

Genetic Journey of the Cherkinsky Ancestors  
Report of Y-DNA Haplogroup Mutations

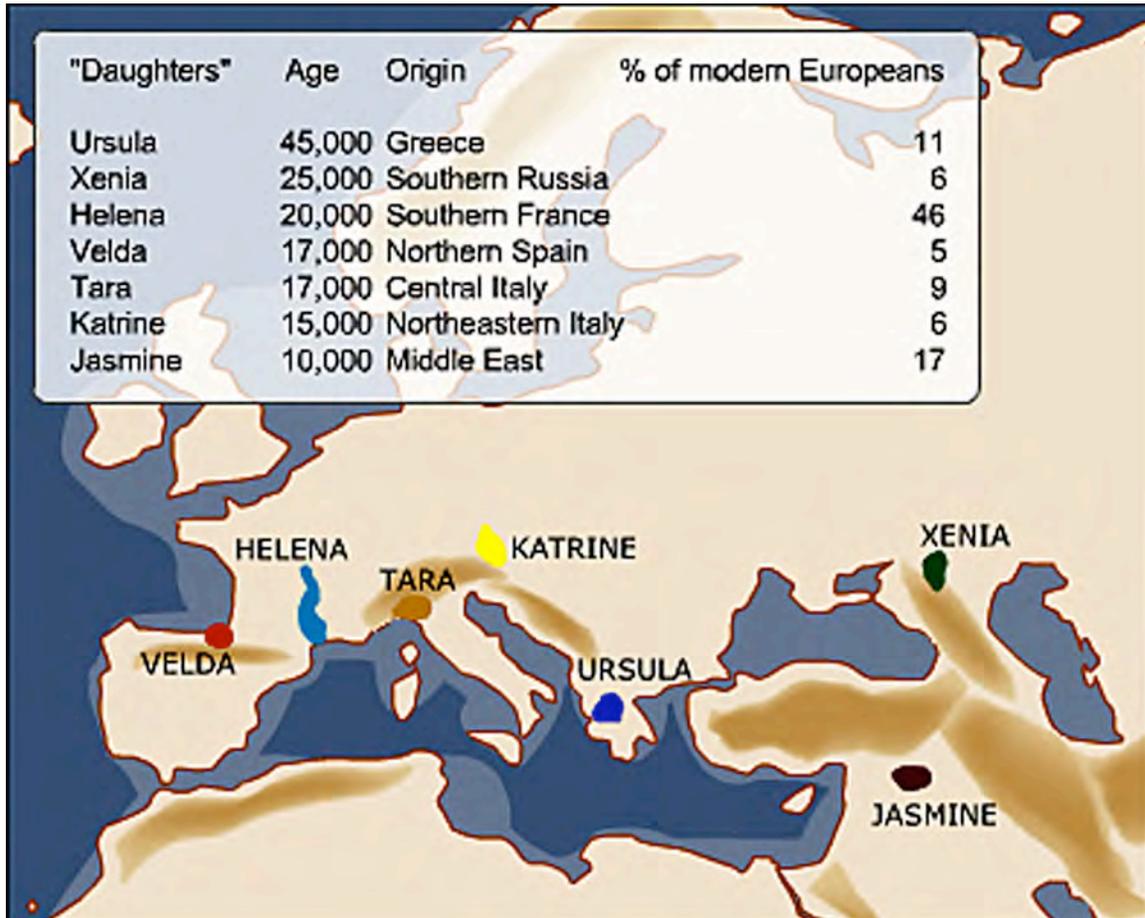
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With the advent of the scientific success of the investigations provided by the Human Genomic Project, relatively inexpensive genetic testing was made available to the public. Several laboratories offer these services, however, the **FamilyTreeDNA** laboratory, under the direction of Professor, Dr. Michael Diamond at the University of Arizona, was selected to analyze the specimens taken from Robert Sherins. Dr. Diamond's laboratory has accumulated a genomic database of about 250,000 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/her data by knowing the sample number and password. As future new information is learned, the laboratory at no extra charge will provide updates to its participants.

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

Mutations in our genetic coding occur about once in every thousand years, although the mutations found in the male Y-DNA occur more rapidly than the mitochondrial DNA (mtDNA) of females. By comparing the molecular chemistry of an individual's DNA to a large database of samples obtained from a given geographical region, Dr. Sykes has calculated the approximate dates of the nearest common female ancestors of a region from the mutation rates determined from our DNA, a common ancestor, who shares identical mutations. In so doing, Dr. Sykes created several fictitious female names, which identified the presumed genetic "mothers." He called those females, "The Seven Daughters of Eve," which are the names given for the genetic mothers of the several European and Central Asian regions involved in his research. Seven females were determined to possess the evidence of the first or most recent common genetic mutations and migrations among regional human populations. Those females transferred their genes with their mutations to successive future offspring. In turn, those genes were transferred to their future generations. The larger the sample population, the more accurate were the predictions of common ancestry. That is the basis of the choice to utilize the FamilyTree DNA laboratory, which could compare my individual genetic sample to a very large database of regional samples, especially those of Eastern European populations.

## Map of Ancestral "Eves"

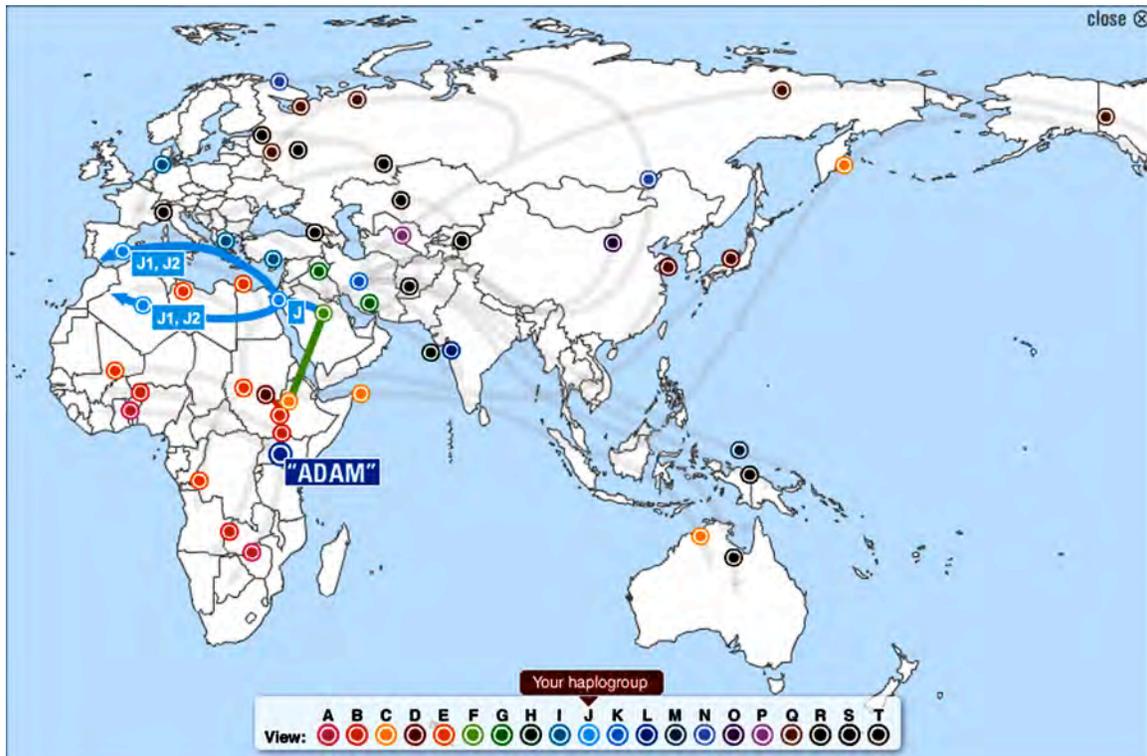


In conception, offspring receive two sex chromosomes, the *Y-chromosome* from the biological father for males, and the *X-chromosome* from the mother. Only sons receive the Y-chromosome. Yet, the male also receives an X-chromosome from his mother as the other half of the chromosomal pair that is inherited. Thus, males receive a set of XY-chromosomes. Fathers cannot contribute an X-chromosome to offspring. Males do **not** receive mtDNA from their fathers because the mitochondrial DNA of the Y-chromosome does not enter the ovum of the mating mother during fertilization – the mtDNA remains outside the fertilized conceptus. Mothers provide both copies of the X-chromosomes to all offspring.

Robert Sherins submitted three sample swabs to the laboratory that were taken from his mouth. The specimens were analyzed for the Y-DNA that was inherited from Robert's Cherkinsky male ancestors. However, Robert's specimen also was analyzed for the X-chromosomal material that he inherited from his mother's Goldenberg ancestors.

The report from FamilyTreeDNA laboratory, which explained the Y-DNA analysis of the 37 genetic targeted molecular sites (instead of the minimal tests for either 12 or 25 alleles), contained fascinating information. A summary of this information is outlined below and supplemented with images of maps, which demonstrated the genomic journey derived from the sub-sets J-2, M-172 and MJ of the “J” Haplogroup.

### Map of J-2 Haplogroup Sub-set Distribution



Robert inherited male Y-DNA only from his male ancestors, who became known to him through the efforts of his genealogical research - as far back as his fourth great grandfather who lived in Konotop, Ukraine, since about 1760. The report showed information of the *general* genomic journey, but remains elusive about certain details of that journey.

Each molecular site of the approximately 20,000 human genes of the 23-pairs of human chromosomes is known as an *allele*. Sex chromosomes are identified as either the X or Y-chromosome; this analysis of the mutations is limited to the Y-chromosome. Each of the mutations was labeled and assigned to a specific “Haplogroup.” A Haplogroup identifies the constellation of mutations in the molecular chemistry of the DNA that has been inherited. Each mutation may be called an *SNP*, specific nucleotide polymorphism (change of molecular chemistry). In Robert’s sample, the analysis was reported as the **J Haplogroup, but with J-2 and M-172 sub-sets.**

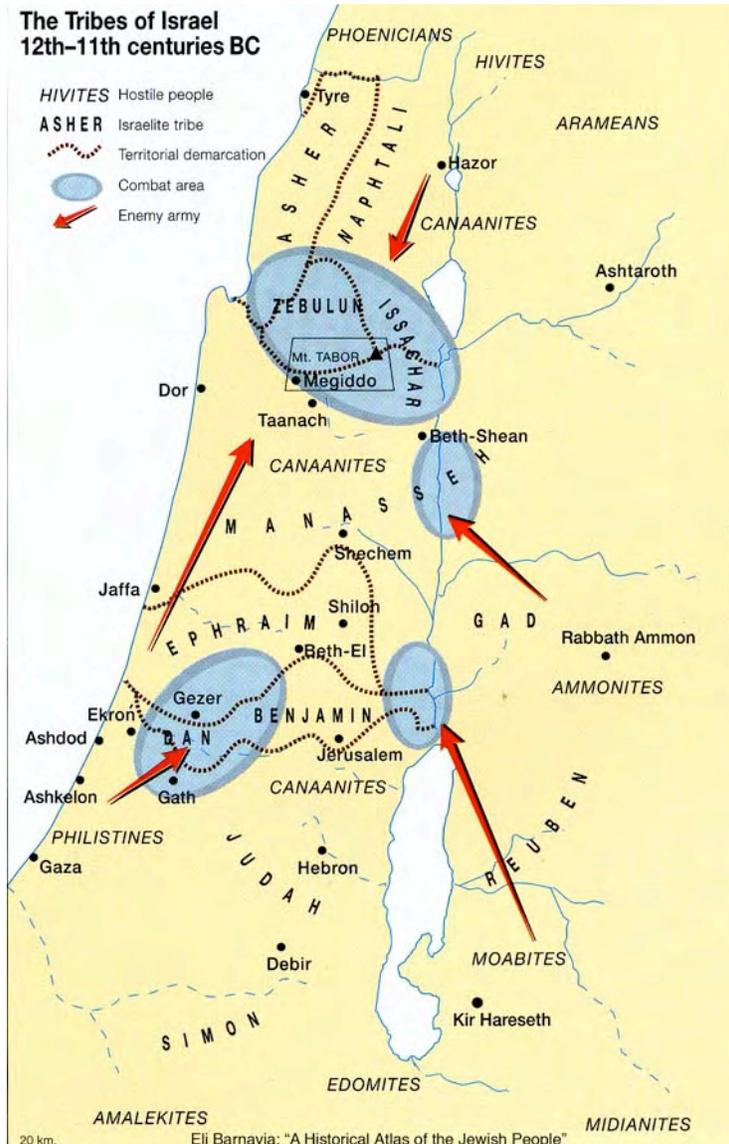
Our human journey began an estimated 150,000 to 200,000 years ago in the Rift Valley of Kenya-Ethiopia, Africa, where modern humans evolved. Skeletal remains have been dated, which have provided part of the basis of the evidence for our human evolutionary journey. A list of those dates is summarized to show the approximate era and region of the early and pre-historic human inhabitation.

**Table of the Human Genomic Journey  
Common to our Haplogroup**

Approximate Date	Region	Haplogroup
150,000 years ago	African Rift Valley; especially Sub-Saharan	L1
90,000	Out of Africa	L3
80,000	Middle East and West Eurasia	N
60,000	East Eurasian	M
60,000 - 45,000	Large sub-set of the N Haplogroup; East and West Central Asia and the Middle East.	R
45,000	Sub-Set of Haplogroup "R"	M89
40,000	Sub-set of M89; Mainly Middle East	J and J-1
10,000	Sub-Set of Haplogroup "J" Located in the Fertile Crescent Region of Mesopotamia	J-2 M-172 or J-M Sub-claves

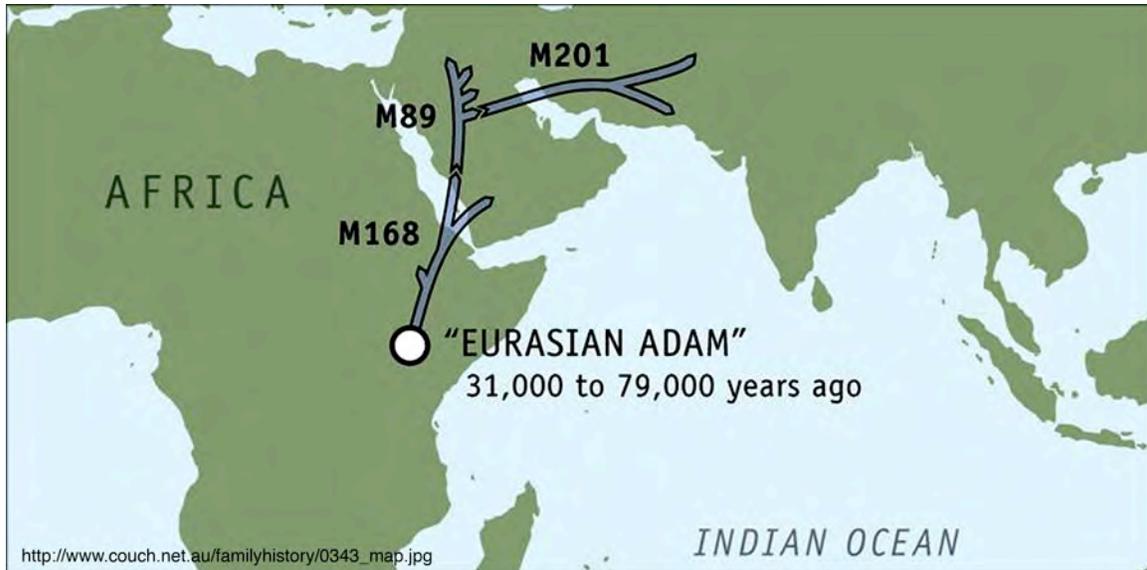
What do the sub-sets of "J" mean? Brian Sykes created the fictitious names of the assumed daughters of Eve (named after the Biblical "Adam and Eve"), denoting the location of the most recent female ancestors of modern humans. In the region of the Mesopotamian Fertile Crescent, the former Assyrian Empire and Northern Iraq, the daughter of Eve was named, "*Jasmine*," or simplified as the letter "*J*." Jasmine appeared about 10,000 years ago and gave rise to the many generations of Semitic tribes of Summeria, the Levant, Kurds, Canaanites, Arabs, Hebrews and long-forgotten names of other tribes of the region.

## Map of the Tribes of the Levant



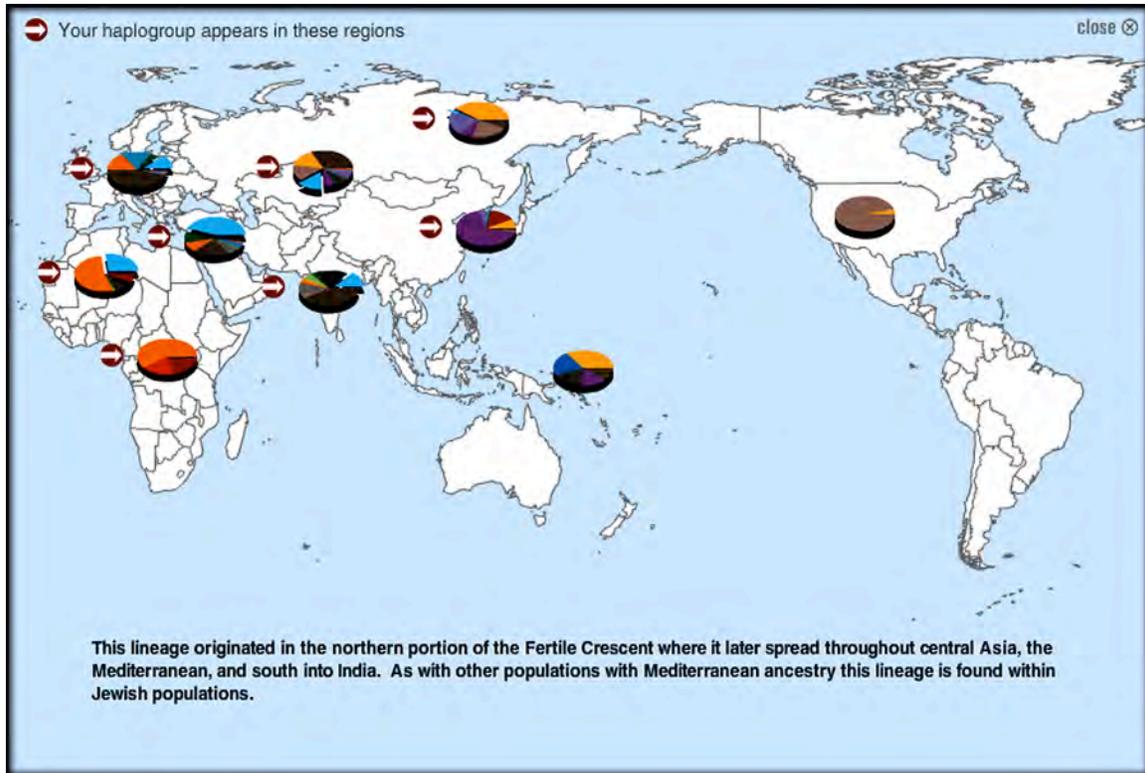
J-1, J-2 and M-172 are major sub-sets of the Haplogroup "J" (Jasmine). Although "J" has minimal distribution, sub-set J-1 is associated with Semitic peoples of the Middle East. **M-172** arose from sub-set J-2, now as **M-89**. That mutation has been identified in many individuals, but, mainly in Southern Europe, Greece, Italy, Spain, as well as. Turkey, Georgia, the Kurds, the Middle East, Central Asia and South Asia.

## Map of M89 Haplogroup Distribution



The J-2 sub-set mutation has been identified in 20% of all Jews. J-2 and M-172 sub-set mutations also were identified in remains uncovered in Jericho and from an excavation near Jerusalem, which were dated about 8,500 years ago. That era was associated with the rather abrupt change in living conditions when the hunter-gatherers appear to have first settled from their nomadic prior lives.

## Map of J-2 and M-172 Haplogroup Sub-Set Frequencies



The DNA mutations associated with the many past pre-historic migrations of modern humans from 150,000 to 8,500 years ago can be identified among all our Cherkinsky ancestors. The surname, Cherkinsky, was adopted only a couple of centuries ago; patronymic naming pre-existed. The oldest genealogical record of the Cherkinsky surname was dated about 1790. We can derived from that information, the name and birth of our third great grandfather, Iosef Cherkinsky, from Konotop and assume that his unnamed father would have been born about 1760.

There is **no** specific genomic information between the dates of our common ancestral Eve, Jasmine, who lived about 10,000 years ago, and the dates of our genealogical records that proved the existence of our Cherkinsky ancestors since the 18<sup>th</sup> century in Konotop, Ukraine. However, indirect genomic evidence is available. There are nine locations where a large group of other samples have been collected and identified by exact J-2 and M-172 matches with our Cherkinsky' Y-DNA mutations. Those matches were located in: Germany/Prussia, Lithuania, Poland, Eastern Austria, Belarus and Ukraine. The Middle Eastern matches can be assumed, since not all ancestors migrated from their original settlements in the Middle East.

## European Matches of Cherkinsky Y-DNA



There is an unfortunate scientific disconnect in the available information between the time of the first Diaspora from the Middle East (5<sup>th</sup> century BCE) to the time of the known relocation of our ancestors in Eastern Europe (18<sup>th</sup> century). Cherkinsky ancestors were known to have lived in the region of Minsk Gubernya, Belarus-White Russia, in the early 18<sup>th</sup> Century before their relocation to Konotop, Ukraine. Records documenting our ancestors are proven from 1790; our ancestors lived in the five villages of Konotop Uyezd (county), Chernigov Gubernya: Konotop, Bakhmach, Hrigorovka, Kuren, and Tynitsia.

One of the most attractive hypotheses about the Cherkinsky migration to Eastern Europe remains the theory that our ancestors first migrated to Crimea and the Black Sea area during the era of the Greek colonies of the Black Sea region that began in the 5<sup>th</sup> century BCE. Jewish traders, some with their families, migrated steadily northward from successful settlements in Crimea, eventually settling in Kiev about the 13<sup>th</sup> century. Jews were evicted by the Russian Czar during the 14<sup>th</sup> century and did not return to Russia until the time of the Partitions of the Commonwealth of Poland-Lithuania in the late 18<sup>th</sup> century, 1772, 1794, and 1795. Our ancestors were thus “Russianized” through the political process that ensued by the Russian occupation of Eastern Poland.

The other hypotheses about Cherkinsky migration in Europe must include:

- Early Jewish migration to Southern Europe along the Mediterranean Sea as far as Spain; secondary migration after the Inquisition, followed by eviction from Spain and Portugal in 1492. Under those circumstances, Cherkinsky ancestors very likely would have migrated to Northwestern Europe,

Netherlands, Prussia or England, before additional migration to Lithuania, Belarus, Poland, and eventually Konotop, Ukraine.

- An alternative hypothesis would include migration from Spain or Portugal to the Ottoman Empire and then secondary migration northward. This latter route seems less likely in our specific case.
- Jewish migration during the time of the Roman Empire from the 1<sup>st</sup> to 6<sup>th</sup> centuries CE with eventual settlement in Italy. Apparently, 60% of the Ashkenazim living in Europe can be traced to the genomes of four women in Northern Italy, “genetic mothers,” from the 6<sup>th</sup> to 10<sup>th</sup> centuries.

Unanswered questions about the Cherkinsky ancestral journey from the era of Abraham, about 2,800 years ago must take into account the anthropological and cultural history of the many Jewish Diasporas.

- The first Diaspora was a result of the Assyrian conquest of the Ten Tribes of the Northern Kingdom of Israel ~750 BCE.
- The “March to Babylon” occurred in 580 BCE and was associated with the second conquest of Israel, when the Babylonians defeated the Southern Kingdom of Israel and destroyed the First Temple in Jerusalem.
- Cyrus, king of Persia, conquered Babylon in 530 BCE and the Jews of the former Babylonian community became traders and merchants, who could travel to the frontiers of the Persian Empire. The frontiers extended from the Indus Valley in the east, to the region of the present “...stan” countries in Central Asia, to the western frontiers of Anatolia, and to Egypt.
- When Alexander the Great defeated Darius of Persia in the 3<sup>rd</sup> century BCE, Jews emigrated to the frontiers of the expanded Greek Empire: India, Middle East, North Africa, Turkey, Crimea, Georgia (Caucasus), and Greece.
- During the period after the Romans defeated the Greeks – the era of Jesus, Jews emigrated to the frontiers of the vast Roman Empire: North Africa, Middle East, Byzantium, Southern Mediterranean as far as Spain, European frontiers as far as England, Germany, France, and parts of Central Europe.
- During the era of the Roman Empire, Jews relocated to communities in Italy, the Balkans, France, and Germany.
- Jews began to trade with the kingdom of Poland and the Grand Duchy of Lithuania after those nations were established in the 10<sup>th</sup> century.
- Jews were first invited by the king of Poland to settle in Eastern Poland in the 13<sup>th</sup> century. They mostly arrived from Western Europe.
- Jews were expelled from Spain and Portugal at the end of the 15<sup>th</sup> century. They mainly relocated to the Netherlands, England, North Africa and the Ottoman Empire.
- Our branch of the Cherkinsky family has the rare B+ blood type. B+ blood type has been detected in the descendants of the Canaanites, specifically in the modern Arab and Jewish populations, as well as among the Kurds and Armenians. Interestingly, it is present among the current population Kazakhstan, which is a very isolated Central Asian community. Inclusion of the genes for B+ blood very likely came from the descendants of Jasmine, those of us who inherited the genes for Haplogroup “J” – and sub-sets of J2

- and M 172. Those genes also may have been passed to the descendants of migrating Asiatic tribes that brought Asiatic Khazars and similar groups into Eastern Europe. The Khazars lived in the peri-Caspian Sea region, coinciding with the region of Modern Kazakhstan. The Kievan Rus (first Viking kings of Russia) defeated Khazaria in the 13<sup>th</sup> century; the Khazar Empire ceased to exist, but the population migrated primarily into the Commonwealth of Poland-Lithuania (Rzeczpospolita). The Khazarian nobility previously had converted to Judaism in 8<sup>th</sup> century CE, built synagogues, and had a legal system that utilized the Hebrew language. What Jewish father in Eastern Europe would have denied his daughter a marriage to a Jewish Khazarian, with “potential,” to be his new son-in-law?
- The genes from other Asiatic tribes also could have been inserted among Jewish offspring by members of tribes from earlier Asiatic migrations, such as the Scythians or other Turkic speaking nomads from the Altai Region of Mongolia, who invaded Eastern Europe; the Mongol and Tatar invasions; or the Rhadanites, who were early Jewish traders of the first several centuries CE, when Jewish traders and merchants traveled to China, India, Central Asia, Persia, Middle East, North Africa and Europe. It has been estimated that many traders, who ventured far from the Middle East, did not bring their families, because the frontier regions were too dangerous and risky. The genomic project has shown that many Jewish descendants carry the genes of the local populations, which could only have been introduced from mating of Jewish men with non-Jewish local wives, the latter having been converted to Judaism and their offspring raised in the Jewish faith. Importantly, the Rhadanites were known for their business acumen, far ranging adventures, and multi-lingual abilities.

Recommended reading:

- Sykes, Brian: *The Seven Daughters of Eve, the Science that Reveals our Genetic Ancestry*, W.W. Norton & Company, New York and London, 2001.
- Internet searches for the detailed explanation of J-2 and M-172 Haplotype sub-sets and maps of their genomic migration routes.