Your Y DNA Results - Netscape

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Latest News

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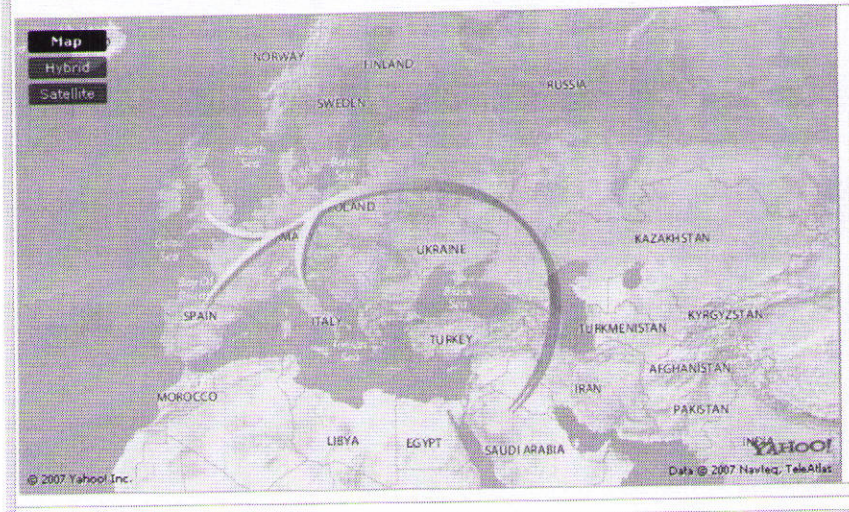
New Tab | Your Y DNA Results

DYS449	DYS452	DYS454	DYS455	DYS456	DYS458	DYS459a	DYS459b	DYS460	DYS461	DYS462
30	30	11	11	16	16	9	10	11	12	11

DYS463	DYS464a	DYS464b	DYS464c	DYS464d	DYS464e	DYS464f	GGAAT1B07	YCAIIa	YCAIIb	Y-GATA-A10
24	15	16	17	17	-	-	10	19	23	15

DYS635	Y-GATA-H4.1
23	21

PATERNAL ANCIENT ANCESTRY



R1b Paternal Ancient Ancestry Haplogroup R1b first arrived first arrived in Europe from West Asia during the Upper Paleolithic period (35,000-40,000 years ago) at the beginning of the Aurignacian culture. This culture is one of the first within Europe to leave cave art, and their stone tools were more refined than previous periods. The Périgordian culture is also thought by some to have existed at this time.
As the last ice age began, it became necessary to move down to below the tree line to hunt game. At its peak, the ice shelf within Europe extended down as far as southern Ireland, the middle of England and across northern Germany. Scandinavia was entirely covered. The sea ice pack extended as far as northern Spain, and tundra covered much of continental Europe. The tree line at the height of the ice age extended as far south as southern France, northern Italy, the northern Balkans and across the Black Sea.

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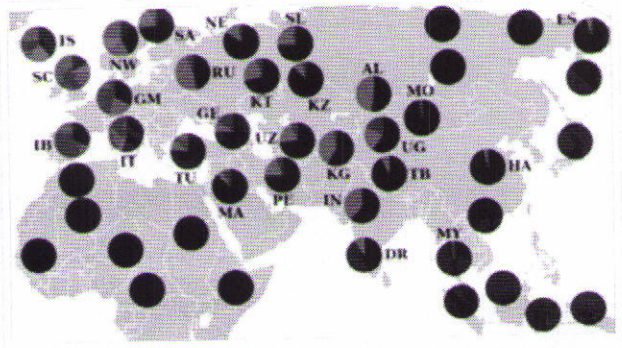
Haplogroup R1b (Y-DNA)

From Wikipedia, the free encyclopedia

In human genetics, **Haplogroup R1b** (**M343**) (previously called **Hg1** and **Eu18**) is the most frequent Y-chromosome haplogroup in Europe.

Its frequency is highest in Western Europe, especially in Atlantic Europe (and due to European emigration, in North America, South America, and Australia). In southern England, the frequency of R1b is about 70%, and in parts of north and western England, Spain, Portugal, France, Wales, and Ireland, the frequency of R1b is greater than 90%.



Distribution of R1a (purple) and **R1b** (red).

Bryan Sykes in his book *Blood of the Isles* gives the populations associated with R1b the name of Oisín for a clan patriarch, much as he did for mitochondrial haplogroups in his work *The Seven Daughters of Eve*. Stephen Oppenheimer also deals with this population group in his book Origins of the British.

Contents

Subclades

Haplogroup R1b is a descendant of Haplogroup R1 (M173). R1b is characterised by the presence of the M343 marker.

- R1b (M343)
  - R1b*
  - R1b1 (P25)
    - R1b1*

- R1b1a (M18)
- R1b1b (M73)
- R1b1c (M269, S3, S10, S13, S17)
  - R1b1c*
  - R1b1c1 (M37)
  - R1b1c2 (M65)
  - R1b1c3 (M126)
  - R1b1c4 (M153)
  - R1b1c5 (M160)
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    - R1b1c9b (S29)
  - R1b1c10 (S28)
- R1b1d (M335)

R1b1c

Most of the present-day European males with the M343 marker also have the P25 and M269 markers. These markers define the **R1b1c** subclade.

It is considered widespread in Europe throughout the Paleolithic already before the last Ice Age.[1] This culture is associated with the Cro-Magnon people, the first modern humans to enter Europe. The Cro-Magnons were the first documented human artists, making sophisticated cave paintings. Famous sites include Lascaux in France, Cueva de las Monedas in Spain and Valley of Foz Côa in Portugal (the largest open-air site in Europe).

European LGM refuges, 20 kya.

The glaciation of the ice age intensified, and the continent became increasingly uninhabitable. The genetic diversity narrowed through founder effects and population bottlenecks, as the population became limited to a few coastal refugia in Southern Europe. The present-day population of R1b in Western Europe are believed to be the descendants of a refugium in the Iberian peninsula (Portugal and Spain), where the R1b1c haplogroup may have achieved genetic homogeneity. As conditions eased with the Allerød Oscillation in about 12,000 BC, descendants of this group migrated and eventually recolonised all of Western Europe, leading to the dominant position of R1b in variant degrees from Iberia to Scandinavia, so evident in haplogroup maps (http://www.scs.uiuc.edu/~mcdonald/WorldHaplogroupsMaps.pdf) .

An alternative belief is that R1b represents the Western or centum-speaking branch of the Proto-Indo-Europeans, although this remains uncertain.

A second R1b1c population, reflected in a somewhat different distribution of haplotypes of the more

rapidly varying Y-STR markers, appear to have survived alongside other haplogroups in Eastern Europe. However, they do not have the same dominance that R1b has in Western Europe. Instead the most common haplogroup in Eastern Europe is haplogroup R1a1.

Note that haplogroup R1b and haplogroup R1a first existed at very different times. The mutations that characterize haplogroup R1b occurred ~30,000 years bp, whereas the mutations that characterize haplogroup R1a occurred ~10,000 years bp.

(Note that in earlier literature the M269 marker, rather than M343, was used to define the R1b haplogroup. Then, for a time (from 2003 to 2005) what is now R1b1c was designated R1b3. This shows how nomenclature can evolve as new markers are discovered and then investigated).

To date about 50% of R1b1c (M269+) men are negative for all of the known R1b1c subclades and are therefore classed as members of the paragroup R1b1c*. R1b1c* is not a subclade. Men of varying haplotypes and places of ancestral origin comprise its membership. Thus R1b1c* should not be considered as a single clade-like entity with any single geographic locus.

R1b1c4 (M153): This haplogroup has been found so far in 39 individuals, most of them Basques, the rest were likely of Iberian ancestry or have not been classified ethnically[2]. The first time it was located (Bosch 2001[3]) it was described as H102 and included 7 Basques and one Andalusian.

R1b1c6 (SRY2627 (M167)): The first author to test for this marker (long before modern haplogroup nomenclature existed) was Hurles in 1999[4]. He found it relatively common among Basques (13/117: 11%) and Catalans (7/32: 22%). Other occurences were found among other Spanish, Béarnais, other French, British and Germans.

In 2000, Rosser[5] also tested for that same marker, naming the haplogroup **Hg22**, and again it was found mainly among Basques (19%), in lower frequencies among French (5%), Bavarians (3%) Spanish (2%), Southern Portuguese (2%), and in single occurrences among Romanians, Slovenians, Dutch, Belgians and English.

In 2001, Bosch[6] described this marker as H103, in 5 Basques and 5 Catalans. Further regional studies[7] have located it in significative ammounts in Asturias, Cantabria and Galicia, as well as again among Basques. Cases in the Azores and Latin America have also been reported. A total of 85 individuals with this haplogroup have been found so far, almost all of them in academic studies, making it the best documented R1b1c subclade[8].

The subclade **R1b1c7** (M222), on the other hand, is associated with the Irish and Scots; in this case, the relatively high frequency of this specific subclade among the population of certain counties in northwestern Ireland may be due to positive social selection, as R1b1c7-M222 is believed to have been the Y-chromosome haplogroup of the kings of the Uí Néill clan of ancient Ireland.

The **R1b1c9** (S21) subclade, although recently discovered by EthnoAncestry, appears to be the most common downstream marker from R1b1c appearing in over 35% of those tested. This group has a maximum in Frisia (the Netherlands) and, in general, is the predominant R1b haplogroup. It may have originated towards the end of the last ice age, or perhaps more or less 7000 BC, possibly in the northern European mainland.[2] (http://www.geocities.com/mcewanjc/s21comment.htm) The exact technical

definition of the SNP was not initially released for commercial reasons, but the same marker was subsequently independently identified (as their "U106") by Sims et al (2007) [3] (http://www3.interscience.wiley.com/homepages/38515/pdf/940.pdf) .

The **R1b1c9a** subclade is defined by the L1/S26 SNP and is downsteam of S21. It occurs in less than a half a percent of R1b males, mainly with roots in the south and east of England and in Germany. **L1** was first discovered by Family Tree DNA, then confirmed and named **S26** by EthnoAncestry. L1/S26 is located in the flanking region of DYS439, and when it occurs, it inhibits the FTDNA primers from binding, thus producing an apparent null allele or "**null439**". FTDNA displays null alleles at DYS439 with a **Blue 12** on public pages, and with a **Blue asterisk** beside 439 on personal results pages. Other testing companies do report detecting null 439s. For further information, see the **null439 project** at [4] (http://www.familytreedna.com/public/null439) .

The **R1b1c9b** subclade is defined by S29 and is downsteam of S21. It was discovered by EthnoAncestry, and has to date been found primarily in southern England (although this may reflect a sampling bias). Recent findings show that it also occurs in Germany in the region previously inhabited by the Saxons. Further studies will serve to ascertain whether this is a native Briton marker, or Continental and having arrived in England with the Anglo - Saxons in the 5th Century.

R1b1c10 (S28) Although sample sizes are relatively small, it appears to reach a maximum in Alpine Germany and Switzerland.

Other subclades

Populations characterised as **R1b1a** (M18), **R1b1b** (M73), and **R1b1d** (M335), with those mutually exclusive distinctive markers but no M269 have been found, in Sardinia, Eurasia, and Anatolia respectively. It is presumed that these are descendants of R1b1 populations which found other refuges from the ice.

An apparent R1b1* population has been found among the Ouldeme of Northern Cameroon in west central Africa. [5] (http://hpgl.stanford.edu/publications/AJHG_2002_v70_p1197-1214.pdf) [6] (http://www.u.arizona.edu/~ewood/Wood_et_al_EJHG_2005.pdf)

Modal haplotypes

Within the R1b haplogroup are modal haplotypes. One of the best-characterized of these haplotypes is the Atlantic Modal Haplotype (AMH). This haplotype reaches the highest frequencies in the Iberian Peninsula and in the British Isles. In the Iberian Peninsula it reaches 33% in Portugal.

There also exists a haplotype of R1b with the DYS393=12 which is known in the literature as Haplotype 35, or ht35, as opposed to the AMH which is known as haplotype 15. They can be found in high numbers in Southeastern Europe and Western Asia. The members of this haplotype are thought to be descended from early R1b's who found shelter in Anatolia during the Last Glacial Maximum instead of in Iberia. They can be found in high numbers in the Armenian Highland and Armenia with smaller numbers throughout the Middle East, in Jewish populations, in Southeastern Europe, and in the Caucasus Mountains. There is also a sizable pocket of ht35 in Uyghur populations in western China, which is thought to be a remnant of the Tocharians, an Indo-European speaking people that inhabited the Tarim Basin in Central Asia until they were later absorbed by various Turkic peoples. Ht35 is also

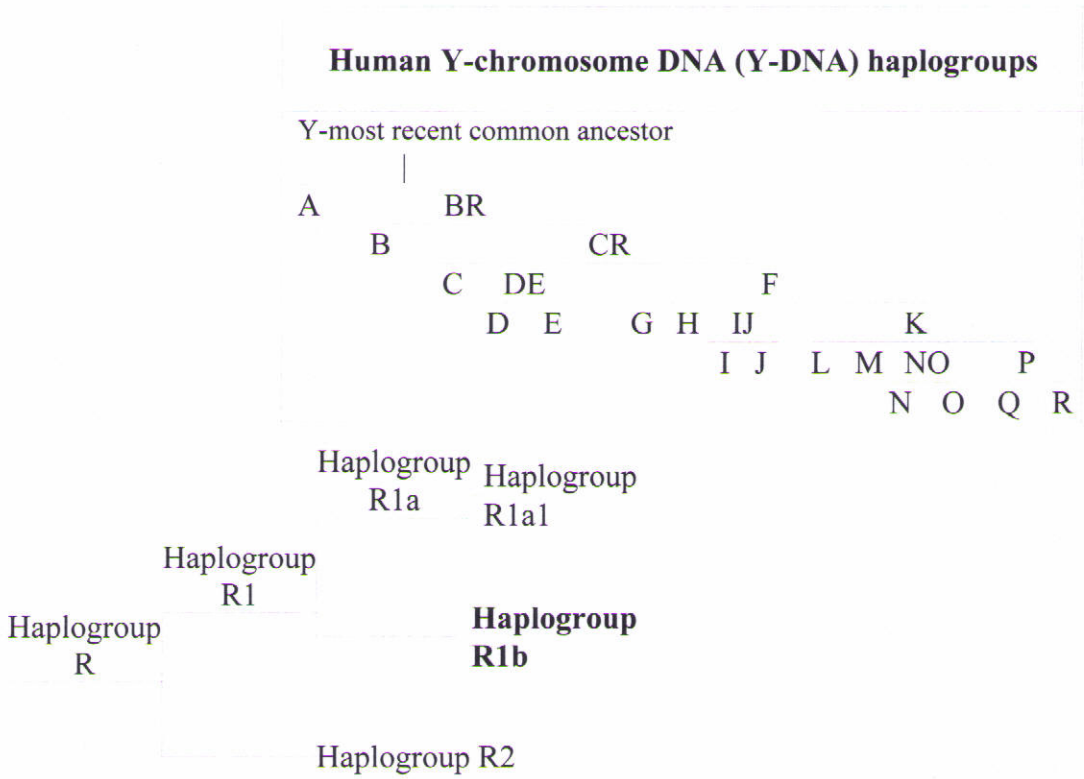
present in Britain in areas that were found to have a high concentration of Haplogroup J, suggesting they arrived together, perhaps through Roman soldiers. For further information and different subgroups of ht35, see [7] (http://freepages.genealogy.rootsweb.com/~gallgaedhil/haplo_r1b_ht35.htm) .

- R1b Modal Haplotype. Ysearch 55GU9 (http://www.ysearch.org/lastname_view.asp?uid=&letter=&lastname=R1b&viewuid=55GU9&p=(
- R1b Modal Ysearch C7BED (http://www.ysearch.org/lastname_view.asp?uid=&letter=&lastname=R1b&viewuid=55GU9&p=(
- R1b (NW Irish) Modal Ysearch M5UKQ (http://www.ysearch.org/lastname_view.asp?uid=&letter=&lastname=modal&viewuid=M5UKQ&
- Comparison (http://www.ysearch.org/research_comparative.asp?uid=&vallist=+55GU9%2C+C7BED%2C+M5

Niall of the Nine Hostages

In 2006, a subgroup of R1b common among people of Irish patrilineal descent was identified as the probable haplotype of many within the septs associated with Niall of the Nine Hostages, an Irish king in the Dark Ages. SNP testing has shown that the cluster of haplotypes purported to be associated with the patrilineal descendants of the Uí Néill clan displays the M222 mutation that defines Haplogroup R1b1c7.

Relationship to other haplogroups



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Paternal Lineage Test

Paternal Lineage and the Y-Chromosome

A male providing his Y-chromosome sample also represents the DNA of his father, paternal grandfather, and so on up the paternal line. Y-chromosome results are generally identical throughout the paternal line. But because mutations do occur, it is possible for a son's results to be slightly different from his father's or his brother's.

Women, in spite of not carrying a Y-chromosome, can still trace their paternal lineage. Using a DNA sample provided by a brother, father, or another paternal relative (for example, a male cousin) a woman can treat these Y results as if they were her own.

Y-chromosome test

The Y-DNA test looks at specific regions of the Y-chromosome. These regions are known to contain a series of repeating sequences of DNA molecules (for more information see short tandem repeat). All men have these repeating segments; what differs between men is the number of times the specific sequence repeats. Counting these repeats is what constitutes the results of the Y-DNA test. DNA Ancestry offers two Y-chromosome tests: Y-DNA 33 or Y-DNA 46 markers (or locations on the Y-chromosome). Testing more markers allows for a more accurate estimate of the relationship between two individuals.

Common Ancestor

Similar to traditional genealogy, finding a common ancestor across pedigrees is the payoff that leads to expanding family trees. DNA testing provides an objective and accurate way to determine a) to what degree you are related and b) approximately how far in the past you may have shared a common ancestor.

The more Y-chromosome markers tested, the greater the precision of the test. For example, an 18 marker Y-chromosome test that matches another participant's test on all 18 markers, allows a common ancestor to be predicted within a range of 1 to 27 generations. Two participants matching on all 46 markers, on the other hand, can narrow their common ancestor to exist within 1 to 10 generations! For most, a Y-DNA test comparison with up to 2 or 3 mismatches will indicate that there is a genealogically relevant relation in past generations.

Paternal Ancient Ancestry

The Y-chromosome test also provides a look into your ancient paternal ancestry through a prediction of your ancient haplogroup, or deep ancestral grouping haplogroups were formed when ancient peoples migrated and branched out from Africa tens of thousands of years ago. As they spread throughout the world and adapted to their new environments, their DNA diversified, creating new groups and subgroups.

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About Paternal Lineage Test Results

Your Paternal Lineage test result consists of two components: Y-DNA results and a paternal ancient ancestry prediction.

Y-DNA Results

Your Y-chromosome results will consist of a table of markers tested (numbering from 1 to 33 or from 1 to 46) and a corresponding value for each. Each marker is a specific location on the Y-chromosome and is referred to by its DNA Y-chromosome Segment number (DYS number).

The portions of the Y-chromosome tested are known to produce repeating patterns of nucleotides (the building blocks of DNA.) These Short Tandem Repeats (STRs) are counted at each marker and reported as your DNA result. The profile of repeats is inherited from your father and is what differentiates your specific paternal lineage from another's.

The extent to which your Y-DNA results match other participants will determine how closely related you might be by providing an estimate of how far in the past you shared a common ancestor.

Each of the names of the Y-chromosome locations available for testing are presented in the table. A dash, "-", shown in specific boxes in the table means that results were not produced for that particular location because of two possible factors. First, for markers DYS19b, DYS464e and DYS464f, a lack of result may be due to the fact that these allele results are very rare. Second, the dash may signify the presence of a marker value that cannot be obtained using the current testing methodology.

Paternal Ancient Ancestry

Your Paternal Ancient Ancestry (or Haplogroup) is predicted based on your Y-DNA results. You will receive the name of the haplogroup, a detailed description of the group, and a map showing how your ancient ancestors migrated out of Africa over 100,000 years ago and split off to populate the different regions of the world.

Because particular patterns are seen within particular haplogroups, on most occasions we can predict which haplogroup you are in. Along with the prediction, we also provide the history, background and mapped distribution of your haplogroup.

Please be aware that, while our comparative database uses up-to-date information, it may not be possible to make an accurate prediction on all occasions and sometimes no prediction can be made.

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What do I do after I receive my Test Results?

Now that you have your results the next thing to do is to compare your results with other participants in the DNA Ancestry database. Click on the DNA Matches tab to see how closely other participants match your results.

Matching Map

The Map shows the approximate current location throughout the world of the most closely matching participants. Clicking on a figure in the map will display the name (if not anonymous), location, and an estimate of Most Recent Common Ancestor (MRCA). The list of participant names is sorted by MRCA, with those most closely related to you at the top of the list.

You can directly compare your DNA results with other closely matching participants by clicking the checkbox by their names and pressing the "Compare" button.

Comparison Table

The table displays your selected participants' results in relation to how similar or different they are from your results. When your markers and repeat values match, you will see a checkmark. Where your markers differ, you will see the value highlighted. The greater the number of differences, the more distantly related you are.

Common Ancestor

If you have found a closely matching participant, you can further analyze how related you might be by clicking on the Participant's name. The Most Recent Common Ancestor (MRCA) calculation is based on the number of markers tested and the number of matching values. The MRCA reports the range of generations in which you and another participant may have shared a common ancestor. The closer you match, the more narrow the range of generations will be.

Comparing Pedigrees

Armed with a range of generations in which you might share a common ancestor, you can now begin communicating with your genetic cousins using Ancestry.com Connection Service as the first step towards comparing the genealogies of your two families. If you're fortunate, the common ancestor analysis will narrow your search to a timeframe and you will find the ancestor that joins your two family trees.

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Statistics for Calculating Most Recent Common Ancestor

MRCA is a term that is used often in discussions of genetic genealogy. MRCA stands for Most Recent Common Ancestor and it refers to a statistical calculation that determines the likely generation in which two individuals share a common ancestor. The MRCA is often reported with a 95% Confidence Interval. The MRCA number itself is the generation in which it is 50% likely that two individuals are related. The 95% Confidence Interval then gives you a range of generation values that encompass 95% of all possibilities. For example, there is a 95% likelihood that two individuals sharing 25 of 26 alleles will have an MRCA within 11.9 generations expanding between 1.7 and 39.5 generations.

Statistics Used in Genetic Genealogy

The MRCA calculation relies heavily on the mutation rate of the loci. Previously, the Y-chromosome mutation rates that have been used for genealogical purposes have ranged from 0.002-0.004, depending upon the testing laboratory. This value is known as the mutation constant and may be represented by the term μ (pronounced my). This value is the rate at which a change (mutation) is identified at a particular locus from a father to a son. Each marker tested on the Y-chromosome has its own mutation rate, these mutation rates are known for many of the Y-chromosome loci across several human populations (publication is in press). The mutation rate can be affected by several different factors such as population, haplogroup within a population, length of the allele, region on the Y-chromosome, and size of the repeat structure. For those loci where the mutation rate has not yet been determined, DNA Ancestry has chosen to use a rate of .0028. As more data on Y-chromosome mutation rates becomes available, we will re-evaluate our statistical calculation to reflect a more precise measurement for each locus.