"Constructing a Family Finder Genomic Journey"

Robert S. Sherins, MD

Introduction

Humans inherit all of their individual characteristics and gender from the genes received from both parents. In males, gender is carried on the Y-DNA of the 23rd chromosome. Males also receive and X-chromosome from their mother, but an XY pairing of the 23rd chromosome will determine male gender of an offspring. On the other hand, women receive an X-chromosome from each parent. This results in an XX-pair of chromosomes that confers female gender to that offspring.

The other 22-pairs of chromosomes, other than the X and Y chromosome, are inherited from both parents nearly equally, one chromosome of each pair from the father and the other from the mother. Any uneven split of the shared chromosomes may result in a mutation of the genetic material, which may be lethal or non-lethal. Those 22 pairs are known as autosomal chromosomes, which provide all of the characteristics of each individual, except for gender. Gender is solely provided by the X- and Y-chromosomes.

In my past publication about the human genomic journey, I showed how the male Y-DNA and the female mitochondrial DNA (mtDNA) are transferred to each subsequent generation in a linked chain that is unbroken from the time of the appearance of the first modern humans. The rate of mutations of the DNA can be measured. From those calculations it was determined that modern human females have birthed offspring since about 150,000 years ago. Males on the other hand, did not demonstrate such an aged genome and the earliest male age was estimated only about 60,000 years ago. The male partner had to exist, but no researchers had yet discovered Y-DNA of that older era.

Last year, an African-American man from Atlanta, Georgia, requested his DNA analysis. His DNA was so different, that the National Geographic Genomic Project sent the tissue samples to another genetics laboratory at Family Tree DNA, inc. in Arizona. The second laboratory was able to determine that the sample Y-DNA mutations dated from 348,000 years ago. It was the oldest modern human DNA ever studied. In fact, the Family Tree DNA laboratory possessed 2 additional human tissue samples of identical haplotype. One sample came from an individual in Algeria and the other from Chad. This demonstrated that modern human DNA was much older than suspected.

This year, I discovered that it was possible to study the DNA from the other 22-pairs of chromosomes, which are known as the autosomal chromosomes. For a reasonable fee of $99, the previously submitted tissue samples were studied. The test is known as the "Family Finder" test. Mutations within the DNA of the 22-pairs of autosomal chromosomes were compared to the DNA from other large indigenous populations throughout the world. From the DNA studies of my wife and me, samples were compared on a statistical basis for similarities to the other populations. The charts and maps shown below demonstrate the extraordinary and exceptional evidence associated with each of our genomes.

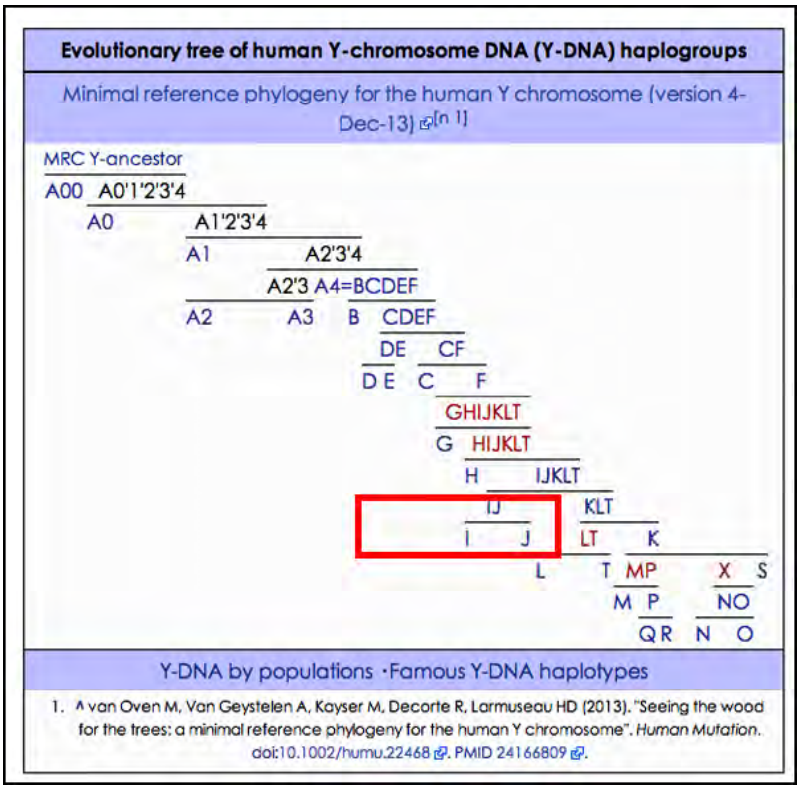
Additional information from newly discovered mutations and nucleotide sequences of the Y-DNA and mtDNA has provided much more detail than previously known with regard to the genomic journey identified with the 23rd chromosomes. Many new sub-clades (sub-groups) and refined interpretations have been announced. I will explain this in greater detail in the article.

**Robert S. Sherins Y-DNA Genome**:
The results of Robert's Y-DNA test showed that his haplogroup and subclade are J2a. Howver, further and deep DNA testing was requested, which further refined the subclade as **Haplogroup M410.**This was determined by analyzing single mutations (SNPs) among the nucleotide sequences binding the

2 chains of the DNA. More recent joint efforts among researchers have resulted in redefining many of the estimates about the evolutionary chronology and timeline.

The chart below demonstrates a reference for the human Y-DNA chronology. We have learned that the ancestor male Y-DNA has been dated to 348,000 years ago. This finding reset the timeline of human evolution back by a huge number of millennia. The oldest estimate of female ancestry is still estimated to be 150,000 years ago. Let's wait a little longer because surely there was a "first" female whose mtDNA would match that of the male. Ancestral DNA may have died out leaving no traces of the "first" human female. However, the genomic researchers are seriously involved in finding "her." To me, the concept of being able to determine the age of an ancestral "Adam" and an ancestral "Eve" is absolutely spellbinding. Of course there had to be a "First Couple."

The chart displayed below[1] depicts the evolutionary development of the Y-DNA haplogroups by their "letter" designations. Robert's Y-DNA is designated J2a (red marquee). The chart demonstrates that the J Haplogroup is a fairly recent development.




The next chart[2] shows that the J2 Haplogroup appeared about 15,000 years ago and is represented by populations in the Northern Mesopotamian region. The results are consistent with previous predictions that the J-M172 (J2a) Haplogroup developed in the region known as the "fertile crescent" – located along the southern border of Turkey with its geographic neighbors: Syria, Iraq and Iran.

[1] www.wikipedia.com
[2] Ibid.

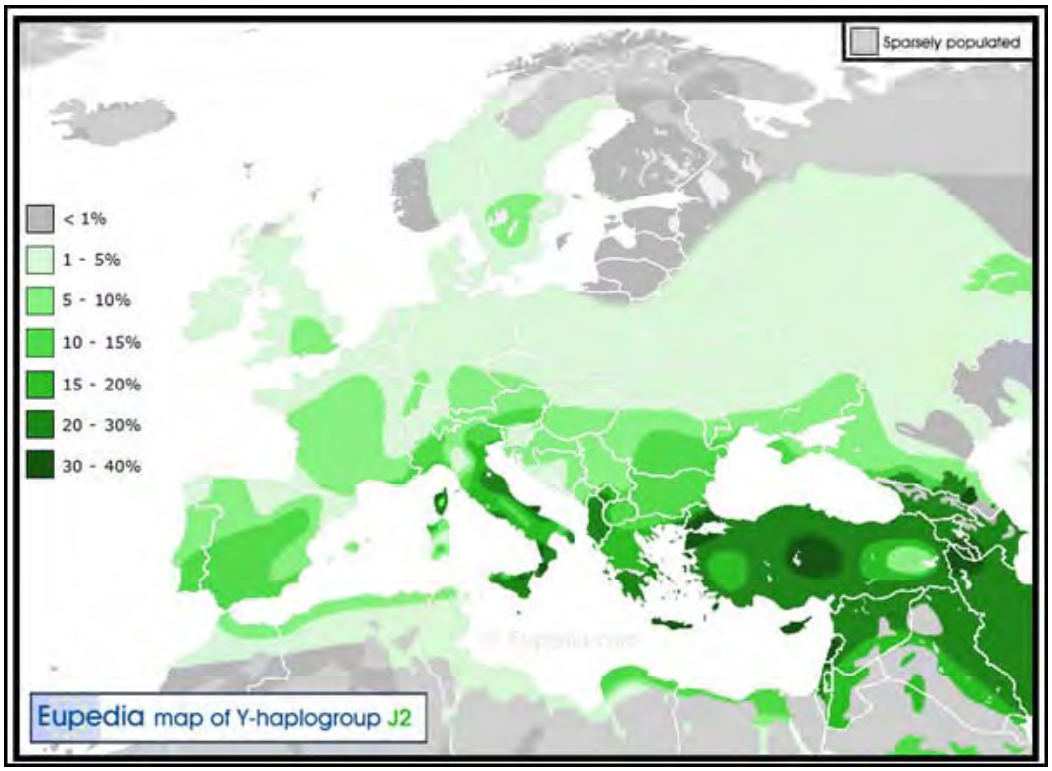
| Haplogroup | Possible time of origin (years ago) | Possible place of origin | Highest frequencies |
|---|---|---|---|
| K | 40,000 | South Asia or West Asia | |
| T | 30,000 | West Asia | |
| J | 30,000 | Middle East | |
| R | 28,000 | Central Asia | |
| E1b1b-M35 | 26,000 | East Africa | |
| I | 25,000 | Balkans | |
| R1a1 | 21,000 | Southern Russia | |
| R1b | 20,000 | Around the Caspian Sea or Central Asia | |
| E1b1b-M78 | 18,000 | Egypt/Libya | |
| G | 17,000 | Between India and the Caucasus | |
| I2 | 17,000 | Balkans | |
| J2 | 15,000 | Northern Mesopotamia | |
| I2b | 13,000 | Central Europe | |
| N1c1 | 12,000 | Siberia | |
| I2a | 11,000 | Balkans | |
| R1b1b2 | 10,000 | North or south of the Caucasus | |
| J1 | 10,000 | Arabian peninsula | |
| E1b1b-V13 | 10,000 | Balkans | Albania |
| I2b1 | 9,000 | Central Europe | Germany |
| I2a1 | 8,000 | Pyrenees[16] | |
| I2a2 | 7,500 | Dinaric Alps | |
| E1b1b-M81 | 5,500 | Maghreb | Berbers |
| I1 | 5,000 | Scandinavia | |
| R1b-L21 | 4,000 | Central or Eastern Europe | |
| R1b-S28 | 3,500 | around the Alps | |
| R1b-S21 | 3,000 | Frisia or Central Europe | |
| I2b1a | < 3,000 | Britanny | |

The 3rd chart shows the distribution of populations with the largest percentage of individuals displaying the J-M172 (J2a) haplogroup – in descending order: Iraq, Lebanon, Iran, Turkey, and Ashkenazim' Jews.[3] The expansion of J-M172 individuals in the Levant/Syria has been associated with the success of the Neolithic agriculturalists, which occurred about 8,000-9,000 years ago. There are other populations of the Caucasus that significantly display the J-M172 haplogroup: Inquish 87%,[4] Chechens 55%, Georgians 21-72%, Azeris 24%, Abkhazia 25%, Ossetians 24%, and Circassians 22%.[5] A more recent analysis of a 37-marker DNA test showed that my Y-DNA can be more specifically identified as the ***subclade M410***. The M410 population is primarily ***located in Georgia and North Ossetia***. This is positioned in the heart of the Caucasus.

[3] J-M172 haplogroup is less frequently represented among Sephardim Jews.
[4] Formerly Inguish-Chechin Soviet Republic; now split into 2 republics of Russia.
[5] Ibid.

| Country/Region | Sampling | N | J-M172 | Study |
|---|---|---|---|---|
| Jewish | Ashkenazim Jewish | 442 | 19 | Behar 2004 |
| Iran | | 92 | 25 | El-Sibai 2009 |
| Iraq | | 154 | 43.6 | Al-Zahery 2011 |
| Israel | Akka | 101 | 18.6 | El-Sibai 2009 |
| Jordan | | 273 | 14.6 | El-Sibai 2009 |
| Lebanon | | 951 | 29.4 | El-Sibai 2009 |
| Oman | | 121 | 10.0 | Abu-Amero 2009 |
| Pakistan | | 176 | 11.9 | Abu-Amero 2009 |
| Pakistan | Chitral District | | | Firasat 2007 |
| Qatar | | 72 | 8.3 | El-Sibai 2009 |
| Saudi Arabia | | 157 | 15.9 | Abu-Amero 2009 |
| Syria | Syria | 554 | 20.8 | El-Sibai 2009 |
| Turkey | | 523 | 24.2 | El-Sibai 2009 |
| UAE | | 164 | 10.3 | El-Sibai 2009 |
| Yemen | | 62 | 9.6 | El-Sibai 2009 |

The following "Eupedia" map depicts the regions with the highest concentration of J-M172 populations. Also displayed are the populations that migrated farthest from the Levant.



FamilyTreeDNA

# Certificate – Haplogroup

Family Tree DNA certifies that a DNA sample from

## Robert Saul Sherins

was analyzed for Haplogroup determination using the Single Nucleotide Polymorphism test. The analysis shows that you are positive for the following SNPs: M410+; and negative for the following SNPs: P81- P279- M68- M67- M47- M419- M340- M339- M319- M318- M289- M158- M137-. According to the current classification, you have been assigned to:

**Haplogroup J2a**

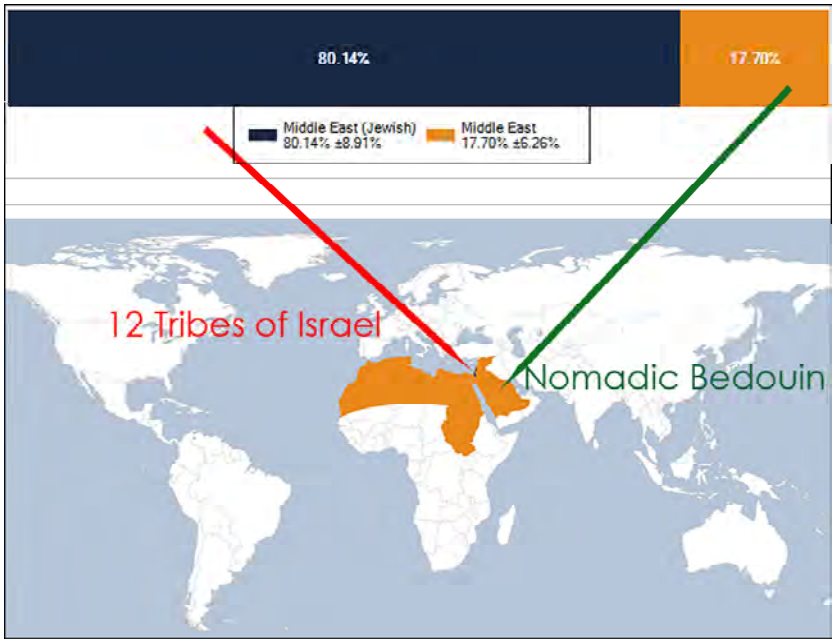
This lineage originated in the northern portion of the Fertile Crescent where it later spread throughout central Asia, the Mediterranean, and south into India. As with other populations with Mediterranean ancestry this lineage is found within Jewish populations.

December 6, 2013

Concetta A. Bormans

Y-DNA Haplogroup/Subclade J2a/J-M172 Haplogroup

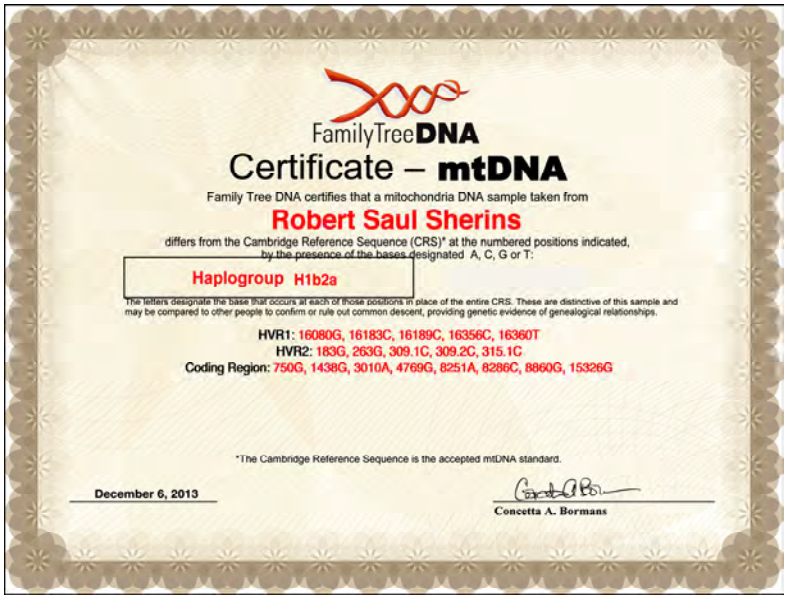

Map of Fertile Crescent Location; Region of 1st Agriculture Settlements




Autosomal Family Finder Locations
80% Hebrew Tribes of Israel; 18% Nomadic Bedouin

**Robert Sherins Autosomal Genome** shows that his appearance and characteristics are most related to Jewish ancestry from the Levant. The study is called the "Family Finder" analysis. About 80% of his autosomal genes were derived from ancestral Hebrew tribes in the Levant. Those genetic ancestors also gave rise to populations of Kurds, Anatolians, Georgians, Armenians and other diverse Semitic tribes. Another deduction from the analysis was the ***absence*** of any Iberian or Iranian population representation. This is significant in its absence, since there are no indications of Sephardic or Mizrahi (Eastern Assyrian, Babylonian or Persian Jewish) autosomal DNA.

Because Robert carries the mtDNA from his mother, it was possible to update the evidence from his maternal lineage. The certificate demonstrates the mtDNA from the **H1b2a haplogroup**.


FamilyTreeDNA

Certificate – **mtDNA**

Family Tree DNA certifies that a mitochondria DNA sample taken from

**Robert Saul Sherins**

differs from the Cambridge Reference Sequence (CRS)* at the numbered positions indicated, by the presence of the bases designated A, C, G or T:

Haplogroup H1b2a

The letters designate the base that occurs at each of those positions in place of the entire CRS. These are distinctive of this sample and may be compared to other people to confirm or rule out common descent, providing genetic evidence of genealogical relationships.

HVR1: 16080G, 16183C, 16189C, 16356C, 16360T
HVR2: 183G, 263G, 309.1C, 309.2C, 315.1C
Coding Region: 750G, 1438G, 3010A, 4769G, 8251A, 8286C, 8860G, 15326G

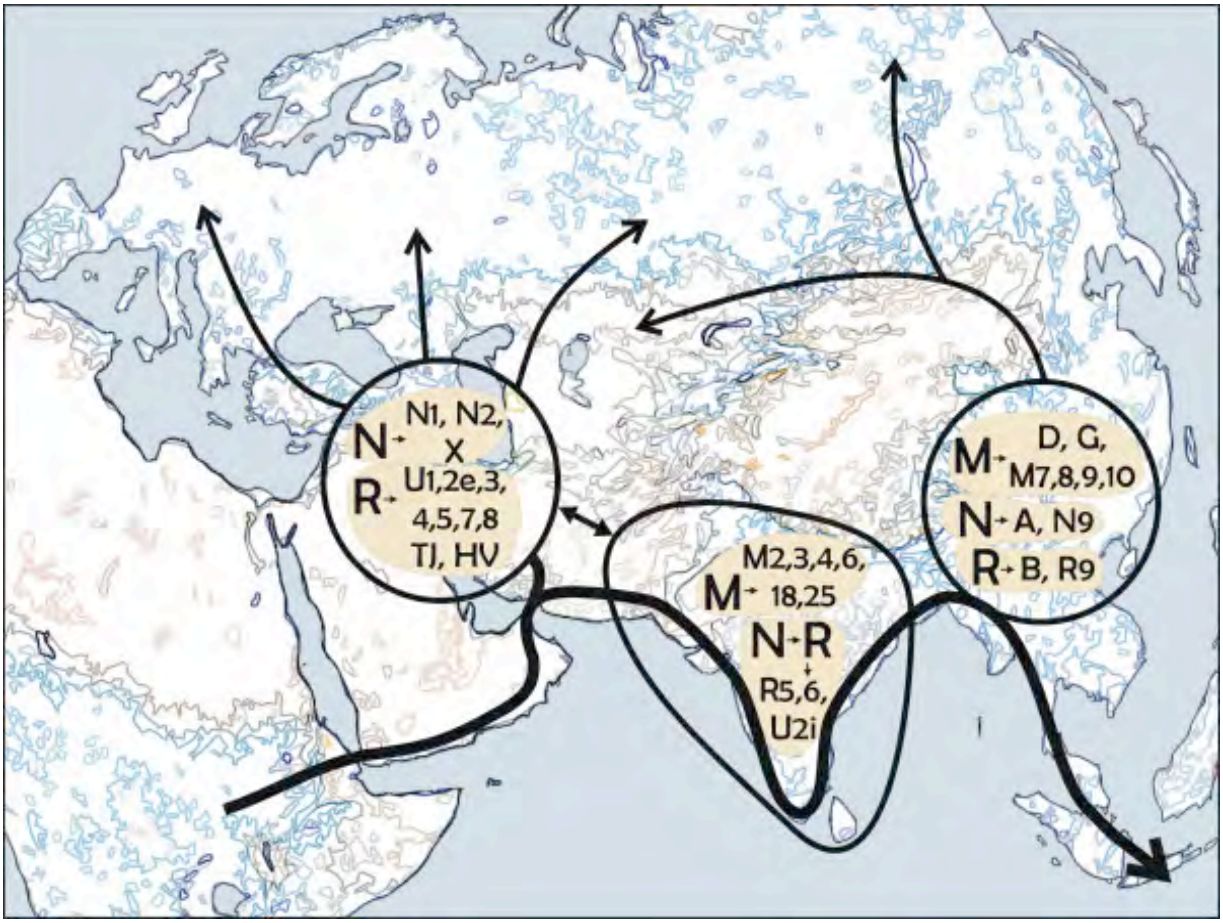
*The Cambridge Reference Sequence is the accepted mtDNA standard.

December 6, 2013

Concetta A. Bormans

mtDNA Haplogroup/Subclade: H1b2a

The following map depicts the genomic journey and expansion of females who carried the ancestral HV and H mtDNA to Europe.




Current data support a conclusion that ancestral females of the mtDNA "N" haplogroup migrated from Western Asia to Europe[6] approximately 15,000 years ago. About 80% of Ashkenazi Jews can trace their ancestors to Eastern Europe. It is believed that the females of that group were local women who were assimilated from indigenous populations and converted to Judaism. Because of the earlier dates of evolution, distribution of their progeny with similar genetic traits can also be found elsewhere in the Near East, in Eastern Africa and India, as well as in East, Central Asia and the Caucasus. The evolution of this haplogroup was a major founding of a new population stemming perhaps from Southern Mediterranean/Italy migrating northward to Central Europe. Also represented is a large cohort of "Levites" (ancient priestly caste). The theories of gene flow during the subsequent millennia have become a fascinating resource for understanding the development of the several prominent Jewish communities of the world.

The first wave of female conversion to Judaism is estimated to be about, or even before, 2,000 years ago, when Jewish traders were first permitted into the Hellenistic Greek and later Roman territories**. It is estimated that those assimilations occurred primarily in the Mediterranean region of Italy with no evidence of assimilation in Eastern Europe, the Caucasus or from the Kazharians.**

Many daughter lineages were founded from the initial appearance of "N" and "HVO" Haplogroups; 81% of the descendants are European populations: HVO (4.1%); H (20.5%); I (1.3 %); J (6.3%); K (31.8%); M1 (1.0%); U (2.2%); W (1.6%); and remaining groups in the Near East and Asia (9.4%).
I

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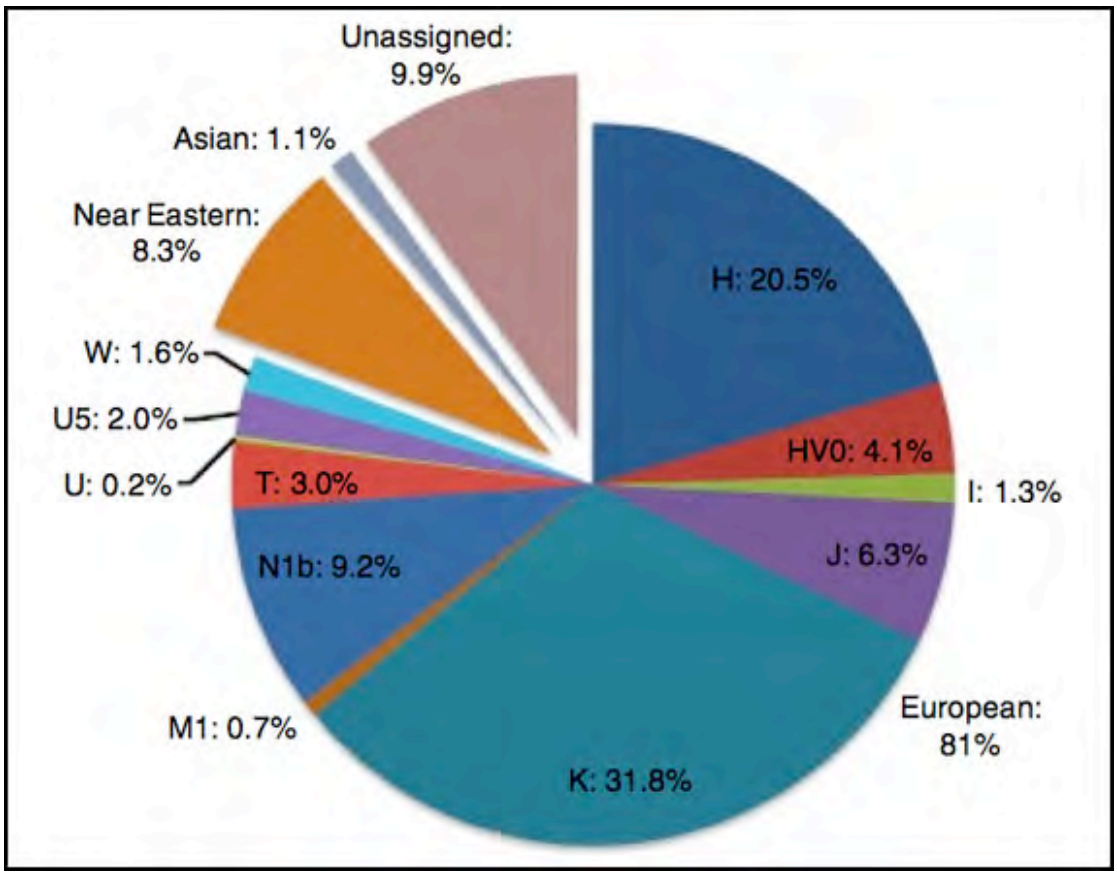
6 http://www.academia.edu/4718697/A_substantial_prehistoric_European_ancestry_amongst_Ashkenazi_maternal_lineages




From the data one can understand why Jewish females are significantly represented in the populations of Belarus, Lithuania, Poland, Russia and Ukraine.

Conclusion:

Genomic testing of the 23rd chromosome (sex-chromosomes X-mtDNA and Y-DNA) and the autosomes of the remaining 22-pairs of chromosomes can provide invaluable information about the journey and culture of our ancestors. The information and interpretation of the testing results is being updated regularly. This is the best reason to support periodically revisiting one's test results. The results of my wife's and my own DNA analyses have been summarized with surprisingly new understanding of our genomic ancestry.