hammer's laboratory at the University of Arizona performs the DNA analyses on the specimens received from the National Geographic Genomic Project and Ancestry.com website applicants.

In 2001, "The Seven Daughters of Eve, the Science that Reveals our Genetic Ancestry," by Dr. Brian Sykes,² was published by W.W. Norton & Company, New York and London. This very readable and basic analysis of the female human genomic journey became a best seller, which created keen public interest in the use of DNA testing for the purpose of determining one's female genetic ancestry.

Dr. Sykes determined that mutations of the genetic coding occur about once in every thousand years, although the mutations found in the male Y-DNA are more varied than the mitochondrial-DNA (mtDNA) of females. The tests are performed and compared to the results in the database of samples obtained from individuals living in varied worldwide regions. Dr. Sykes identified and calculated the approximate dates of origin and the approximate geographic locations of the mutations. The results produced the estimated dates of the appearance and the dates of the *most recent common female mutations in Europe*. Those females were called genetic "Eves". They were provided with fictitious given names, by which he identified the seven regional European genomic regions.

Anthropologist and geneticist Spencer Wells, PhD, renowned authority on this subject, popularized genomic testing through public media supported by the National Geographic Society (The Genographic Project, 2005). Dr. Well's comments summarize the subject very well:

"Some 99% of the human genome is shuffled from one birth to the next. The Genographic Project traces the 1% of the genome, which is not shuffled—

²Sykes, Brian: "[*The Seven Daughters of Eve*](#)^[1] is a book by [Bryan Sykes](#) that presents the theory of [human mitochondrial genetics](#) to a general audience. Sykes explains the principles of [genetics](#) and [human evolution](#), the particularities of mitochondrial DNA, and analyses of ancient [DNA](#) to genetically link modern humans to [prehistoric](#) ancestors. Oxford University Professor of Genetics at the Institute of Molecular Medicine, 2015.

mitochondrial DNA (mtDNA) through the maternal line and the Y-chromosome through the paternal. These jokers in the pack allow geneticists to work back to our common ancestors. Our mtDNA appears to coalesce in a single woman, who lived on the African savannah 150,000 years ago (now estimated to be ~300,000 years ago). Our Y-chromosome survives from a single man, who lived in the Rift Valley of Kenya and Tanzania about 348,000 years ago.

[It is estimated that...] About 60,000 years ago, our species had crashed to about 2,000 individuals, then recovered with the help of language and conceptual thinking. The speed of our spreading is alarming set against evolutionary time, as if we are bacteria. The journey of each individual is arranged by haplogroup, a branch of migration marked by a genetic mutation. Since the 1848 revolutions, the spread of mechanized transport and the rise of “isms” culminating in globalism, couples have been shuffling their distinct genetic families, or haplogroups, some representing tiny indigenous peoples, others much of western Europe.

In many respects the Genographic Project is a race against time. Indigenous peoples amount to just 350m of the 6.8 billion people on the planet. The number of languages has gone from 15,000 in 1492 to 5,900 today. The ancient bloodlines are almost gone [because of the assimilation of populations].”

Modern humans may have first appeared in the Rift Valley of northeastern Africa about 348,000 years ago³. For about the first 100,000 years, three identifiable mutations in the mitochondrial DNA appeared among the first groups of humans. Original male equivalent DNA from our most recent common ancestors has not yet been discovered. Those small bands of individuals migrated, but remained within Africa for at least 250,000 years. The people of the San-Bushman tribe are genetically the descendants of the first modern humans.

³ *Y-DNA evidence of the Aoo male haplogroup.*



San Busman Village



<http://nissan4x4.co.za>

Diaspora “Out Of Africa”

It is estimated that about 80,000 years ago, small bands of humans migrated out of Africa and crossed over to the Southern Arabian Peninsula over or through the region of narrowing of the Red Sea as it passes to the Gulf of Aden. The isthmus is quite restricted and in ancient times, there may have been a land bridge.

The routes of migration out of Africa have been determined by the measuring molecular changes (mutations) of the gender-determining chromosomes, the Y-DNA and the mitochondrial DNA, (mtDNA) of the indigenous populations living in both geographic regions. The first group has been identified as the “DE” haplogroup, which appeared in Arabia 80,000 years ago. Descendants of those first individuals continued to migrate along the coastline of South Asia, reaching India, Indonesia and Australia by about 60,000 years ago.

The first genetic “Adam” was estimated to be 348,000 years ago. Published in *The American Journal of Human Genetics*⁴ was an article that identified the Y-DNA of an African-American male from South Carolina, who had genetic mutations estimated to have originated at least 348,000 years old. This archaic genome preceded all previously examined Y-DNA dates. The haplogroup has been identified at the A00 haplogroup, which is the currently oldest human male lineage from Africa. Testing of indigenous populations has confirmed several other individuals with identical mutations presently living in Cameroon. None have been found in sub-Saharan Africa, but it does not confirm that Cameroon was the location of origin of this haplogroup.

Other recent analyses of African haplotypes among indigenous populations has shifted the location of the presumed “genetic Adam.” Haplogroup A1b has been associated with Bakola pygmies from Southern Cameroon and one individual male who is an Algerian Berber. Since the discovery of the South Carolina male who exhibited the earliest Y-DNA haplotype, the classification identification of this archaic DNA has been changed to A00.

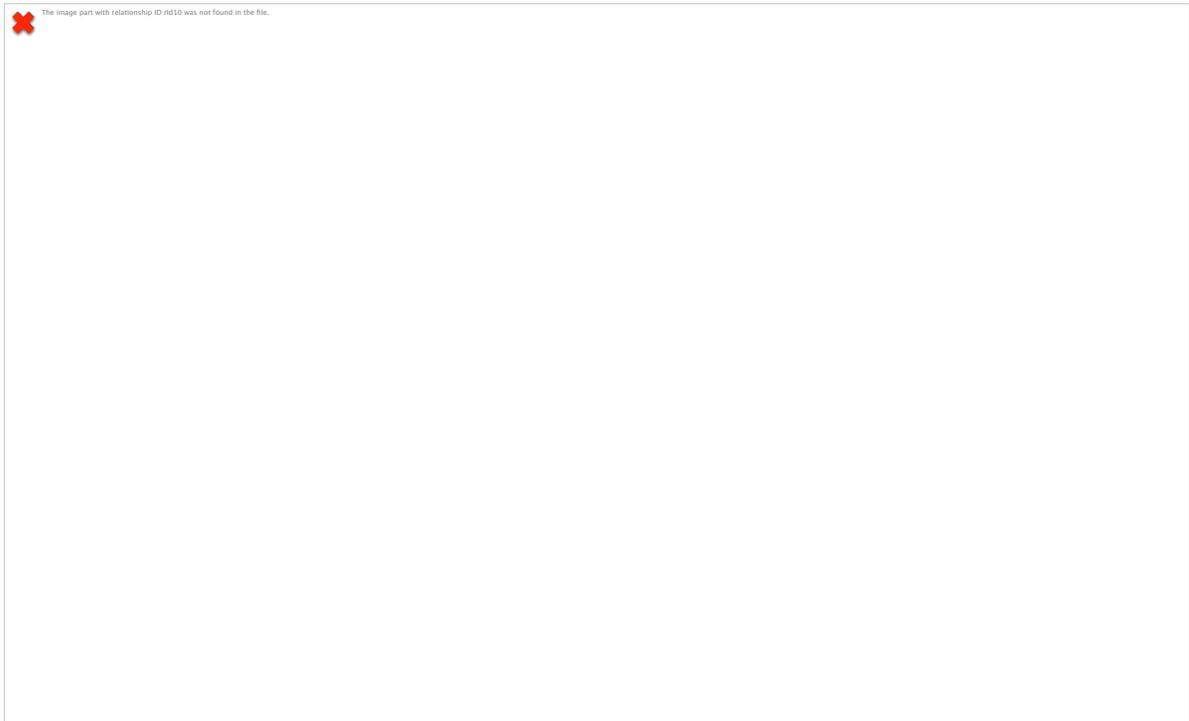
⁴ Vol. 92, pages 454-459, March 7, 2013.



“D” Haplogroup - First Out of Africa, 80,000 Years Ago (<http://earth.google.com/>)

A second wave of humans migrated out of Africa approximately 60,000 years ago. They migrated northward into the Middle East. Some of those individuals remained in the Middle East, but others continued to migrate northward and reached Central Asia and the Caspian Sea region about 55,000 years ago. By 45,000 years ago, an ice-age maximum appeared, during which the ice cap increased and retreated northward to the pole and thereby opened new grasslands in Europe and Asia. Early modern humans followed the herds of animals into Europe for the first time. Those individuals are known as the Cro-Magnon. By 35,000 years ago, other territories in Asia became accessible to wildlife. Following their food sources, modern humans migrated eastward as far as Siberia. By 18,000, the seas were lowered due to the Polar ice-maximum and a Siberian land bridge to North America formed, Small bands of humans entered North America for the first time. When the seas rose again, the humans, who had migrated to North America, were unable to return to Siberia. Instead, they continued to move southward. During the next millennium, a relatively short time, descendants from those early Amerasians reached Central and South America.

The initial human migration out of Africa has been genetically identified as Y-DNA Haplogroup “DE” haplogroup. However, only about 10% of living persons today are classified as the descendants of those genetic “DE” ancestors. Everyone else (90% of living persons) is related to the individuals who comprised a second wave of humans, who migrated from Africa to Central Asia about 60,000-55,000 years ago. The second wave of human migration out of Africa has been genetically identified as “M” or “N” haplogroups.



Second Wave of Human Migration to Central Asia

<http://www.google.com/maps>



Cro-Magnon Migration to Europe - 45,000 Years Ago



Asian Migration about 35,000 Years Ago

Let me summarize the information that we have learned thus far. It took 7-million years for the bipedal hominids of Africa to have evolved to a state of having larger brains, creating hand tools, and surviving within Africa as hunter-gatherers. Dentition shows that omnivorous diets prevailed, which may have had direct consequences in providing for the high protein diets required to build the more complex brains of the later species.

Within the period of 500,000 to 300,000 years ago, Neanderthal species appeared in the Middle East, Europe and Central Asia. We now understand that by 348,000 years ago the first modern human males appeared in Africa as attested by the recent discovery of the A00 Y-DNA haplogroup of the African-American male in South Carolina and 3 other individuals in Cameroon (2) and Algeria (1). Thus, we can say with confidence that for a period of time, perhaps 50,000 years, modern humans had evolved within the time frame of Neanderthal evolution. The appearance of both species may have been concurrent for 50,000 or so years, but Neanderthal was NOT present in Africa. At least, no fossil records of Neanderthal have been found in Africa so far.

Female mitochondrial DNA has been analyzed (mtDNA) from many indigenous populations of Africa and other global communities. By using the same calculus used with the Y-DNA project, it has been estimated that the earliest female modern humans evolved in Africa about 200,000 to 150,000 years ago. With the discovery of the male A00 haplogroup from 348,000 years ago, we can assume that a female counterpart may be discovered from the same archaic period. Modern human female counterparts were required for successful matings.

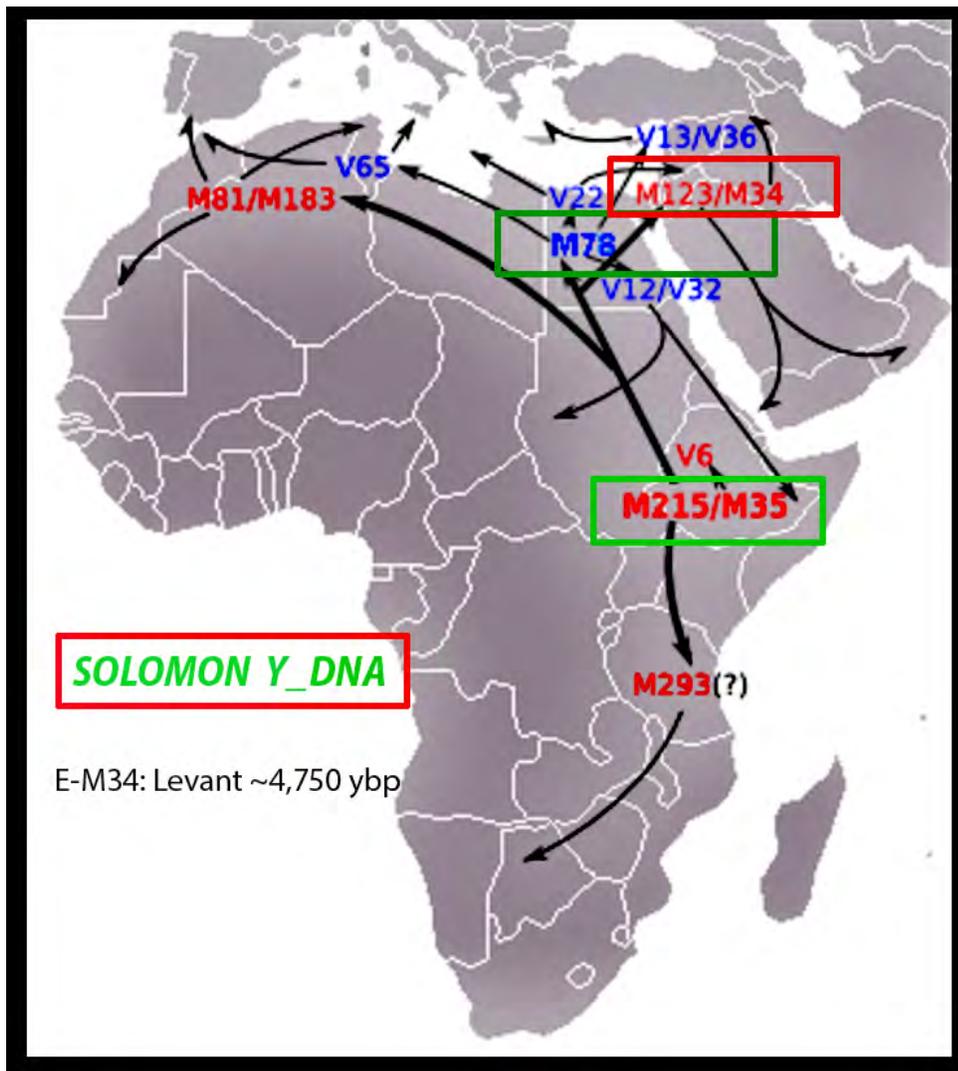
Modern human evolution within Africa continued for about another 250,000 years before any known mutations appeared in Africa. Male individuals who demonstrated "A" and "B" Y-DNA haplogroups survived within Africa. Female individuals with mtDNA of the L0, L1, L2 and L3, Haplogroup evolved within Africa. Today, the descendants with those individuals live among the San/Bushman tribes.

Our knowledge and interest in the human genomic journey begins with the first modern human treks out of Africa. Although *Homo erectus* migrated to Europe and Asia (1.8 million ybp) and Neanderthal (800,000 to 30,000 ybp), modern humans remained within Africa until 100,000 to 80,000 years ago. Y-DNA "DE" haplogroup has been identified in the Arabian Peninsula and dated to about 80,000 years ago. The next mutation was

ascertained to be “E” haplogroup and dated to about 60,000 years ago in the region of the Ho9rn of Africa (Northeast Africa). Both “D” and “E” have been identified along the coasts of Southern Asia, India, Indonesia and Australia dating from over 60,000 years ago.

Genetic mutations, Defining Haplogroups and subclades.

Based upon the most recent genetic evidence, the appearance of Haplogroup “E” has been calculated to be about 65,000 ybp in the Northeast region of the Horn of Africa. This is a different interpretation of the more recent data.



MAP African Migration Y-DNA E-M34 – 4,750 ybp

Our maternal grandfather, Saul Solomon from Pungesti, Moldavia, Romania, was a descent of an ancient male, who gen0mic identity has been discovered. The ancestral line of their male Y-DNA has been calculated, including several subclades (sub-groups) identified as to approximate date and geographic location (see charts below). An index

of genetic markers has been constructed that shows the descendants of the original genetic ancestral relative. Very importantly, it is now estimated that males of the particular subclade we Solomons display on our Y-DNA genes is E1b1b1b, previously called E3b. This individual appeared about 42,000 ybp in Northeastern Africa. The genetic male descendant, E-M35 appeared about 34,800 ybp, from which we are derived. Several significant descendant sub-clades appeared about 20,000 ybp, from which we carry additional identifying genetic markers (mutations). We also carry the following genetic subclade markers: Z827 (20,000 ybp). It is estimated that the proto-Semitic language, "Afro-Asiatic," appeared in the same region at that time and place before spreading into the Middle East. Among Jewish descendants, we carry the E-M34 mutation that separates us from other E-M35 descendants that migrated to Europe.

That critical next mutation marked the historic migration of our Hebrew ancestors, appearing about 20,000 – 18,000 ybp. The E-M34 ancestors migrated to the region of Morocco in Northwestern Africa. The genetic journey carried that group to the Iberian region where several new mutations appeared about 12,000 ybp, which spread in diffuse directions: Sardinia, Germany, Eastern Europe (Czech), Greece and Italy.

Most importantly for us Solomons, E-M34 next appeared in Eastern Anatolia (Turkey) about 5,500 ybp (3,500 BCE). Eastern Anatolia is a region of great importance historically, as well as to our Solomon (and Sherins-Cherkinsky) family history. Anatolia is a region well represented by the Kura Araxes culture, which originated in Georgia and North Ossetia (Caucasus) about 6,500 ybp (4,500 BCE). Based upon fundamental archeological research and anthropological, historical and linguistic studies, the trail of the unique pottery developed by the Kura Araxes culture can be traced to Antioch, Godin tepe in Western Iran and Tel Bet Yerah at the Southwestern region of the Sea of Galilee where the origin of the Jordan River exits the Sea.

Evidence of the Kura Araxes culture residing in the Levant appeared about 2,800 ybp (800 BCE), during an Era dominated by the Hittites, whose Empire extended from the upper Fertile Crescent, Anatolia and Caucasus to Egypt. WE SOLOMON MALES CARRY THE CRITICAL Y-DNA MARKER, E-Y6923, which appeared in the Levant about 1,200 ybp.

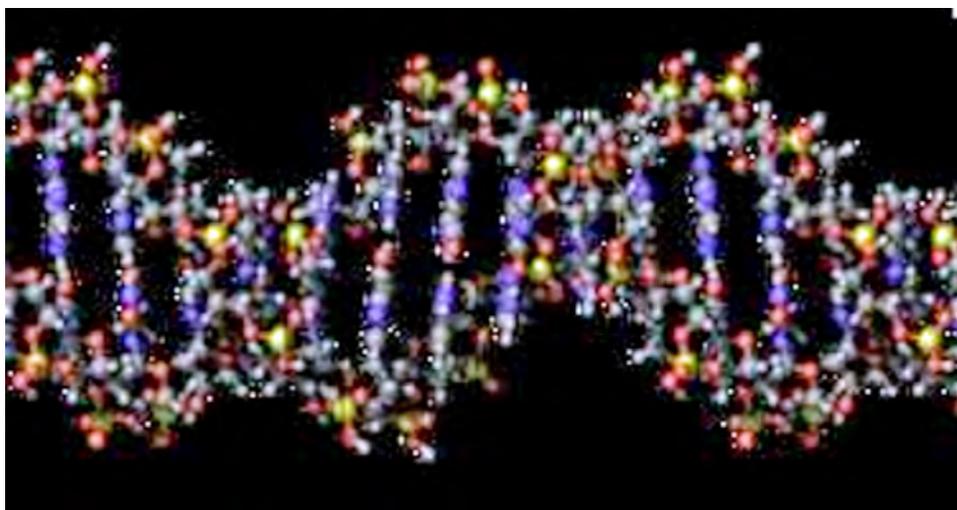
Basic Understanding of Human Y-DNA Haplogroups⁵

Y-chromosome DNA (Y-DNA) haplogroups is determined by single nucleotide polymorphisms (SNP = MUTATION) tests. SNPs are locations on the DNA where one nucleotide has "mutated" or "switched" to a different nucleotide.

Because a *haplogroup* consists of similar haplotypes, it is possible to predict a haplogroup from the haplotype. A SNP test is required to confirm the haplogroup prediction. Not all the testing companies offer SNP testing, and consequently their customers' haplogroup predictions are sometimes inaccurate. For advice on SNP testing it is recommended that you join the appropriate Y-DNA haplogroup project and seek advice from the volunteer project administrators.

ISOGG⁶ maintains the most up-to-date version of the Y-SNP tree. The tree is updated as and when new branch-defining SNPs are discovered. The criteria for inclusion of SNPs in the tree are published here.

Phylotree maintains a minimal reference phylogeny for the human Y-chromosome, an abbreviated version of the Y-tree showing only the principal branches. The Y-Phylotree can be found there. Background information on the methodology of the tree and the SNPs included can be found here.⁷



Double Helix DNA Connected by Nucleotides

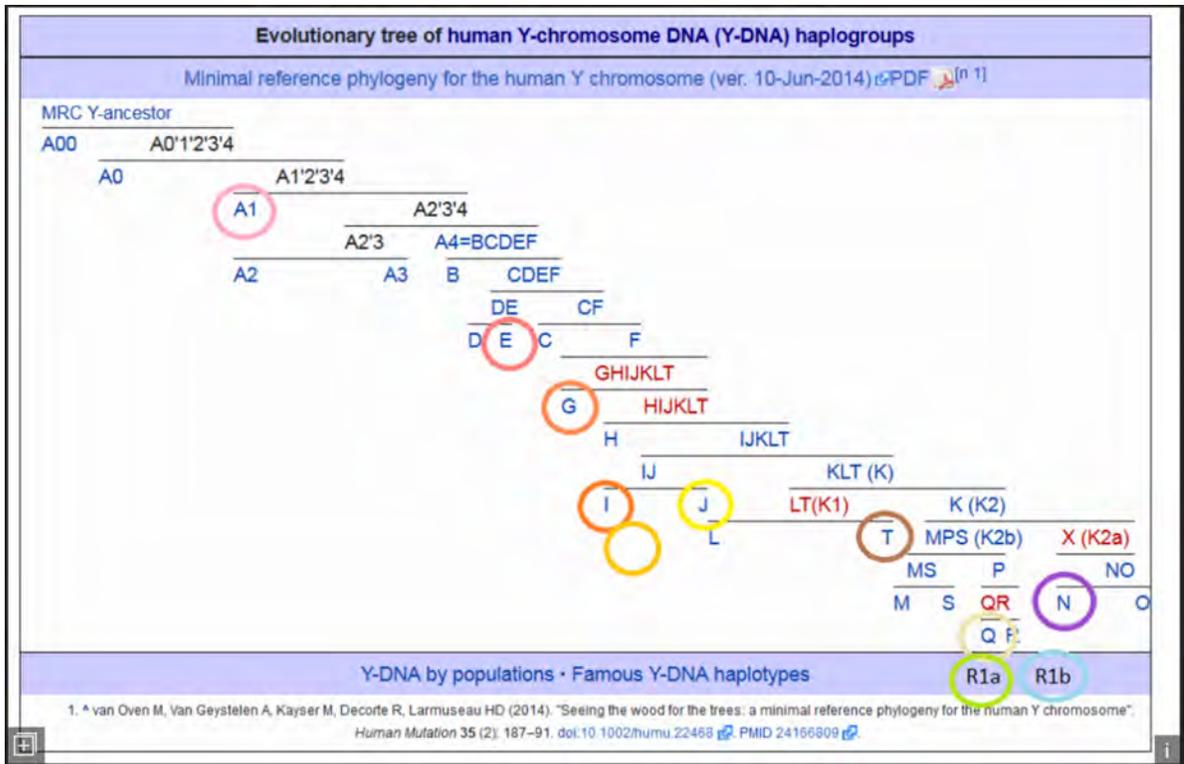
⁵<https://isogg.org/wiki/Haplogroup>

⁶

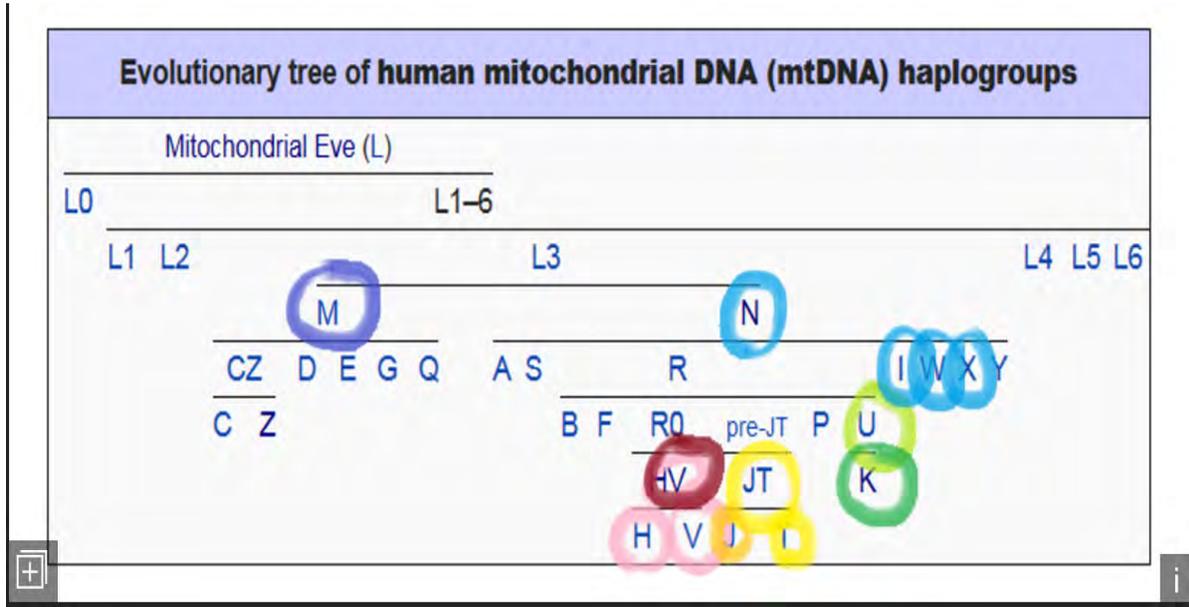
⁷ ISOGG: International Society of Genetic Genealogy.



DNA Electrophoresis Scanning



Graph Y-DNA Haplotree



Graph mtDNA Haplotree



Certificate DNA Robert Sherins -- J-M410

Family Tree DNA Analysis 2015

[J>J2a>J-M172>J-M410]

Origin Haplogroup J2a-M410

From: Haplogroup J (Y-DNA)⁸

Haplogroup J-M304, also known as J is a Y-chromosome DNA haplogroup. It is believed to have evolved in Western Asia.^[2] The Clade spread from there during the Neolithic, primarily to North Africa, the Horn of Africa, Socotra, the Caucasus, Southeast Europe, West Asia, Central Asia, South Asia. Haplogroup J-M304 is divided into two main subclades (branches), J-M267 and J-M172.

<i>Haplogroup J-M304</i>	
Possible time of origin	48,000 years ago ^[1]
Possible place of origin	<u>Western Asia</u>
Ancestor	<u>IJ</u>
Descendants	<u>J-M172</u> , <u>J-M267</u>

Haplogroup J-M304 is believed to have arisen roughly 48,000 years ago in Western Asia.^[1] It is most closely related to the haplogroup I-M170, as both lineages are haplogroup IJ subclades. Haplogroup IJ and haplogroup K derive from Haplogroup IJK, and only at this level of classification does haplogroup IJK join with Haplogroup G-M201 and Haplogroup H as immediate descendants of Haplogroup F-M89. J-M304 is defined by the M304 genetic marker, or the equivalent 12f2.1 marker. According to a genetic study in China by Shou et al., J*-M304 is found among the Sibe people, Kazakhs, Dongxiangs and Uzbeks in Northwest China.

The main current subgroups J-M267 and J-M172, which now comprise between them almost all of the population of the haplogroup, are both believed to have arisen very early, at least 10,000 years ago. Nonetheless, Y-chromosomes F-M89* and IJ-M429* were reported to have been observed in the Iranian plateau (Grugni et al. 2012).

⁸ [https://en.wikipedia.org/wiki/Haplogroup_J_\(Y-DNA\)](https://en.wikipedia.org/wiki/Haplogroup_J_(Y-DNA))

On the other hand, it would seem to be that different episodes of populace movement had impacted southeast Europe, as well as the role of the Balkans as the phylogenetic unification of Hgs I and J show a long-standing corridor to Europe from the Near East by the basal M429 mutation. This proof of common ancestry suggests that ancestral Hgs IJ-M429* probably would have entered Europe through the Balkan track sometime before the LGM. They then subsequently split into Hg J and Hg I in Middle East and Europe in a typical disjunctive phylogeographic pattern. Such a geographic hall is prone to have encountered extra consequent gene streams, including the horticultural settlers. Moreover, the unification of haplogroups IJK creates evolutionary distance from F–H delegates, as well as supporting the inference that both IJ-M429 and KT-M9 arose closer to the Middle East than central or eastern Asia.

Haplogroup J has also been found among two ancient Egyptian mummies excavated at the Abusir el-Meleq ar chaeological site in Middle Egypt, which date from a period between the late New Kingdom and the Roman era.

Distribution

Haplogroup J-M304 is found in its greatest concentration in the Arabian Peninsula. Outside of this region, haplogroup J-M304 has a significant presence in North Africa and the Horn of Africa. It also has a moderate occurrence in Southern Europe, especially in central and southern Italy, Malta, Greece and Albania. The J-M410 subclade is mostly distributed in Anatolia, Greece and southern Italy. Additionally, J-M304 is observed in Central Asia and South Asia, particularly in the form of its subclade J-M172. J-12f2 and J-P19 are also found among the Herero (8%).

Basal J*(xJ1, J2) is found at its highest frequencies among the Soqotri (71.4%). In Ethiopia, haplogroup J has been found to be strongly associated with elite endurance. J sublineages are the most common paternal clades borne by such athletes (30% of 5K-10K runners; 43% of marathon runners), with a lower frequency in the general population (25%).

Phylogenetic trees

There are several confirmed and proposed phylogenetic trees available for haplogroup J-M304. The scientifically accepted one is the Y-Chromosome Consortium (YCC) one published in Karafet 2008 and subsequently updated. A draft tree that shows emerging

science is provided by Thomas Krahn at the Genomic Research Center in Houston, Texas. The International Society of Genetic Genealogy (ISOGG) also provides an amateur tree.

The Genomic Research Center tree

This is Thomas Krahn at the Genomic Research Center's Draft tree , Proposed Tree for haplogroup J-P209 (Krahn & FTDNA 2013). For brevity, only the first three levels of subclades are shown.

- J-M304 12f2a, 12f2.1, M304, P209, L60, L134
 - M267, L255, L321, L765, L814, L827, L1030
 - M62
 - M365.1
 - L136, L572, L620
 - M390
 - P56
 - P58, L815, L828
 - L256
 - Z1828, Z1829, Z1832, Z1833, Z1834, Z1836, Z1839, Z1840, Z1841, Z1843, Z1844
 - Z1842
 - L972
 - M172, L228 [Sherins/Cherkinsky]
 - M410, L152, L212, L505, L532, L559 [Sherins/Cherkinsky]
 - M289
 - L26, L27, L927
 - L581
 - M12, M102, M221, M314, L282
 - M205
 - M241

From: Haplogroup J2 (Y-DNA)⁹

⁹ https://en.wikipedia.org/wiki/Haplogroup_J-M172

Author: Maciamo Hay.

January 2017

Origins:

“Haplogroup J2 is thought to have appeared somewhere in the Middle East towards the end of the last glaciation, between 15,000 and 22,000 years ago. The oldest known J2a samples at present were identified in remains from the Hotu Cave in northern Iran, dating from 9100-8600 BCE (Lazaridis et al. 2016), and from Kotias Klde in Georgia, dating from 7940-7600 BCE (Jones et al. (2015)). This confirms that haplogroup J2 was already found around the Caucasus and the southern Caspian region during the Mesolithic period. The first appearance of J2 during the Neolithic came in the form of a 10,000 year-old J2b sample from Tepe Abdul Hosein in north- western Iran in what was then the Pre-Pottery Neolithic (Broushaki et al. 2016).

Notwithstanding its strong presence in West Asia today, haplogroup J2 does not seem to have been one of the principal lineages associated with the rise and diffusion of cereal farming from the Fertile Crescent and Anatolia to Europe. It is likely that J2 men had settled over most of Anatolia, the South Caucasus and Iran by the end of the Last Glaciation 12,000 years ago. It is possible that J2 hunter-gatherers, then goat/sheep herders, also lived in the Fertile Crescent during the Neolithic period, although the development of early cereal agriculture is thought to have been conducted by men belonging primarily to haplogroups G2a (northern branch from Anatolia to Europe), as well as E1b1b and T1a (southern branch, from the Levant to the Arabian peninsula and North Africa).

Mathieson et al. (2015) tested the Y-DNA of 13 Early Neolithic farmers from the Barcın site (6500- 6200 BCE) in northwestern Anatolia, and only one of them belonged to haplogroup J2a. Lazaridis et al. (2016) tested 44 ancient Near Eastern samples, including Neolithic farmers from Jordan and western Iran, but only the above-mentioned sample from Mesolithic Iran belonged to J2. Likewise, over 100 Y-DNA samples have been tested from Neolithic Europe, covering most of the important cultures, and only two J2 sample was found, in the Sopot and Proto-Lengyel cultures in Hungary, dating from 7,000 years ago. J2 was also absent from all Chalcolithic and Bronze Age Indo-European cultures, apart from one J2a1b sample in Hungary dating from the end of the Bronze Age (c. 1150 BCE, see Gamba et al. 2014), in the minor Kyjatice culture, an o

shoot of the Urn field culture, which differs from typical Indo-European cultures by its use of cremation instead of single-grave burials.

No Neolithic sample from Central or South Asia has been tested to date, but the present geographic distribution of haplogroup J2 suggests that it could initially have dispersed during the Neolithic from the Zagros mountains and northern Mesopotamia across the Iranian plateau to South Asia and Central Asia, and across the Caucasus to Russia (Volga-Ural).

- *The first expansion of Y-DNA J2 probably correlated with the diffusion of domesticated cattle and goats (starting c. 8000-9000 BCE), rather than with the development of cereal agriculture in the Levant.*
- *A second expansion would have occurred with the advent of metallurgy. J2 could have been the main paternal lineage of the Kura-Araxes culture (Late Copper to Early Bronze Age), which expanded from the southern Caucasus toward northern Mesopotamia and the Levant.* After that J2 could have propagated through Anatolia and the Eastern Mediterranean with the rise of early civilizations during the Late Bronze Age and the Early Iron Age.

Quite a few ancient Mediterranean and Middle Eastern civilizations flourished in territories where J2 lineages were preponderant. This is the case of the Hattians, the Hurrians, the Etruscans, the Minoans, the Greeks, the Phoenicians (and their Carthaginian offshoot), the Israelites, and to a lower extent also the Romans, the Assyrians and the Persians.

- *J2 men dominated all the great seafaring civilizations from the middle Bronze Age to the Iron Age.*

There is a distinct association of ancient J2 civilizations with bull worship. The oldest evidence of a cult of the bull can be traced back to Neolithic central Anatolia, notably at the sites of Çatalhöyük and Alaca Höyük. Bull depictions are omnipresent in Minoan frescos and ceramics in Crete. Bull-masked terracotta figurines and bull-horned stone altars have been found in Cyprus (dating back as far as the Neolithic, the rest presumed expansion of J2 from West Asia). The Hattians, Sumerians, Babylonians, Canaanites, and Carthaginians all had bull deities (in contrast with Indo-European or East Asian

religions). The sacred bull of Hinduism, Nandi, present in all temples dedicated to Shiva or Parvati, does not have an Indo-European origin, but can be traced back to Indus Valley civilization. Minoan Crete, Hittite Anatolia, the Levant, Bactria and the Indus Valley also shared a tradition of bull leaping, the ritual of dodging the charge of a bull. It survives today in the traditional bull fighting of Andalusia in Spain and Provence in France, two regions with a high percentage of J2 lineages.

Geographic distribution

Distribution of haplogroup J2 in Europe, the Middle East & North Africa

http://www.eupedia.com/europe/Haplogroup_J2_Y-DNA.shtml

4/12/2017 Haplogroup J2 (Y-DNA) - Eupedia

“The world's highest frequency of J2 is found among the Ingush (88% of the male lineages) and Chechen (56%) people in the Northeast Caucasus. Both belong to the Nakh ethnic group, who had inhabited that territory since at least 3000 BCE. Their language is distantly related to Dagestani languages, but not to any other linguistic group. However, Dagestani peoples (Dargins, Lezgins, Avars) belong predominantly to haplogroup J1 (84% among the Dargins) and almost completely lack J2 lineages. Other high incidence of haplogroup J2 are found in many other Caucasian populations, including the -

- *Azeri (30%), the Georgians (27%), the Kumyks (25%), and the Armenians (22%). Nevertheless, it is very unlikely that haplogroup J2 originated in the Caucasus because of the low genetic diversity in the region. Most Caucasian people belong to the same CTS6804 subclade and share a common patrilineal ancestor who lived some 7,500 years ago, at the time of the Neolithic expansion to the Caucasus.*

The Chechens and Ingushs belong almost exclusively to the Y7800 clade, which formed only 2,000 years ago and has a TMRCA of approximately 1,500 years. The high local frequencies observed would rather be the result of founder effects, for instance the proliferation of chieftains and king's lineages through a long tradition of polygamy, a practice that the Russians have tried to suppress since their conquest of the Caucasus in the 19th century.

- *Outside the Caucasus, the highest frequencies of J2 are observed in Cyprus (37%), Crete (34%), northern Iraq (28%), Lebanon (26%), Turkey (24%, with peaks of 30% in the Marmara region and in central Anatolia), Greece (23%), Central Italy (23%), Sicily (23%), South Italy (21.5%), and Albania (19.5%), as well as among Jewish people (19 to 25%).*

One fourth of the Vlach people (isolated communities of Romance language speakers in the Balkans) belong to J2, considerably more than the average of Macedonia and northern Greece where they live. This, combined to the fact that they speak a language descended from Latin, suggests that they could have a greater part of Roman (or at least Italian) ancestry suggests that they could have a greater part of Roman (or at least Italian) ancestry than other ethnic groups in the Balkans.

http://www.eupedia.com/europe/Haplogroup_J2_Y-DNA.shtml 4/12/2017 Haplogroup J2 (Y-DNA) - Eupedia

Subclades:

If you are new to genetic genealogy, please check our Introduction to phylogenetics to understand how to read a phylogenetic tree.

1K

1.1K SHARES

http://www.eupedia.com/europe/Haplogroup_J2_Y-DNA.shtml 4/18
4/12/2017 Haplogroup J2 (Y-DNA) - Eupedia

Two main subclades divide haplogroup J2: J2a and J2b:

- (M410, L152, L212/PF4988, L559/PF4986) and J2b (M12, M102, M221, M314).
- J2a1-M67 is the most common subclade in the Caucasus (Vainakhs, Ingushs, Chechens, Georgians,

http://www.eupedia.com/europe/Haplogroup_J2_Y-DNA.shtml

History

Middle-Eastern and European J2a: from Kura-Araxes to the Greeks and Romans:

- It is very likely that J2a, J1 and G2a were the three dominant male lineages the Early Bronze Age Kura-Araxes culture, which expanded from the South Caucasus to eastern Anatolia, northern Mesopotamia and the western Iran. From then on, J2

men would have definitely have represented a sizeable portion of the population of Bronze and Iron Age civilizations such as the Hurrians, the Assyrians or the Hittites. It is very possible that bronze technology spread from the South Caucasus across the Iranian plateau until the Indus Valley, giving rise to the Harappan Civilization (see below).

- The Phoenicians, Jews, Greeks and Romans all contributed to the presence of J2a in Iberia. The particularly strong frequency of J2a and other Near Eastern haplogroups (J1, E1b1b, T) in the south of the Iberian Peninsula, suggest that the Phoenicians and the Carthaginians played a more decisive role than other peoples. This makes sense considering that they were the first to arrive, founded the greatest number of cities (including Gadir/Cadiz, Iberia's oldest city), and their settlements match almost exactly the zone where J2 is found at a higher frequency in southern Andalusia.
- The high incidence of J2a in Italy is owed in great part to the migration of the Etruscans from western Anatolia to central and northern Italy, and to the Greek colonization of southern Italy. Immigration from the eastern Mediterranean to Rome during the Roman Empire, then from Anatolia, Thrace and Greece during the Byzantine period (particularly in north-eastern Italy) further increased the incidence of J2 in the peninsula.
- Several common Italian J2a subclades are found mainly in the south of Italy (M319, M92, Z467, Z7671, all under L558) and are likely to be of Greek origin. The highest concentrations of J2a in Europe are found in Crete (32% of the population) and Calabria (26%). M319, one of the principal J2a1 subclades in Greece, Italy and Western Europe, reaches its maximum frequency in Crete (6-9%).

Roman J2a1-Z435

http://www.eupedia.com/europe/Haplogroup_J2_Y-DNA.shtml

4/12/2017 Haplogroup J2 (Y-DNA) - Eupedia

The Romans probably helped spread haplogroup J2 within their borders, judging from the distribution of J2 within Europe (frequency over 5%), which bears an uncanny resemblance to the borders of the Roman Empire (once concessions are made for the Germanic invasions that appear to have lowered the frequency of J2 between Belgium and Switzerland). There is a high diversity of J2a in Italy, but the most common branch found all over the peninsula and therefore most likely linked with a Roman diffusion is L70, and particularly its subclade Z435. All L70 carriers today descend from a single patrilineal ancestor who lived about 5,000 years ago. This corresponds to the time when the Proto-Indo-Europeans started invading Central Europe from the Pontic Steppe. It is not yet clear where J2-L70 was located at the time. It could have been present in the Steppe and tagged along the predominantly R1b branch of the Proto-Indo-Europeans that moved to the Balkans and Central Europe. Or it could have been one of the lineages of Chalcolithic Southeast and Central Europe. A third alternative is that L70 originated in Anatolia or Greece and moved to Italy with the migration that gave rise to the Etruscan civilization.

Z435 was formed about 3,600 years ago and has a TMRCA of only 3,100 years (± 300 years). The latter corresponds roughly to the timing of the invasion of Italian peninsula by Italic tribes from the Alps. Z435 has numerous subclades of its own, and most have been identified in central Italy. This could either mean that Z435 was one of the founding Italic lineages, or that it was already in Italy and was assimilated by the Italic tribes. The PF5456 subclade is barely 2500 years old, and would have emerged and propagated after the founding of Rome. Outside Italy, it is now found in such varied places as Portugal, Spain, France, Britain, Belgium, southern Germany, Austria, Bulgaria, Tunisia or Lebanon, all regions colonized by the Romans. Z2177, another subclade of Z435, is a bit under 3,000 years old. It has various subclades of its own which are scattered today around Italy (northern Italy, Tuscany, Latium, Sicily, Sardinia) and in places like Switzerland, south-west Germany, Britain, Spain, Romania, Greece, Turkey and Syria - also all these regions were part of the Roman Empire. Italy has by far the highest concentration of Z2177 of any country.

J2a in Central & South Asia: the Harappan and Oxus Civilizations

Within the Indian subcontinent, J2a peaks at frequencies of 15-25% around the Indo-Pakistani border, from Punjab to Gujarat and Sindh. This region matches exactly the Bronze Age Indus Valley Civilization, also known as the Harappan Civilization, that existed from 3300 BCE to 1300 BCE and which practiced bull worship like other J2a civilizations. Bronze started being used by the Harappan Civilization circa 3000 BCE, a few centuries after its earliest known regular use around the Caucasus by the Maykop culture (from 3700 BCE) and the Kura–Araxes culture (from 3500 BCE). While the Maykop culture was closely linked to the Yamnaya culture in the Pontic- Caspian Steppe and is thought to be associated with Proto-Indo-European speakers and Y-haplogroups R1a and R1b, the Kura-Araxes culture would have allowed the diffusion of Y- haplogroup J1 and J2a around the Middle East, taking over the Neolithic societies primarily associated with Y-haplogroup G2a and G2b.

Archeological evidence of a massive migration from the southern Caucasus to the Indus Valley is elusive at present, but it cannot be excluded as it has been proven now that large-scale Indo- European migrations took place during the same period from the Pontic-Caspian Steppe to Europe and Central Asia. There is no reason to believe that J2a people from the Kura-Araxes culture couldn't have expanded in the same way westward toward Anatolia, Greece and Italy and eastward to Iran, southern central Asia, Pakistan, India.

There is another cluster of J2a with a frequency approximating 15% in Bactria, in southern- central Asia, in what is now northern Afghanistan, eastern Turkmenistan, southern Uzbekistan and western Tajikistan. This region corresponds to the Bactria–Margiana Archaeological Complex (BMAC), also known as the Oxus civilization, which flourished between 2300 and 1700 BCE. Oxen were used to draw wheeled carts and camels were domesticated in this region c. 2500 BCE, just before the start of this civilization. The BMAC was eventually overrun by the Indo-Iranian migrations from the Andronovo culture and the Sintashta culture further north, and became Indo-Europeanized. The Indo-Aryans pursued their southward expansion, invading northern Pakistan and northwest India from 1800 BCE to 1500 BCE, and eventually bringing about the demise of the Indus Valley Civilization around 1300 BCE.

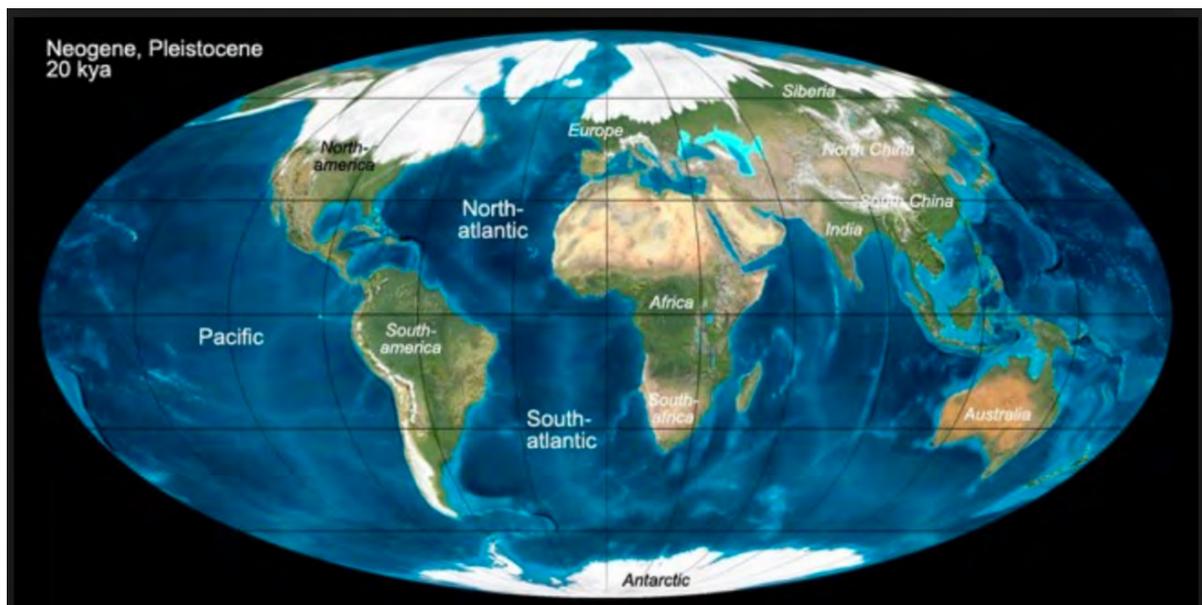
From http://www.eupedia.com/europe/Haplogroup_J2_Y-DNA.shtml

4/12/2017 Haplogroup J2 (Y-DNA) – Eupedia

There are a wide variety of J2a branches found in South Asia. Some are over 10,000 years old (CTS6002, F3133, M68, M319, PF5174, Z6065) could have migrated from West to South Asia during the Neolithic, Chalcolithic or Early Bronze Age. Based on their phylogeographies, F3133 and M319 could be associated with the Kura-Araxes expansion. Y21500 has a TMRCA of 3700 years and is also found in Russia, which suggests an Indo-Aryan origin - perhaps one of the J2a1 subclades assimilated by R1a invaders in Central Asia before conquering the Indian subcontinent. A few much younger clades are also found in western India and Pakistan, such as L534 (TMRCA 2,800 ybp) and YSC246 (TMRCA 1,750 ybp) and would have come to India in historical times, for example with the Mughals.

From Nomads to Settlers and Nation States

The advent of the last ice-age resulted in warming of the latitudes of Central Asia, Europe and Asia. Nomadic humans followed the animals to the new fertile fields, where food was abundant. Small settlements began to appear where the first evidence of agriculture began. This was the beginning of the Neolithic era. Settlements became more permanent, which was the cultural forerunner of the evolution of Urbanization. Great civilizations evolved that produced the written language, city-states, arts and sciences and the advancement of human cultures in the “Cradle of Civilization.”



Last Ice Age Maximum -- 24,000 ybp

Our genomic ancestors were very well situated in the evolution of human culture. We have a great advantage in our pursuit of our ancestral history and to be able to review an area of cultural anthropology where so much prior research has been accomplished in the knowledge of the development of Western Civilization.

I have copied images of maps that show the evolution of the regional kingdoms/empires of the Near East. Each of those cultures impacted the evolution and distribution of our ancestors.



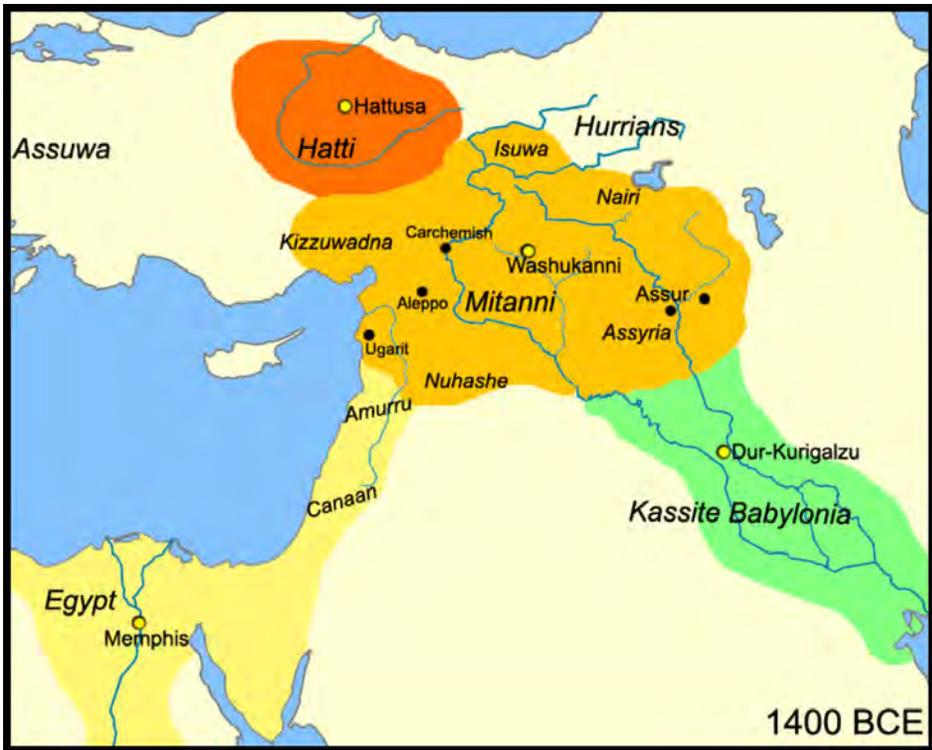
Map Hurrian, Amurru, Subartu and Early Hittite Kingdoms
 ~ 2,400 BCE



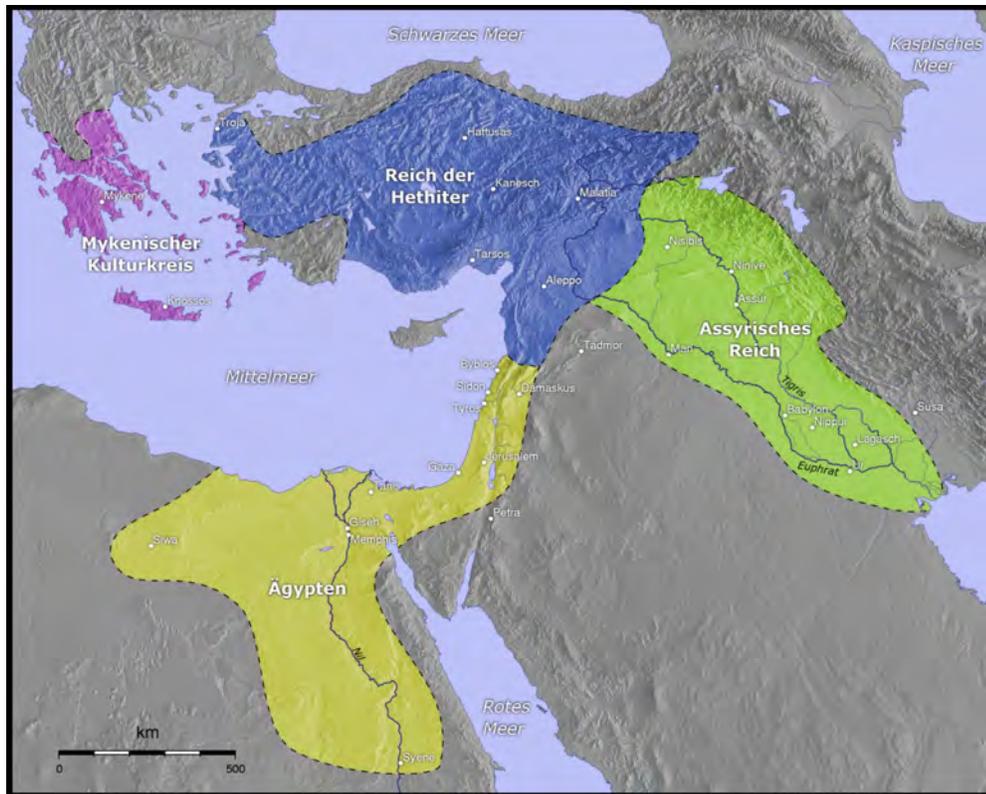
Hurrian Incense Burner



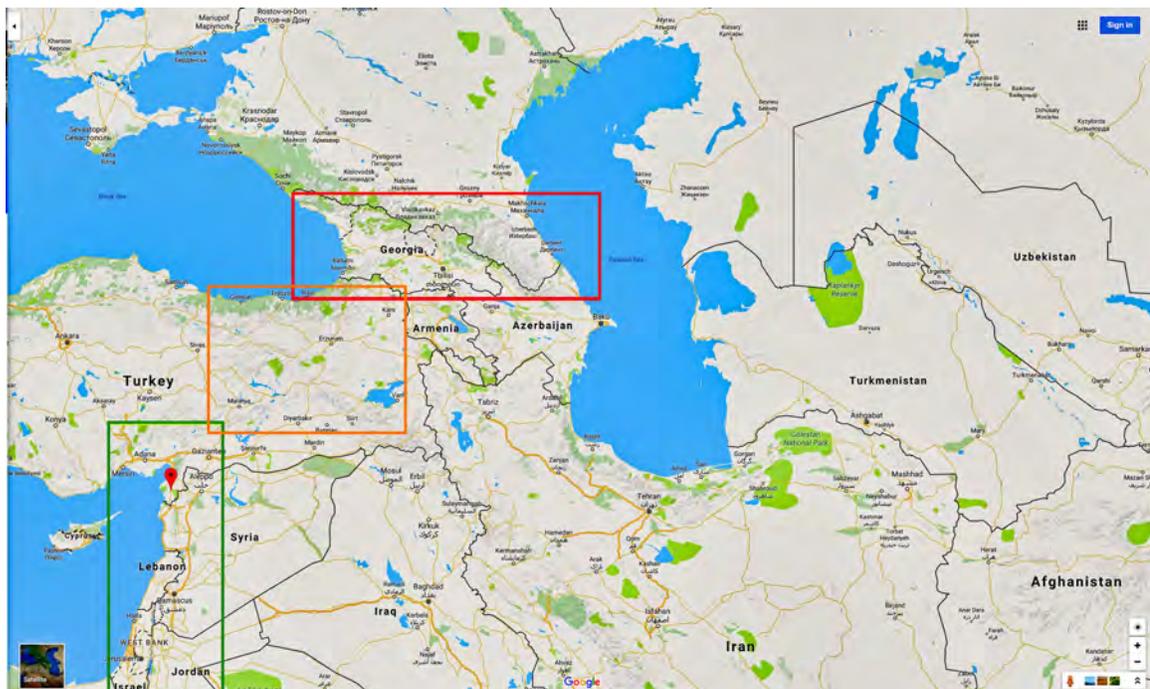
Urartu Kingdom
 Caucasus, Anatolia and Cilicia
 Foundation of the Armenian Nation



Map Hurrian, Hatti (Hittite) and Mitanni Kingdoms
 ~ 1,400 BCE



Map Hittite Empire ~ 1,300 BCE



Our Genomic Ancestors Migrated through the Zones Displayed on this Map



Our Genomic Ancestors Migrated to the Levant/Canaan about 2,800 ybp

Historically, Semitic-speaking tribes migrated from the Amorite (Syria) region to the Eastern Nile Delta about 1720 BCE. They were known as the Hyksos. Several became Pharaohs of Lower Egypt before their early “Exodus” from Egypt in the 16th millennium BCE. They resettled in Canaan.





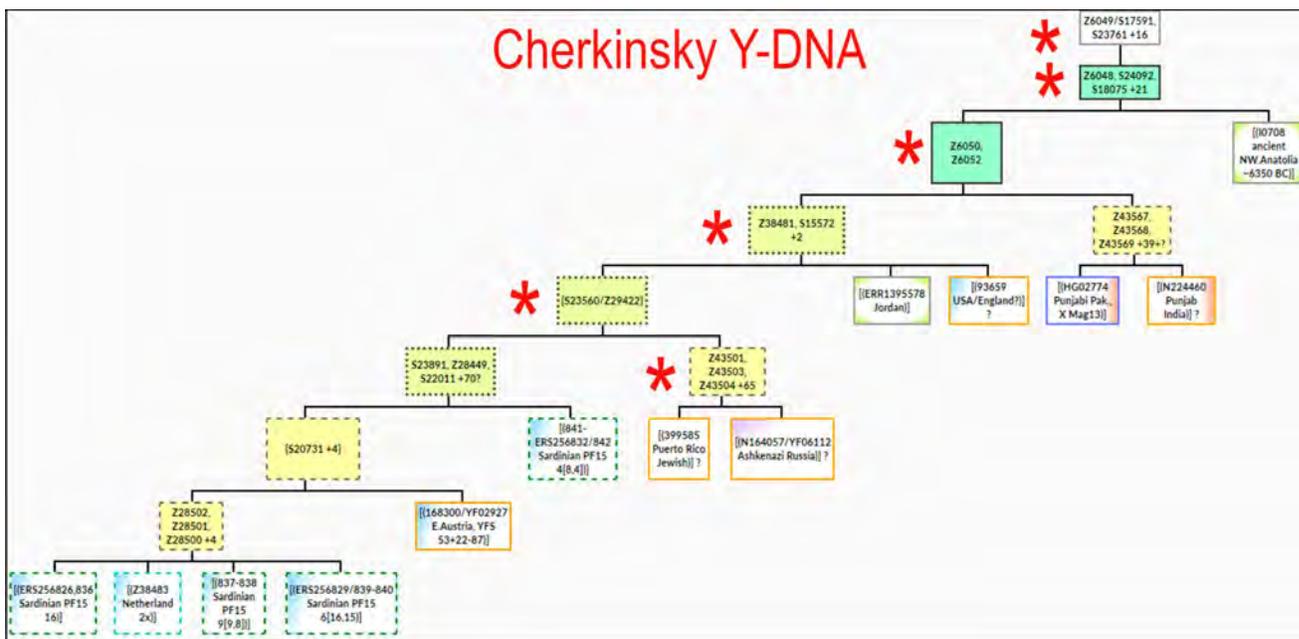
Realm of the Semitic Hyksos, 1720 – 1570 BCE
 The Hyksos Capital city was established at Avaris



Deeper DNA Probes

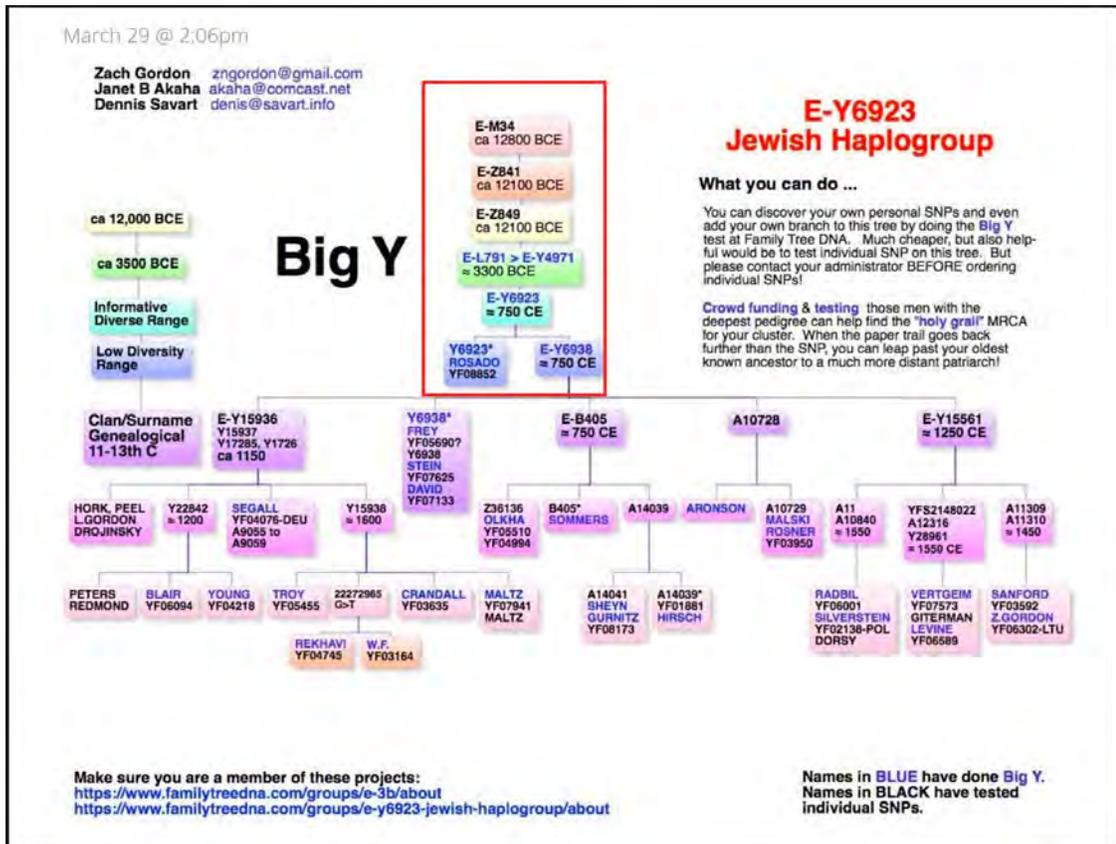
Deeper Y-DNA probes of our paternal and maternal ancestry yielded astonishing results. Both of our male ancestral genetic lines [Cherkinsky and Solomon] coalesced in the Near East by about the 6,000 to 3,000 ybp. Specifically, both ancestors became part of the Kura Araxes culture in Eastern Anatolia by 3,000 ybp!!!

Deeper Genetic probes of our Y-DNA by Family Tree DNA Company produced 2 new identifying subclades of our ancestors: J2a<M410<PF4610<J-Z6048 and S23891 [Cherkinsky]; E1b1b1b<M96<M215<M35<M34<E-Y6923 [Solomon]. The graphs shown below depict the genetic data published by YFull research group in Russia. The administrative project directors of the Family Tree DNA project consultants have further substantiated this.



Cherkinsky genomic journey:

- J2a-M172 27,899 ybp [Primary SNP Mutation]
- J2a-M410 25,800 ybp [Primary SNP Mutation]
- PF4610 19,000 ybp
- J-Z6049 18,000 ybp
- J-Z6048 15,000 ybp
- J-S238991 ~8,000 ybp [Most Recent Mutation]



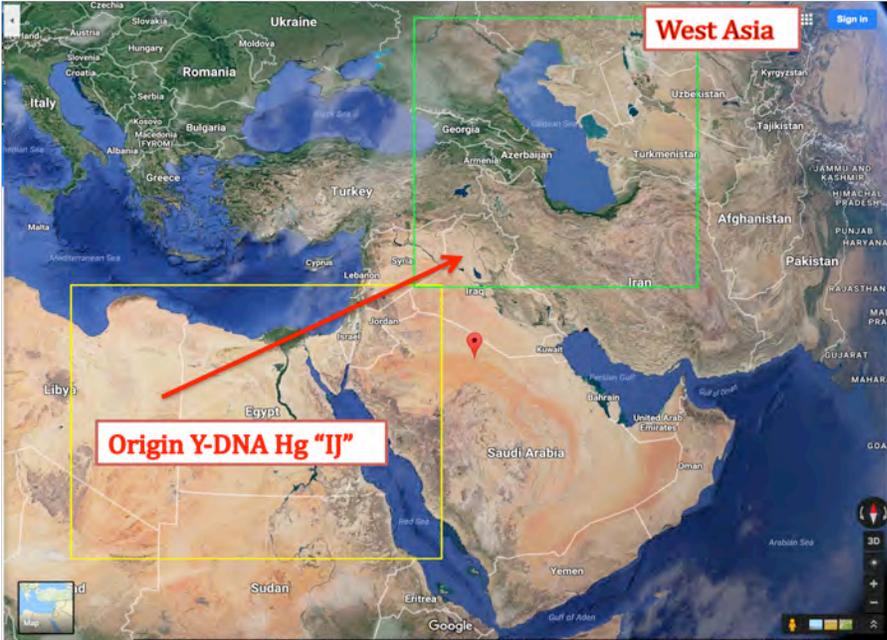
Graph Solomon Y-DNA E1b1b1b>E-Y6923

Migration of Ancestor Solomon to Europe in the 8th Century CE

Our paternal male Y-DNA ancestor appeared in Western Asia or Middle East about 30,000 ybp. His descendant, haplogroup J2a-Z6048 has been documented in the Caucasus, specifically part of the Kura Araxes Valley in Georgia about 15,000 ybp. The next documented genetic descendant, J-S23891, appeared during the Neolithic Revolution, but also in the Kura Araxes Valley of Georgia. Anthropological evidence of the culture included nomadic settlements, establishment of mud-brick homes, canals for irrigation of crops and a special pottery style ["ETC"].

Origin of Our Y-DNA “J” Haplogroup

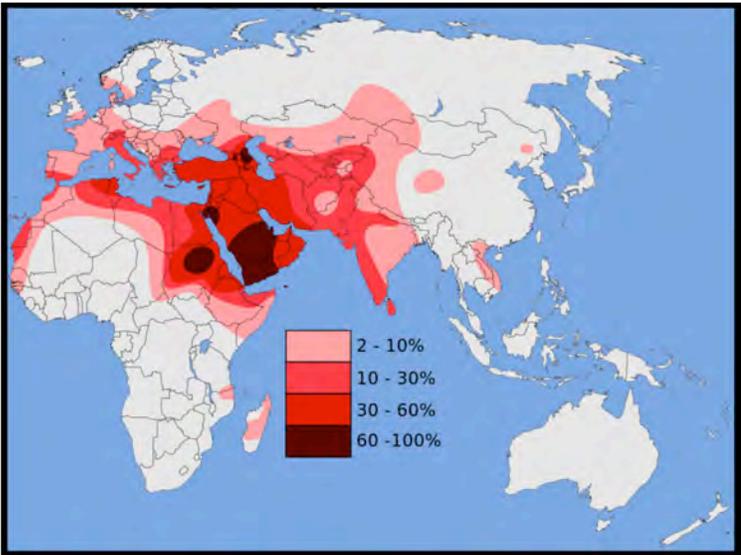
Origin Y-DNA Haplogroup “IJ”
55,000 ybp



76

Map of Origin of Haplogroup IJ [Western Asia]

Origin Y-DNA Haplogroup “J”
48,000 ybp

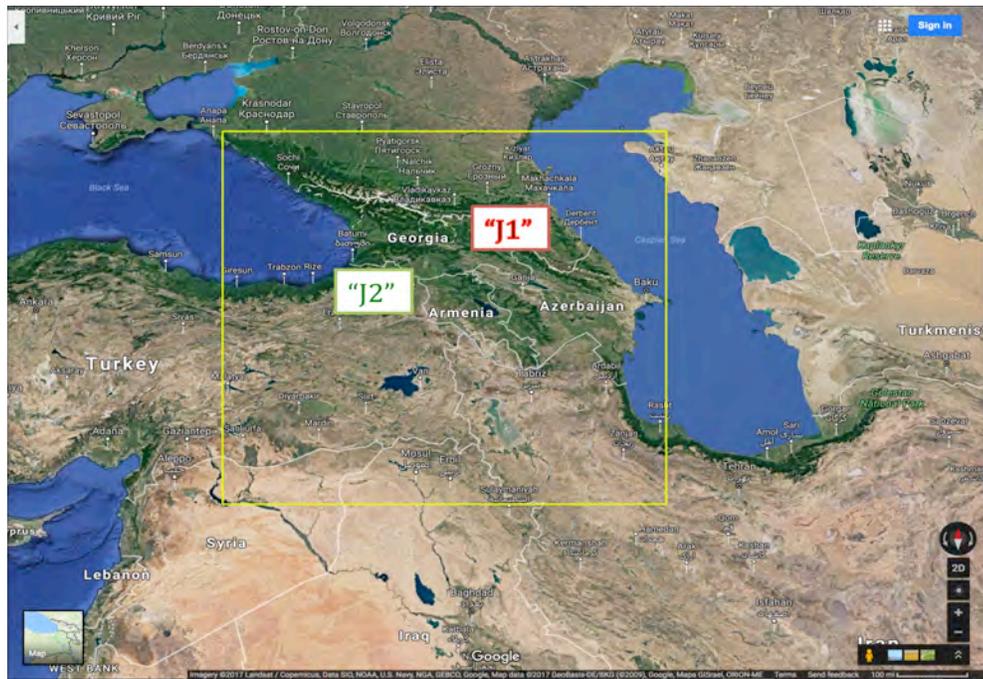


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Distribution Map of Genetic Male Ancestor “J” - 48,000 ybp

Origin Y-DNA Haplogroup

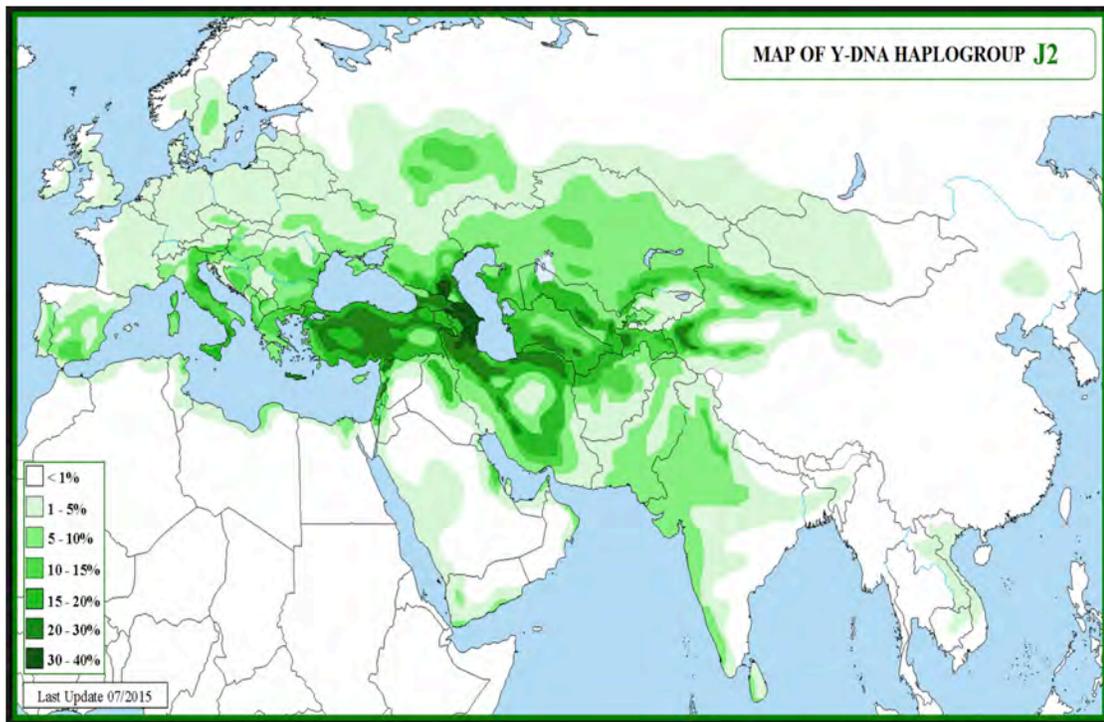
"J1" (24,000 ybp) -- "J2" (27,800 ybp)



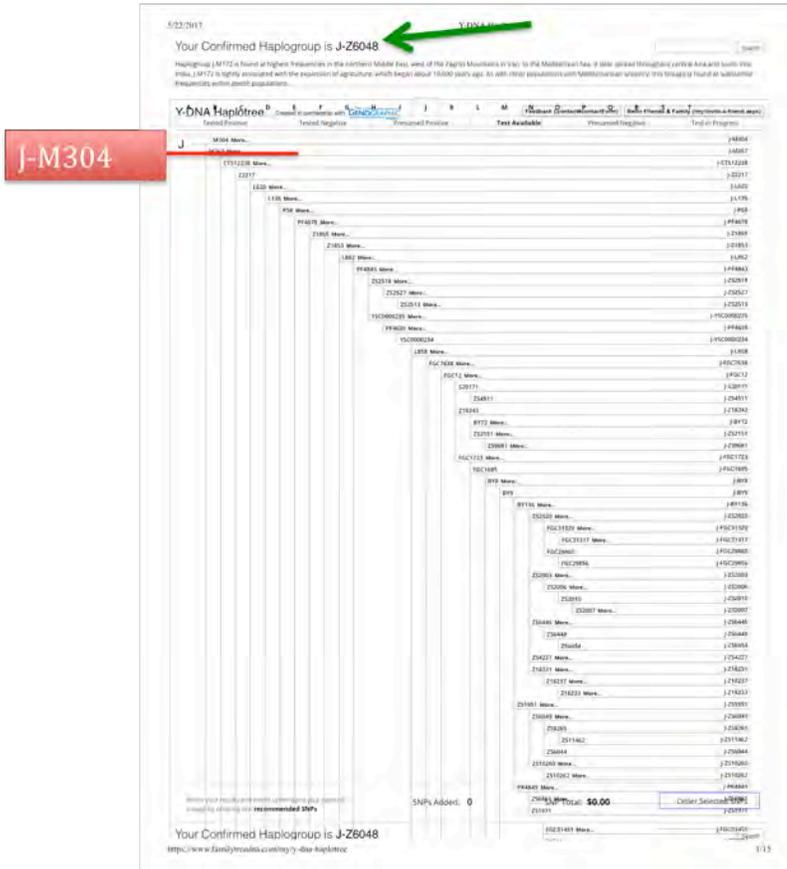
99

Distribution of Y-DNA, Haplogroups J1 and J2

Distribution Y-DNA Haplogroup J2



103

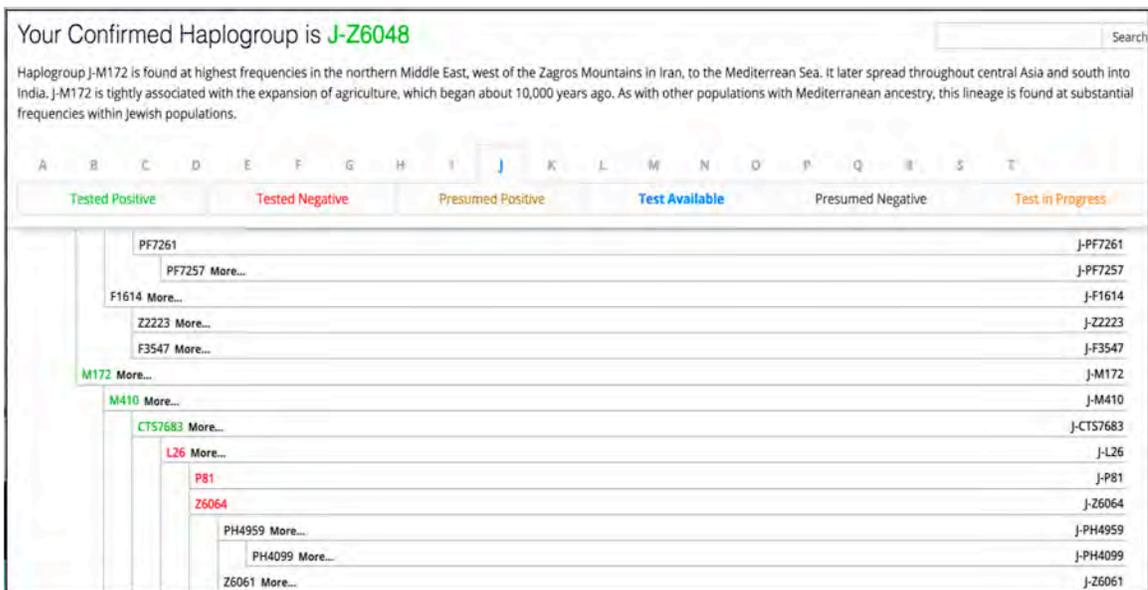


Haplotree "J" (15-pages)

- J-M304 (J)
- J-M267 (J1)
- J-M172 (J2)
- J-M410 (Georgia)
- J-Z6048

(Downstream Sub-Clade)

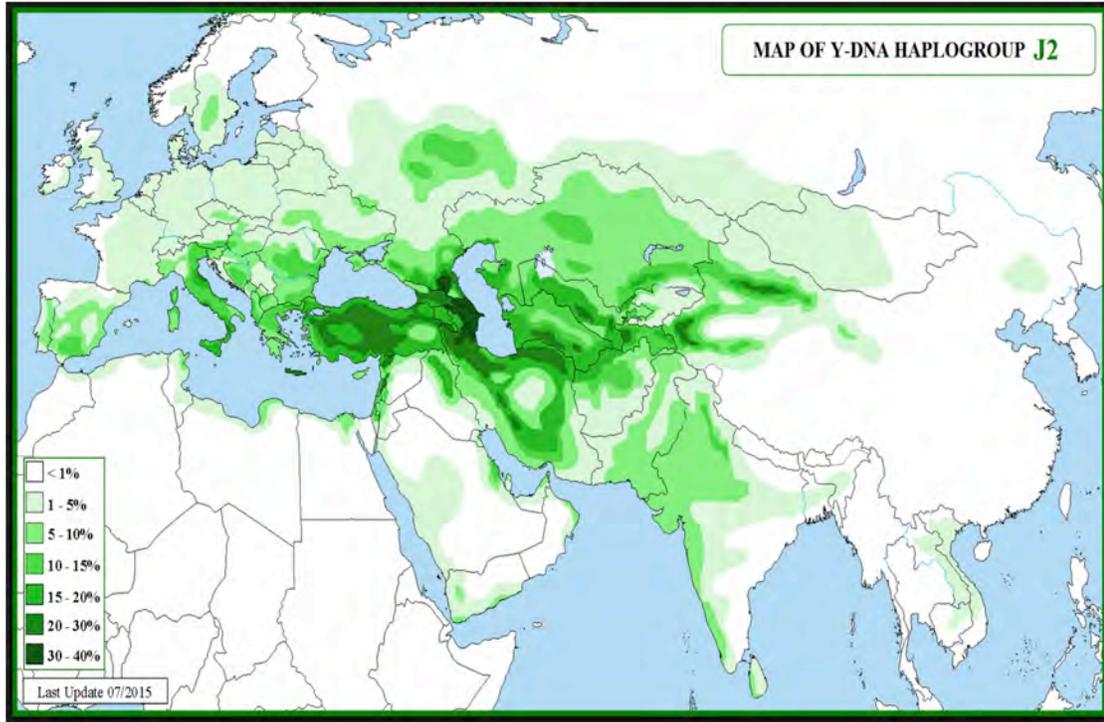
Y-DNA Haplogroup Sub-Clade J-Z6048



Genomic Distribution of Y-DNA: J2a-M410<J-Z6048

Anthropological Aspects

Distribution Y-DNA Haplogroup J2

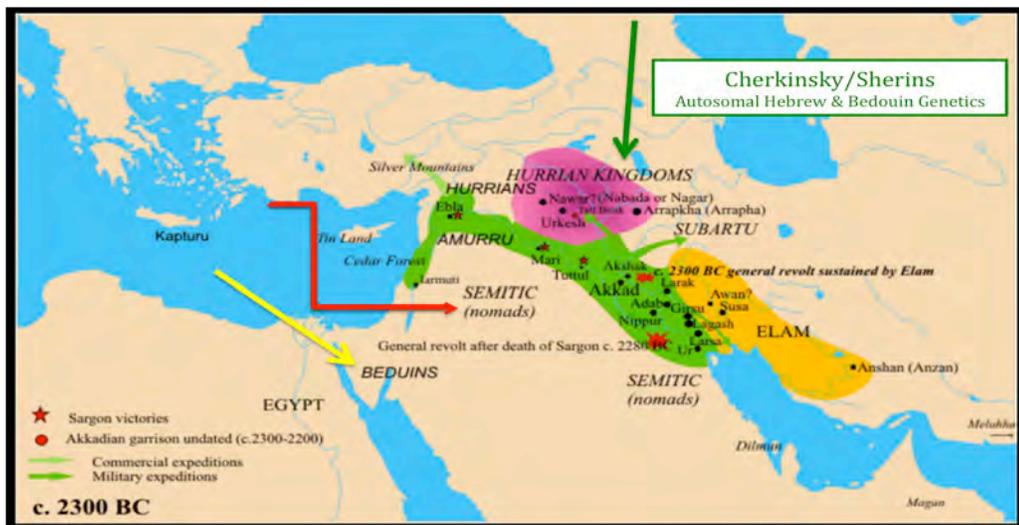


103

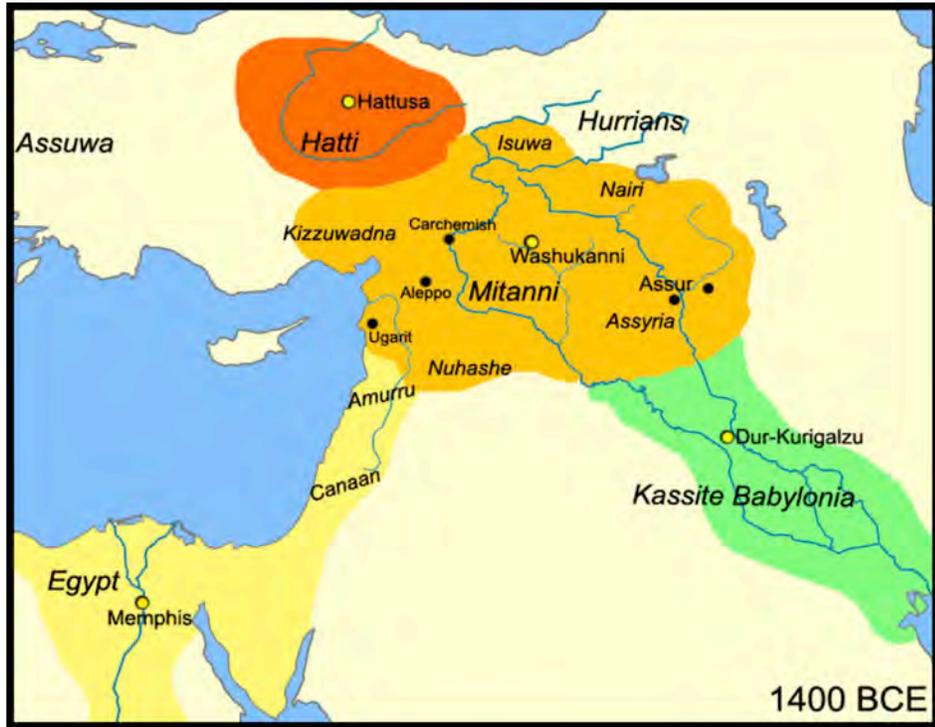


Map Akkadian Empire
 Tigris Euphrates River Valley [present-day Iraq]
 Cuneiform Writing First Appeared

Map Hurrian Kingdom
 Semitic Akkadians appear 2,300 BCE

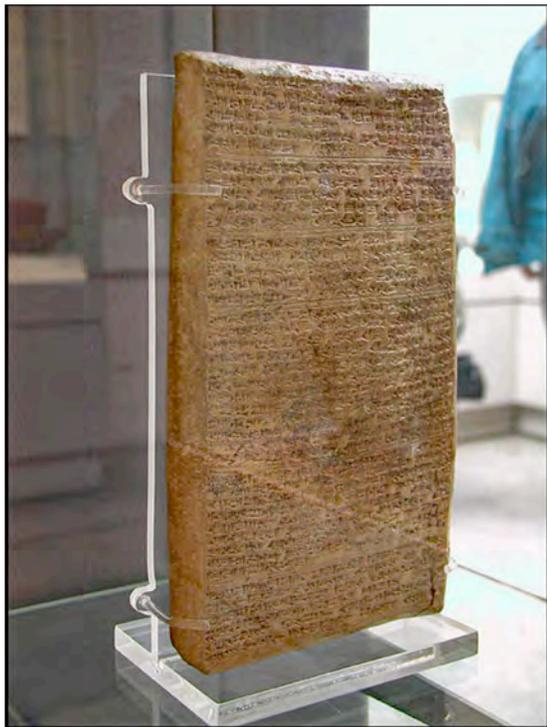


Map Mittani Empire
1,400 BCE



85

Mitanni Cuneiform Tablet
1,400 BCE



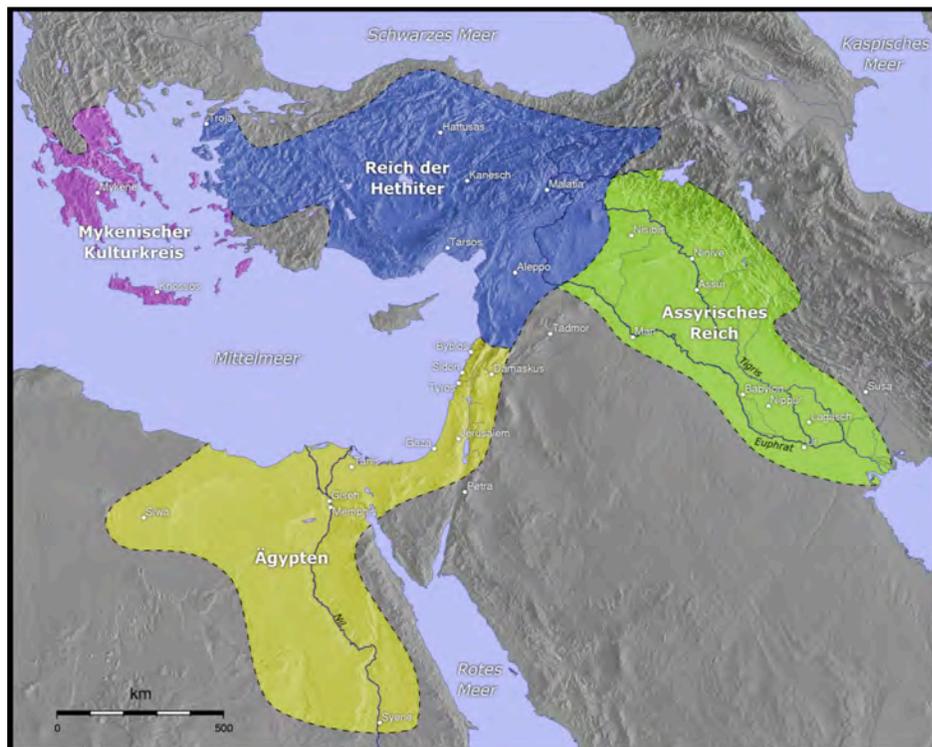
86

Map Hittite Empire
1,350 – 1,295 BCE



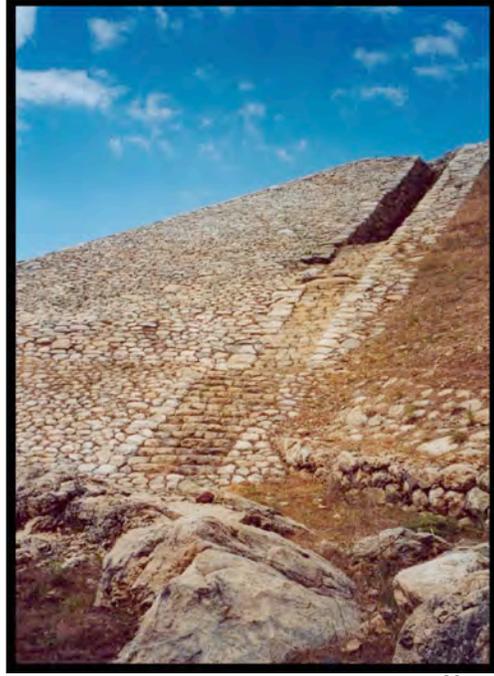
87

Map Hittites
1,300 BCE



88

Hittite Cultural Monuments



89

Hittite Artisan Craftsmanship Relief of Hittite Gods



90

Hittite Bulls



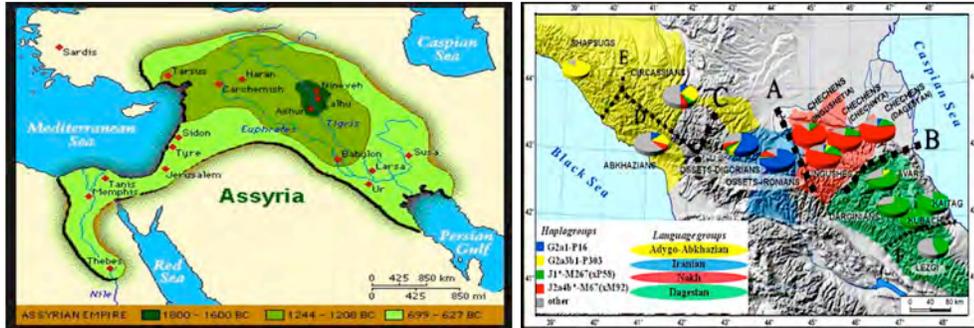
91

Urartu Kingdom of Van (Anatolia)
800-500 BCE



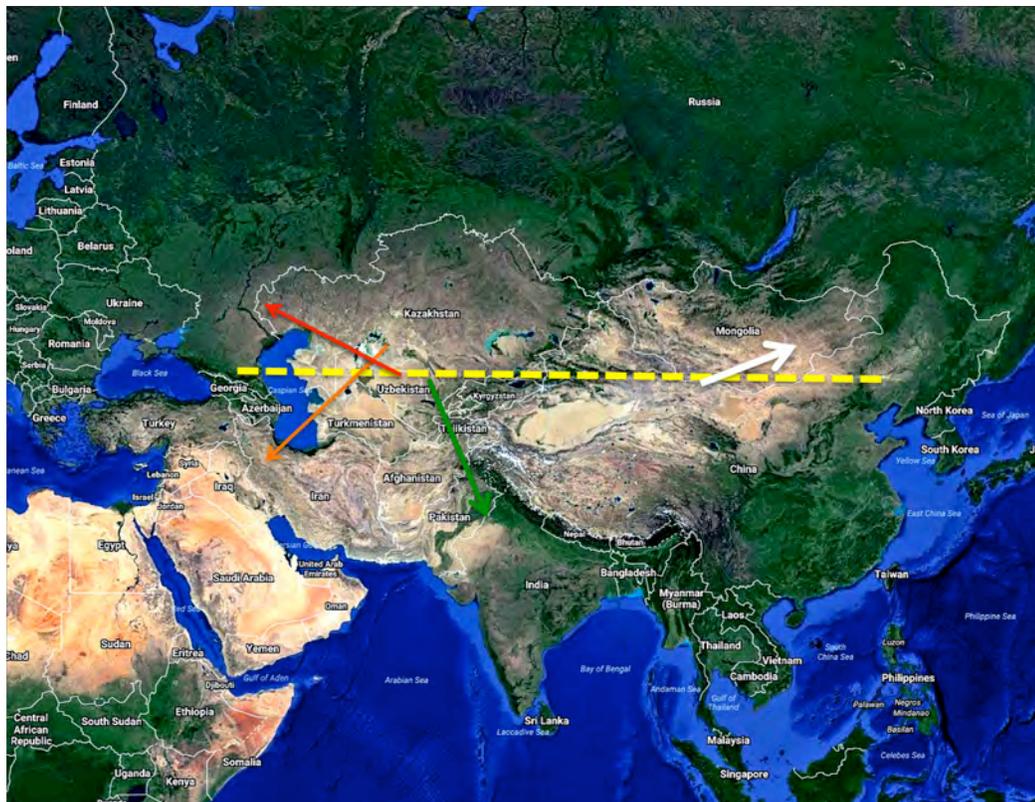
32

Fertile Cradle of Civilization



98

Nomadic Migration Through Mountainous Passes Spread of Horse Culture, Military Power & Linguistics



17

Map Eurasia Demonstrates Mountain Barrier of the Nomadic Steppe Populations and Languages

Ancient Modes of Transportation

- Paleolithic Walking
- Neolithic Walking, Raft, Animal
- Calcolithic Horse, then Sheep, Cattle
- Ancient Wheeled Cart
- Rivers Tribal Migration with Herds
- Levant Camel

118

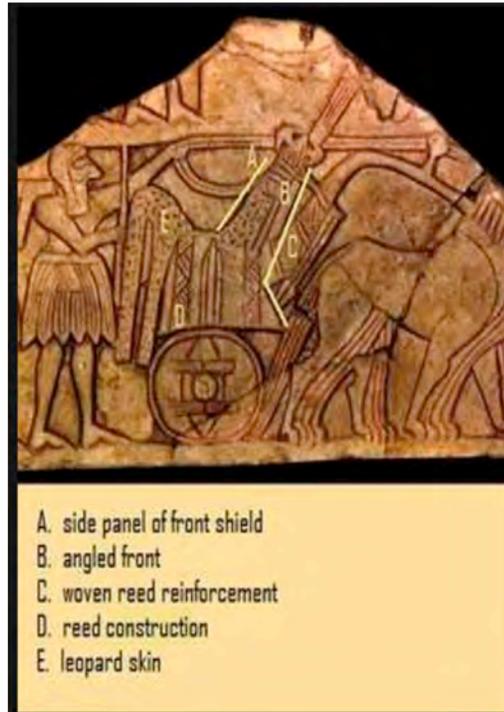
Yurts Essential for Mobility



18

Wheel Invention

Ancient Mesopotamia Advanced Urban Expansion & Military Power



21

History of the Wheel

- The Halaf culture of 6500–5100 BCE is sometimes credited with the earliest depiction of a wheeled vehicle, but this is doubtful as there is no evidence of Halafians using either wheeled vehicles or even pottery wheels.
- Precursors of wheels, known as "tournettes" or "slow wheels", were known in the Middle East by the 5th millennium BCE (one of the earliest examples was discovered at Tepe Pardis, Iran, and dated to 5200–4700 BCE). These were made of stone or clay and secured to the ground with a peg in the center, but required effort to turn. True (freely-spinning) potter's wheels were apparently in use in Mesopotamia by 3500 BCE and possibly as early as 4000 BCE,^[4] and the oldest surviving example, which was found in Ur (modern day Iraq), dates to approximately 3100 BCE.
- The first evidence of wheeled vehicles appears in the second half of the 4th millennium BCE, near-simultaneously in Mesopotamia (Sumerian civilization), the Northern Caucasus (Maykop culture) and Central Europe (Cucuteni-Trypillian culture), so the question of which culture originally invented the wheeled vehicle is still unsolved.

22

Spoke Wheels

Lighter, Faster, Stronger for Chariots



23

Concept of Time



24

Concept of Astronomy & Astrology



26

Urartu – Georgia – Anatolia 715 – 713 BCE



Extensive Urartu/Armenian Boundaries Compare to Modern Armenian Borders (Dynasty - 570 BCE)



35

Map Greater Armenia Seleucid (Persian) & Mede Neighbors (7th Century BCE)



50

Parthia Empire Roman Era - (247-242 CE)



40

Indo Iranian Languages Nomadic Merging With Adjacent Regions



41

Map Greater Armenia

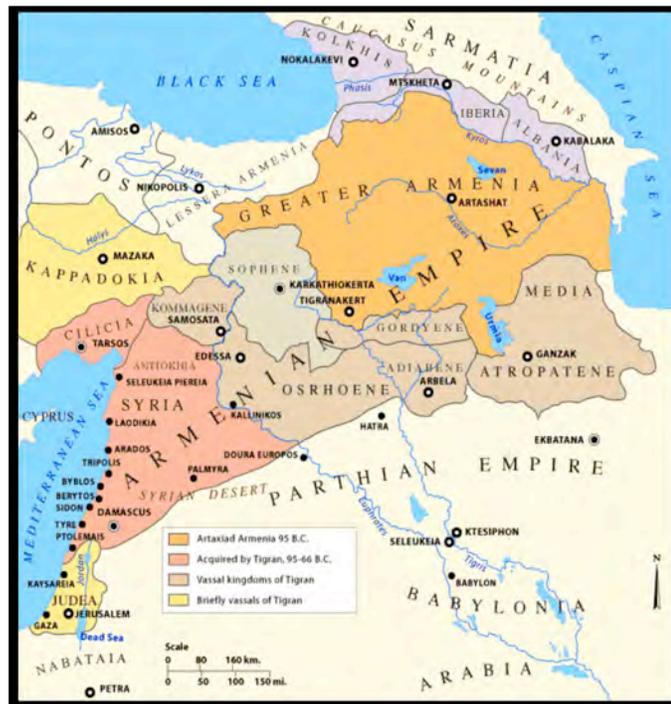
Seleucid (Persian) & Mede Neighbors (7th Century BCE)



50

Tigranes The Great

96 – 66 BCE



42

Extent of Islamic Revolution

7th - 11th Centuries CE

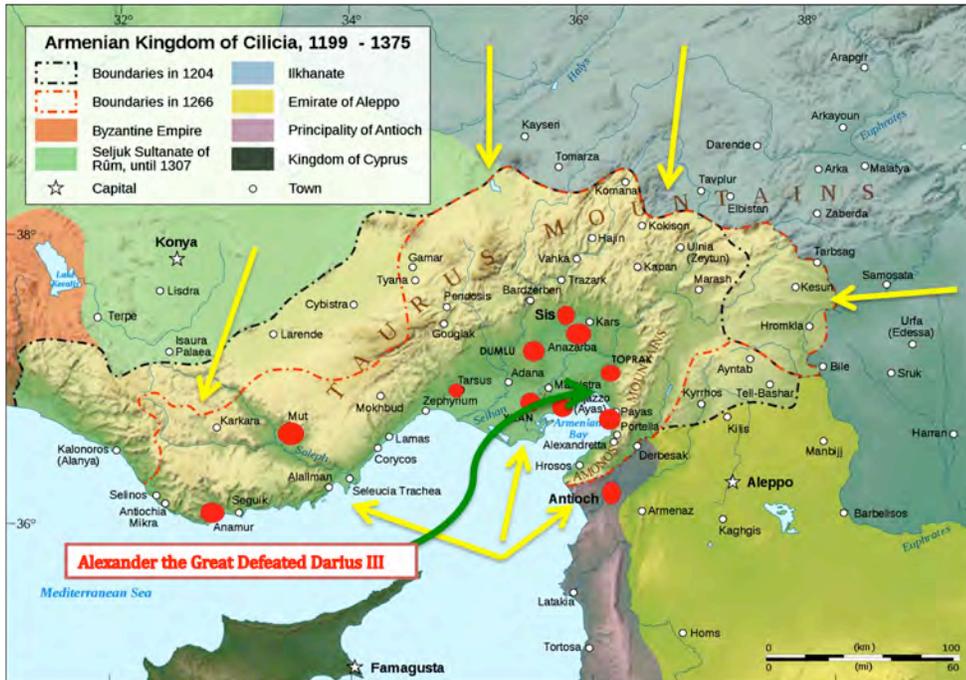


47

Armenian Kingdom of Cilicia

1199-1375

Plain of Isis, Alexander The Great Defeated Persian King Cyrus III



55

Captain Robert S. Sherins, MD
USAF Flight Surgeon, NATO Airbase, Incirlik (Adana), Turkey
December 4, 1964 – December 1, 1966

Captain Sherins and his wife, Marlene Joyce Mager Sherins were stationed at Incirlik Airbase in Cilicia, Southeastern Turkey. They travelled throughout Anatolia during their 2-year military service. They had no prior knowledge that Robert's genomic ancestors had migrated from the Caucasus (Kura Araxes Valley, Georgia) to Anatolia during the period of 6,000 – 3,000 BCE. Published below are images of scenes of their travels in their ancient homeland, Anatolia.

Genomic J2a is the most common Y-DNA haplogroup represented in Anatolia. This SNP mutation is found frequently among: Armenians, Turks, Kurds, Arabs, Zazas and other, such as Ashkenasi Jewish males who have about a 15% incidence of J2a. In the past, this region also was occupied by Greeks, Romans, Urartians, Armenians, Akkadians, Hittites, Mitanni, Medes, Assyrians, Persians, and European Crusaders, among others. All of those populations imparted significant inventions (i.e.; wheel), spiritual observances and rituals, foods (Neolithic agricultural revolution) and later on metallurgy technology.

Doctor's Draft Vietnam Era – Barry Plan Deferment,
United States Air Force, School of Aerospace Medicine,
San Antonio, Texas - 1964

Assignment to USAF NATO Airbase, Incirlik, Turkey
(Adana, Cilicia, Turkey 1964 – 1966

At the height of the Vietnam War, all eligible physicians were drafted, While those in school, internship, residency or fellowship were defered until the doctor had completed training and was licensed to pracice. Dr. Robert S. Sherins' military duties were deferred until 1964.

Based upon the equestrian training at the USAF School of Aerospace Medicine, Dr. Sherins decided to become an Ophthalmologist. However, he was first ordered to complete his tour of military duties that were assigned in Turkey.

Dr. Sherins was enrolled in the Flight Surgeon's program at Brooks Airbase, School of Aerospace Medicine, San Antonio, Texas. He was commissioned as a 1st Lieutenant. After 3 months, he was transferred to Incirlik NATO Airbase, Adana Turkey, and was promoted to the rank of Captain. He served under Col. Samuel Chunn, Hospital Commander. Robert's duties included: Health care of all flying personnel at the base; oversight of public health issues: water, sewage, food handling safety; vaccination for infectious and communicable diseases; maintaining minimum of 4-hours monthly active flying in military aircraft to best understand their unique issues; safety issues of flying personnel; special weapons safety and health issues; high altitude intelligence personnel; isolated tours of duty in remote locations; hospital emergency room night and weekend duties and several high level administrative duties on the airbase.

Robert was a photographer at heart with his first camera. Often, he was asked if he was composing his own "Air Force Story." However, the photographs became an invaluable resource later in his life when he applied the many lessons learned from the variety of military and overseas experiences and duties. Little did Robert know that his genomic ancestors had lived in this region of Anatolia, Turkey, since 30,000 years before.

After becoming fascinated by learning his family history (researched from 1973-2017), the advent of scientific genomic research became available. Robert began his genetic testing in 2002, a few years after he retired from his clinical practice of Ophthalmology at Saint John's Health Center in Santa Monica, California (1970-1997).

A detailed gallery of photographic images has been created to show visually the many varied experiences the Dr. Sherins participated and enjoyed as a result of his USAF Air Force responsibilities.

Image Gallery from USAF Experiences
At the Brooks School of Aerospace Medicine, Texas, and in
Turkey



Capt. Robert S. Sherins
Flight Training T33 1964

Brooks School of Aerospace Medicine
San Antonio, Texas
T-33 Flight Test Flight - School - Graduation (Capt. Sherins Rt.)
1964



Flight Surgeons Graduation
Brooks School of Aerospace Medicine
Capt. Robert S. Sherins, MD -Right



Flight Surgeon's Training: Parachute, Ejection Seat



Lt. Robert S. Sherins, MD
Parachute Training Dropped From 30' Tower



Lt. Robert S. Sherins, MD
Ejection Seat Trail

Incirlik Airbase, Adana, Turkey



Helicopter View Adana, Turkey



Residential Area Adana

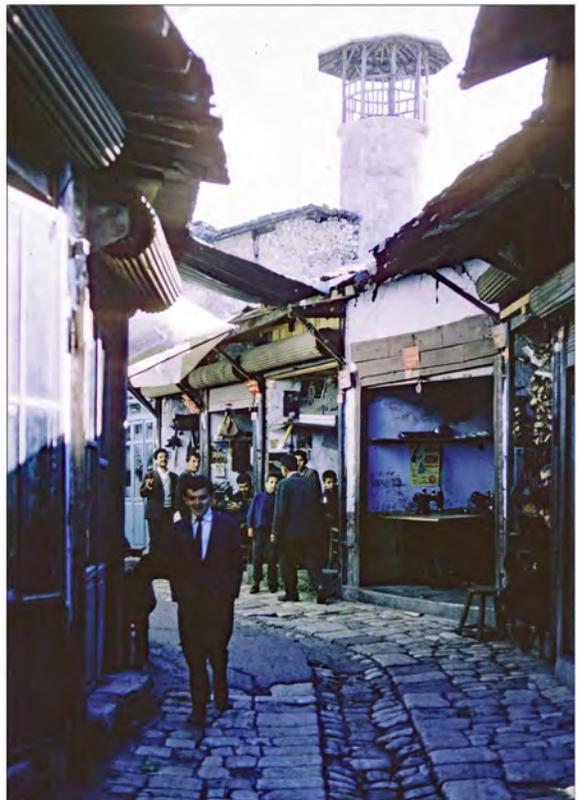


Sherins Modern Apartment, Adana



Turkish Vegetable Vendor , Adana







Adana Fruit Vendor



Adana Lamp Production



Public Water Resource



Old Adana Market Street

Air Transportable Medical-Surgical Hospital & Other Military Responsibilities



Incirlik Medical Staff, Air Transportable Hospital



Capt. Dr. Robert Sherins & Sally Our Lab Blood Source

Capt. Sherins, (right)



Capt. Dr. Robert Sherins Inspecting Safe Water Bag



Base Sewage Imhoff Tank



USAF Helicopter HH43 Oversea Rescue Operation



Air to Air Refueling in Radio Silence Over Mediterranean Sea



Exploring Anatolian Castles

Robert & Marlene Sherins

Tumlu Kale (Armenian Castle, Cilician Plain – 1965)



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Anavarza Castle

