

Where did I come from? - Your predicted Y-DNA ancestral origins

- Y-DNA Haplogroup: R-M207

- Subgroup: R1-M173
- Confidence: Medium

Y-DNA Haplogroup R-M207 Summary

Haplogroup R is defined by a DNA [marker](#) known as M207. Everyone who carries this marker today descends from a common paternal ancestor who lived about 30,000 years ago in west Asia. To date, over thirty [subclades](#) of haplogroup R have been identified, of which, R1a1-M17 and R1b1b2-M269 (historically called R1b3) are the most well described. Both of these subgroups are indicators of European ancestry with haplogroup R1a1-M17 most representative of Eastern Europeans and R1b1b2-M269 most characteristic of Western Europeans.

HISTORY AND GEOGRAPHY OF HAPLOGROUP R

As members of the human family, all people living today can trace their earliest paternal ancestors to populations that lived approximately 100,000 years ago in eastern Africa. These early humans became spread throughout the African continent, and beginning ~50,000 years ago, a series of complex [migrations](#) moved them out of Africa into regions of Asia and beyond to eventually populate every major area of the world.

Approximately 26-30,000 years ago haplogroup R emerged in west Asia descending from a widespread Asian haplogroup known as K-M9. Representatives of haplogroup R expanded to the west and south migrating throughout central and southwest Asia into India, the Middle East, and Europe. During this time, subgroups R1-M173 became frequent throughout central and western Eurasia while R2-M124 distributed mainly within regions of Central and South Asia. Today, members of haplogroup R*-M207 who carry the R-M207 marker, but neither R1-M173 nor R2-M124 markers, can still be found in Central and South Asia.

Haplogroup R2-M124 expanded in the Asian subcontinent following the last Ice Age which manifested its maximum severity ~18,000 years ago and today is found in India, Pakistan, Central Asia, and Turkey with decreasing frequencies respectively. Little is currently known about the subgroups of R2-M124.

Haplogroup R1-M173, represented primarily by subgroups R1a1-M17 and R1b1b2-M269, became well established in Europe during the Upper Paleolithic Period (Late Stone Age) contributing to the spread of Aurignacian or Gravettian culture, characterized by advanced artistic and technological achievements. During this period, populations were ranging across Europe and subsisted mostly by hunting and gathering. An impending Ice Age, reaching its maximum (the LGM=Last Glacial Maximum) beginning ~18-20,000 years ago and lasting several thousands of years, subsequently covered most of Europe with massive glaciers forcing populations to retreat to geographically isolated refuge areas where they were able to persist. Individuals of R1a1-M17 withdrew primarily to refuges located in present day Ukraine and Asia Minor while representatives of R1b1b2-M269 became most concentrated in the Iberian refuge.

As the Ice Age began to abate ~13,000 years ago and living conditions slowly improved across Europe,

localized populations migrated from refuge areas to repopulate Europe and areas of Asia. Specifically, representatives of haplogroup R1a1-M17 expanded into eastern Europe and into parts of Asia whereas those of R1b1b2-M269 moved primarily throughout western Europe, creating opposite geographic distributions which are still evident today. Currently, R1a1-M17 is rare across Western Europe but is found throughout eastern Europe in countries such as Poland, Hungary, and Ukraine; in central Asia with highest prevalence in Altaic-speaking populations of eastern Kyrgyzstan and Indo-European-speaking populations of Tajikistan; and in areas of northwest India. In contrast, R1b1b2-M269 is found at very high frequencies (50-80%) throughout western Europe particularly in the Ireland, Wales, Scotland, England, Portugal, France, Germany, and northern Italy, with diminishing frequencies towards the east although representation stretches as far as central Asia and India.

Once the Ice Age ended haplogroup R would continue to play significant roles in subsequent phases of European history, including the adoption and spread of farming and agriculture, Greek and Roman influences, and the Middle Ages. These and other historic events are currently being studied within the context of Y-DNA haplogroups. This ongoing research will surely enrich our current understanding of world history as well as our own personal and family histories.

IBERIAN R1b HAPLOGROUPS

Haplogroups R1b1b2a2c-M153 and R1b1b2a2d-M167 are considered indigenous to the Iberian Peninsula which encompasses Portugal, Spain, Andorra, Gibraltar, and a portion of France. Evidence suggests that R1b1b2a2c-M153 originated ~18,000 thousand years ago among the Iberian Basques, an ethnic group whose non-Indo-European language, Euskara is the oldest surviving language in Europe. Haplogroup R1b1b2a2d-M167 also originated in Iberia but evolved among its non-Basque population.

HAPLOTYPES OF HAPLOGROUP R

A Y-DNA haplotype consists of a series of [STR \(Short Tandem Repeat\)](#) markers located along the [Y-chromosome](#). Each STR marker has a very high mutation rate and therefore changes rather quickly through time. Because of their high variability STR haplotypes can identify recent relationships within a haplogroup. One well known example is the 6-marker Atlantic Modal Haplotype§ (AMH), which is shared at high frequencies by members of haplogroup R1b1b2-M269 living in the European Atlantic facade, specifically Celtic-speaking populations of Ireland and Wales, Scandinavian countries of Netherlands and Norway, and the Basque population. Additionally, a 17-marker haplotype known as the Irish Modal Haplotype§§ (IMH) accounts for 17% of haplogroup R1b1b2-M269 members in northwest Ireland.

The Y-STR marker, DYS458 is commonly tested by genetic-genealogy companies and is included in many public databases. An unusual "0.2" value (ex. DYS458 = 17.2) is relatively common and typically associated with the Middle Eastern haplogroup J1-M267. However, DYS458.2 values have recently been found to also exist within haplogroups R1b1b2-M269 and R1b1b2a1-M405. Haplogroups J and R do not share this unusual marker because of common ancestry but due to chance independent mutation events. This result underscores the weakness of using a single STR marker or too few STR markers as indicators of common ancestry, even when those values are relatively rare.

FAMOUS MEMBERS OF HAPLOGROUP R

One of Scotland's greatest warriors, Somerled of Argyll, who is credited with driving the Vikings from Scotland, belonged to haplogroup R1a1-M17. Members of Clan Donald, which Somerled founded, were tested to determine Somerled's Y-chromosome membership. In 2005, Oxford University further found that Somerled possibly had 500,000 living descendants. If that is correct, he would be the second most common ancestor after Genghis Khan.

Possible descendants of Niall of the Nine Hostages, an Irish king in the Dark Ages, are members of R1b1b2a2e-M222. These descendants are associated with the U' NŽill clan.

American presidents John Adams and Franklin Pierce belonged to Y-DNA haplogroup R1b1b2-M269.

Joseph Smith Jr., founder of the Mormon Church with current worldwide membership exceeding 13 million, belonged to haplogroup R1b1b2a2e-M222.

Anderson Cooper, an Emmy Award winning American journalist, author, and anchor of the CNN news show Anderson Cooper 360° belongs to haplogroup R1a1-M17.

HAPLOGROUP R AND THE GENETREE DATABASE

The GeneTree haplogroup predictor reports the following R-haplogroups: R1a1-M17, R1b-M343, R1b-M343, R1b1b2*-M269, R1b1b2-M269, R1b1b2a*-S127, R1b1b2a-S127, R1b1b2a1*-M405, R1b1b2a1-M405, R1b1b2a1a-M467, R1b1b2a2e-M222, and R1b1b2a2g-U152, with more on the way!

Approximately 45% of the GeneTree and SMGF databases are members of haplogroup R.

Notes:

** A haplogroup designation followed by a "*" signifies the presence of a haplogroup defining marker but the absence of any other known subclade markers. For example, R1*-M173 is a member of haplogroup R1 but not a member of its subgroup R1a-SRY1532.2.*

§ AMH: DYS388,DYS393,DYD392,DYS19,DYS390,DYS391: 14,24,11,13,13,14

§§ IMH: DYS19, DYS388, DYS390, DYS391, DYS392, DYS393, DYS434, DYS435, DYS436, DYS437, DYS438, DYS439, DYS389I,DYS389B, DYS460, DYS461, DYS462: 14,12,25,11,14,13,9,11,12,15,12,12,13,16,11,10,11

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Frequency Distribution of Y-DNA Haplogroup R-M207



This map shows the geographic distribution of haplogroup R-M207 as measured in various geographically and ethnically defined populations from around the world. The value displayed at any geographical location indicates the percentage of individuals at that location who belong to this Haplogroup.

Y CHROMOSOME DNA TEST RESULTS (PATERNAL-LINE)

DYS385a	DYS385b	DYS388	DYS389I	DYS389II	DYS390	DYS391
11	14	10	13	32	25	10
DYS392	DYS393	DYS394/19a	DYS394/19b	DYS426	DYS437	DYS438
11	13	15	-	12	14	12
DYS439	DYS441	DYS442	DYS444	DYS445	DYS446	DYS447
10	14	18	14	12	12	25
DYS448	DYS449	DYS452	DYS454	DYS455	DYS456	DYS458
20	32	31	11	11	-	15
DYS459a	DYS459b	DYS460	DYS461	DYS462	DYS463	DYS464a
9	10	12	11	11	24	12
DYS464b	DYS464c	DYS464d	DYS464e	DYS464f	GATA H4.1	GGAAT1B07
14	14	17	-	-	13	9
YCAIIa	YCAIIb	YGATAA10	YGATAC4			
19	23	16	24			

Understanding your DNA test results

Your Y-STR haplotype Y-chromosome DNA (Y-DNA) is a type of DNA that is only carried by men and is inherited directly from their fathers. Men who share a common paternal ancestor will have virtually the same Y-DNA, even if that male ancestor lived many generations ago.

The Y-chromosome contains 59 million bits of information, each of which is encoded by a "base pair." Looking at all of these base pairs is impractical, so geneticists have identified a number of specific chromosome locations that can be used for analysis and comparison.

These unique locations are called "markers" and when they occur on the Y-chromosome, they are typically given names starting with "DYS".

At some Y-chromosome locations, there are small segments of base pairs that are repeated in the DNA. Markers with these types of repetitions are called "STR markers," where STR stands for "Short Tandem Repeat."

For instance, a particular genetic sequence at marker location DYS391 might be:

TGTCTG/TCTA/TCTA/TCTA/TCTA/TCTA/TCTA/TCTA/TCTA/TCTA/TCTG
CCT

Note there are ten repeats of the segment TCTA. The number of repeats is the "value" that is shown on your Y-DNA test report for the marker.

Your Y-DNA test report shows a series of markers and their corresponding values. These results are referred to as your "haplotype." For instance, the sequence:

12 15 13 12 29 22 10 11 12 16 11 15 is a 12-marker haplotype.

An analogy that might be useful in here is to think of telephone numbers. The same seven-digit telephone number, 428-1040, might appear in both Boston and Miami. However, adding more numbers ("area codes") allows us to distinguish between regions.

The same thing is true of DNA results. If we compare a limited number of DNA markers (for example, 12), then it's possible for two individuals to have the same marker values, yet not be closely related. Testing for more markers helps avoid this possible ambiguity by providing more accuracy. In general, the more markers tested, the easier it is to distinguish individuals and family tree branches. For this reason, GeneTree only offers tests that provide adequate coverage for most situations.

Haplogroup prediction Each haplogroup is defined by a specific mutation that occurs infrequently throughout history, and is thought to be a unique event when it happens. These type of mutations are often referred to as "Single Nucleotide Polymorphisms" (SNP markers). Everyone who carries a particular haplogroup-defining marker descends from a common paternal ancestor who typically lived many thousands of years ago. Due to historical and environmental forces that have shaped each haplogroup's distribution over time, haplogroups are often associated with certain geographically- or ethnically-defined populations.

We do not currently test for haplogroup-defining SNPs. Instead we predict your haplogroup membership from your Y-DNA haplotype. Our haplogroup predictor uses information from thousands of SNP tested haplotypes to estimate your haplogroup. Our predictor is continually refined and updated to provide the most accurate prediction possible.

Subgroup prediction Haplogroups diverge into more specific lineages which are also defined by particular Y-DNA mutations. For example, haplogroup R splits into haplogroups R1 and R2. You can find the location of your subhaplogroup (or subclade) on the Y-DNA tree by [clicking here](#).

Using your test results The combined information of your haplogroup, subgroup, and Y-haplotype enable you to understand your connections with early ancestors, more recent relatives, and others living today. Although each piece of information is useful by itself, together they link

you to others in a hierarchical way from the past to the present; with your haplogroup indicating your earliest ancestors, your subgroup showing intermediate connections, and your haplotype identifying your nearest relationships.

Your haplogroup designation reveals clues about your deepest paternal ancestors and how they participated in pre-historic population movements. Likewise your subhaplogroup membership provides additional resolution within your haplogroup by identifying sublineages.

People living today who are members your haplogroup also share a common paternal ancestor with you, one who lived in the ancient past. Similarly, those who share your subgroup are connected to you through a more recent common ancestor, but who probably still lived thousands of years ago.

Your closest connections are with those people who are members of your haplogroup and/or subgroup, and with whom you share a similar Y-STR haplotype. In general, the more matching markers that two people have, the closer their connection is.