

# Y-Chromosome Marker S28 / U152

## Haplogroup R-U152

### Resource Page

**David K. Faux**

To use this page as a resource tool, click on the blue highlighted words, which will take the reader to a relevant link.

**How was this marker discovered?** In 2005 Hinds et al. published a [paper](#) outlining the discovery of almost 1.6 million SNPs in 71 Americans by [Perlegen.com](#), and which were deposited in the online [dbSNP database](#). Gareth Henson noticed three SNPs that appeared to be associated with M269, what was then known as haplogroup R1b1c. Dr. James F. Wilson of [EthnoAncestry](#) developed primers for these Single Nucleotide Polymorphism (SNP) markers on the Y-chromosome, one of which was given the name of S28 (part of the S-series of SNPs developed by Dr. Wilson).

**Who were the first to be identified with this SNP?** In testing the DNA of a number of R-M269 males (customers or officers of EthnoAncestry), two were found to be positive for S28 (U152). These were [Charles Kerchner](#) (of German descent) and [David K. Faux](#), co-founder of EthnoAncestry (of English descent).

**How is this marker classified?** In 2006 the International Society of Genetic Genealogists (ISOGG) developed a [phylogenetic tree](#) since the academic grouping (the Y Chromosome Consortium – [YCC](#)) set up to do this task had lapsed in 2002. They determined, with the assistance of Dr. Wilson, that the proper placement would be R1b1c10, in other words downstream of M269 the defining marker for R1b1c. Karafet et al. (2008) (including Dr. Michael Hammer of the original YCC group) published a new [phylogenetic tree](#) in the journal *Genome Research*. The designation for S28 / U152 became R1b1b2h\*. Recently a group of genetic genealogists, using findings from the 23andME testing, discovered a SNP between M269 and S28 / U152, called S116 by EthnoAncestry, and P312 by the Hammer group (YCC), which caused ISOGG to revise their [phylogenetic tree](#). The most up to date classification for the YCC is Karafet et al. (2008) [Errata](#). Presently [Family Tree DNA](#) has termed U152+ as R1b1b2a1b4, if L2/S139+ add a “c” and if also L20/S144+ add a “1”. [ISOGG](#) (2009) has the category as R1b1b2a1a2d, and with L2/S139+ add a “3” and if L20/S144+ add an “a”. Perhaps the most sensible or parsimonious designation is R-U152 for most purposes.

**What is the general nature of the S28 / U152 mutation?** S28 is a neutral transition mutation (it does not adversely affect the functioning of any known gene) where an ancestral Guanine was replaced by the derived Adenine at a single location on the Y-

chromosome. The event presumably happened only once in the history of mankind. Thus some thousands of years ago a spot mutation occurred during meiosis in an R-P312\* father. The mutation was passed to his son who in turn passed it on to every one of his descendants in the direct male line. Thus all R-U152 males have the same ancestor in the Y-line, although the age of the mutation (when S28 / U152 first appeared) has not been determined.

**How old is the mutation?** There is no molecular clock which will provide an absolute dating such as dendochronology (tree ring dating). The date depends on a host of assumptions such as generation age, whether to consider back mutations, accepting a mutation rate and so on. Robert McGregor used the Zhivotovsky et al. (2006) approach and obtained a date for the Most Recent Common Ancestor of 11,400 years (plus or minus 1000 years) of all those in the author's database. Vince Vizachero has estimated the age of S28 as 6600 years (Neolithic), and Dr. Ken Nordtvedt has obtained a date of about 3700 years (Bronze Age). While due consideration must be given these estimates, it is highly likely that what is being detected is an expansion of this haplogroup, whereas its origin lies in the Mesolithic, about 10,000 years ago. Thus the present author is inclined to accept the McGregor estimate since it accords best with all other data sources. Ultimately only ancient DNA samples are going to settle the matter to everyone's satisfaction.

**What are some of the technical aspects of the S28 / U152 SNP?** The essential facts can best be expressed in chart form:

Marker	Rs #	Forward PCR primer (5'-3')	Reverse PCR primer (5'-3')	Product Size (bp)	SNP position (bp)
U152	rs1236440: G>A	cttagctatacagcctcttttgg	aacattccacgcttgaggataa	172	127

What does the G to A mutation of a male who is S28 / U152+ look like along the sequence of base pairs in the vicinity of the marker? This can best be viewed by a [pherogram](#) / chromatogram printout from the program Sequencher to see the difference between an ancestral and derived Y-chromosome at this location.

**Where on the Y-chromosome is the S28 / U152 mutation?** This marker can be viewed via the [Y-chromosome browser](#) created by Thomas Krahn.

**Is there any way to relate S28 / U152 to the broad east – west classification system for R-M269?** There appears to be an important division between the most common forms of R-M269 from Bulgaria eastward versus westward. An “old – fashioned” marker that is seldom used in studies today is the p49a,f Taq haplotype system. [Cinnioglu et al. \(2004\)](#) used this in describing their samples from locations such as Turkey and Armenia and those from Iberia and other locations in western Europe. The division is dramatic, Haplotype 35 is characteristic of most R-M269 east of the Balkans, whereas Haplotype 15 is most common in western Europe. Unfortunately no company at present will do commercial testing for this marker, but Vincent Vizachero has found a set of markers that can act as surrogates. The evidence is very clear, if someone has DYS393=12, DYS461=11, and DYF385=9,10 or 10,10 then it would appear that they are of the

“Eastern” Haplotype 35 variety. Similarly the motif characteristic of Haplotype 15 or “Western” variety is DYS393=13, DYS461=12, and DYF385=10,11. All R-U152 that have been tested for these markers fit into the latter pattern and hence are of the “Western” variety of R-M269 which according to Cinnioglu et al. (2004) likely expanded out of the Franco-Cantabrian refugium after the Last Glacial Maximum (whereas the “Eastern” type likely expanded from the West Asian area at this time).

**[How does the new SNP found via deCODEme testing, known as S116 / P312, relate to S28 / U152?](#)** Recent testing by [Thomas Krahn](#) at FTDNA has revealed that that R-U152, R-M153, R-M167, R-M222 and some R-M269\* test positive for S116 / P312, meaning they have the derived A allele; whereas those who are R-U106 plus all Eastern R-M269\* should have the ancestral C allele on this marker. This will perhaps link in a broad sweeping way those whose ancestors belonged to a Celtic culture (Insular or Continental) who will all share the S116 / P312+ polymorphism, dividing them from the S21 / R-U106 “Germanic” group as well as the large group of R-M269\* “Eastern” found from Bulgaria to Kazakhstan and Anatolia.

**[Why is S28 also known by another name – U152?](#)** In 2007 Sims et al. published a [paper](#) in *Human Mutation* which identified the markers developed by Dr. Wilson, but using new names. Hence S28 is comparable to U152 in their paper.

**[Which companies test S28 / U152?](#)** From April of 2005 until February 2008 only EthnoAncestry offered this SNP. Presently [Family Tree DNA](#) tests the markers developed by Dr. Wilson, which they call the “U-series” or the “Garvey Panel”, which includes what they termed U152 (using the Sims et al. 2007 classification). This testing is only available to those who have tested at least 12 Y-STR markers (the standard Y-chromosome test in genetic genealogy) with FTDNA. Presently [deCODEme](#) and [23andME](#) also test this marker and the latter also tests for L2/S139 and L20/S144 (see later).

**[What do the certificates look like?](#)** Click for examples of [EthnoAncestry’s](#) and [FTDNA’s](#) certificates attesting to a positive finding for S28 and U152 respectively.

**[What databases are available for S28 / U152?](#)** Soon after S28 was identified [David K. Faux](#) began collecting haplotypes and genealogical information (particularly the place of birth of the earliest known ancestor in the Y-line). He also included research testing of his Shetland Islands samples, as well as some as yet unpublished data from academic research. Data is screened to ensure that, particularly in the case of those who are of Colonial American ancestry in the Y-line, that they have a solid paper trail lineage back to a European country. The data includes those tested at EthnoAncestry and FTDNA (and any other company who will offer this testing). In March 2008 it was announced that [Charles Kerchner](#) would be administering a FTDNA sponsored R-U152 project. It is only open to those who have SNP tested U152+ at FTDNA. Recently Tibor Fejer assumed the role of co-administrator and succeeded in clustering all of the meaningful groups within U152 together (e.g., a separate category for those who are R-U152\* with DYS492=12 and another for those who have 14 repeats at his marker). [Adriano Squecco](#) is collecting

all of the raw data from individuals who test with deCODEme and 23andME (Versions 1 and 2) and has presented in a spreadsheet database. In addition, [Ysearch](#) includes those who are identified as S28 or U152 and chose to include their data in this database. At present the database appears to be in the process of shifting from the R1b1b2h to the current FTDNA designation, but much data seems to have vanished in the process (hopefully this will be corrected shortly). Another database is that of [John McEwan](#) who for many months collected data from those who tested positive on one of the subclade tests in relation to R-M269. There is a lot of other material here that would be of interest to those who are U152+. Unfortunately the database has not been updated since July 2007.

***[Is there a website devoted to S28 / U152?](#)*** [Jacques Beaugrand](#) has established a website for this haplogroup, which includes links to many items of interest to those who fall into the R-U152 haplogroup. More recently [Richard Rocca](#) has set up a website devoted to the study of this haplogroup.

***[Can the relationship between individuals who are identified as U152 positive be seen in a graphic form?](#)*** [Dale Bricker](#) has constructed a network diagram to graphically portray the relationships between U152+ individuals. What is interesting is that the closest neighbors of someone from say England may be Italy or Switzerland. However a definite clustering is seen for those in the DYS492=14 category (likely L2 ancestral, described later), which appears to include 1B07=8 also. The larger grouping with DYS492=12 (likely L2 derived) is clustered into 6 groupings with the important markers noted above, as well as DYS456 which appears to have structure in these classifications. [Beau Gunderson](#) has created a pdf contour map (preliminary, first draft) which clearly shows the apparent point of origin of R-U152 (shown as R1b), but which at this time shows the biases in the data with more from Britain and Ireland as well as southern Italy, and less from locations such as France, Spain, and Eastern Europe,

[Gary Felix](#) has established a set of slow moving Y-STR markers and has a table showing how far each haplotype diverges from the modal.

***[Is there a map showing the geographical distribution pattern of S28 / U152?](#)*** [Jacques Beaugrand](#) has drawn a number of maps to illustrate where S28+ are found, which allows viewers to see patterns and overlap with historical and archaeological cultures. [Vince Vizachero](#) has placed pins on a Google map of Italy showing the location of each of the R-M269 SNP tested individuals in the Italy Geographic Project. With the assistance of John Laws and Robert Tarin the author has learned to use Google Maps to depict aspects of the distribution of R-U152 across Eurasia. This resulted in the following maps:

- 1) [Google Map](#) (Part 1) showing all who know their specific village of earliest origin in Continental Europe.
- 2) Since only 200 data points (balloons) can be placed on one page with the Google format, it was necessary to break the map in 1) into a Part 2 which includes the newer entries. [Click here](#) for Part 2. It is best to view the two together by opening both simultaneously.

- 3) For the reasons noted above, it has been necessary to construct a separate [Google Map](#) to show “Insular R-U152” (British Isles) since the original map has become so large that Google split it into two pages (all new entries going to page 2). This is less than acceptable so the division of Eurasia makes more sense. The British Isles are highly over represented in all Y-DNA databases, thus what appears to be a large number of R-U152 there is an illusion – it is a relatively rare haplogroup in that region.
- 4) A third (forth) [Google Map](#) shows the distribution of those who are L20+.
- 5) The next set of maps can be used as overlays by simultaneously opening one or more of the above and any of the following:
  - a) A [Google Map](#) which shows the boundaries of the Continental Celtic world as depicted in Koch (2007). This haplogroup downstream of R-U152 is found in Central France, the Italian Lake District, Switzerland, Southern Germany, and Belgium. It is found in the British Isles but only in England to date, and only along the eastern coastal margins from Lincolnshire to Kent. A more sophisticated map in KML format can be seen [here](#).
  - b) A [Google Map](#) illustrating the regions where tribes from the Continent are known to have settled circa 100 AD, there being little evidence of any post – Neolithic migration of any significance before this date.
  - c) A [Google Map](#) showing the extent of the Angle Kingdoms and presumably early Angle settlement from Jutland; as well as the region where the Jutes also from that area are known to have migrated.
  - d) A [Google Map](#) illustrating the boundaries of Denmark in Viking times circa 800 AD.
  - e) A [Google Map](#) portraying the extent of the Viking settlements in Britain and Ireland based on historical, archaeological, and linguistic (place name) evidence.
  - f) A [Google Map](#) showing the results of the published and unpublished academic studies which include U152. The two most comprehensive articles are Cruciani et al. and Myres et al. 2010.

A more recent addition to the mapping of U152 is that of Richard Rocca seen on the home page of his U152 website by [clicking here](#).

The reader will then be able to come to their own conclusions in relation to whether the distribution of R-U152 follows closely the known Celtic world; and which source or sources are responsible for the presence of R-U152 in the British Isles.

**How common is S28 / U152?** The percentage of R-U152 in Europe or the regions to which Europeans expanded (e.g., USA) is not clear at present. What seems apparent from the database noted above is that there are “hotspots” and so that for example in Switzerland S28 / U152 is going to be relatively common if not the predominant haplogroup. However, despite heavy sampling, to date no one with an aboriginal surname from Ireland (or the western regions of Scotland) has been assigned to the R-U152

category. Hence, its frequency will vary dramatically from country to country. In the McEwan study above (October 2006) he observed that at that time, of the 47 people from Ireland tested (R-M269 being higher in Ireland than anywhere else in Europe), none were R-U152; but 5% of the 21 from Scotland, 12% of 30 individuals from England, and 37% of 12 people from the Continent did test R-U152.

*Are there any published studies using S28 / U152?* In the Simms et al. (2007) study above using a European American sample from the USA (largely from the states of Virginia and South Dakota), 46% were some variety of R-M269, however only 3% were R-U152 (or 7% of the R-M269 population). The most recent study is that of [Niederstatter et al. \(2008\)](#) which examined the percentages of U106 and U152 in the M269 samples from Innsbruck, Austria. In that region the overall numbers of R-M269 were relatively low at 31% (N=42) of the sample of 135 males. About 62% of the M269 were S21 / U106, 21% were S28 / U152, and 19% were “unresolved” R-M269 (neither of the former two). Hence the fraction of both haplogroups was considerably higher in the Austrian (Central European) sample than the European American (probably Western European origin) sample of Simms et al. (2007). A study was published by Ramos-Luis et al., 2009 which focused on the haplogroup structure of France, but only noted one fact of interest, that the haplogroup predominates in Alsace. Fortunately Richard Rocca wrote to the primary author and was able to obtain the precise values of U152 for each region. This data can be seen on his website by [clicking here](#). The breakdown as sent to me by Richard is as follows:

Alsace: 22.5%

Nord-Pas-de-Calais: 17.65%

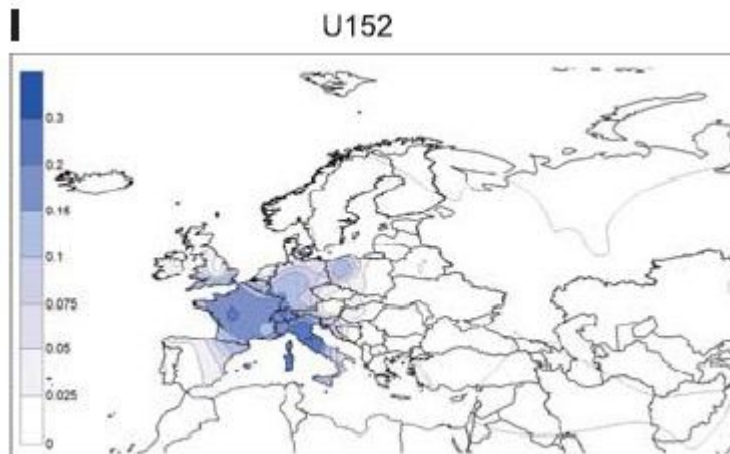
Auvergne: 16.85%

Ile-de-France: 14.29%

Midi-Pyrenees: 13.43%

Provence-Alpes-Cote d'Azur: 11.11%

Two academic studies, which included U152, were published literally back to back in [August 2010](#). [The Myres et al.](#) study has the most comprehensive coverage of Eurasia. [Dienekes](#) has provided a very excellent summary in relation to the findings pertaining to U152 and so will be quoted in full:



”Of interest is the fact that while **R-U152** has a clear French-Italian center of weight, the locations exhibiting highest STR variance are Germany and Slovakia, i.e., Central Europe. My guess is that R-U152 originated in Central Europe spreading to the west and south, perhaps with Italo-Celtic speakers or some subset thereof. In its home territory of Central Europe, its frequency decreased by the introduction of the Germanic and Slavic speaking elements which dominate the region.

Irrespective of what the ultimate origin of R-U152 is, it provides us with a good diagnostic marker for population movements out of the French-Italian area. In Italy for example it is noted at 26.6% for the north and 10.5% in the south. It would be extremely interesting to see its occurrence in Balkan Vlachs, as this would confirm/disprove the Italian component in their origin. However, **R-U152 occurs in 7.3% of Cretans**, suggesting introgression Y-chromosomes of North Italian (Venetian) origin, from the 4-century period of Venetian rule of the island. It also occurs in 4.1% of Greeks, where it might come from any period since the Roman annexation of the Hellenistic states to the Vlachs. However, its presence at only **1.8% of Romanians** makes a large Italian contribution to the Romanian population unlikely. Balkan R-U152 chromosomes should be better resolved to determine when they arrived from the northwest.

The paucity of **R-U152 in Turks** (0.6%) make tales of wandering Galatians less likely to be true. There is no doubt that Galatians settled in Anatolia, but they were probably so few in numbers that they did not permanently alter the population. Knowledgeable readers should chime in about the [Lebanese Christian R1b](#) which was posited as a signature of the Crusades a couple of years ago, and its position in the phylogeny.”

The [supplemental materials](#) are very important, and contain all the raw data for each population, found in Table 4.

[The Cruciani et al. paper](#) also includes only a generic U152, without L2, L4, or L20. While the list of regions is less in number and less specific, the data confirms the general

positioning of the distribution of the haplogroup, illustrating the Swiss “hotspot”, and reflecting that in general, U152 is a reverse mirror image of U106 (which is clearly almost exclusively “Germanic” and from Northern Europe). The peak concentrations of U152 were found in Northern Italy / France.

The above two studies have been summarized quantitatively in a series of three Excel sheets by Tibor Feher. [Click here](#) to access this database. What follows is a summary chart:

Regional rank of frequency (U152+ in all men)				
Italy North+Central+Corsica	482	23.1%		111
Switzerland	175	18.3%		32
France	503	16.7%		84
Germany	398	10.6%		42
Italy South + Sardinia	647	10.2%		66
Bashkirs	586	9.0%		53
England	102	8.8%		9
Greece	410	5.1%		21
Central Europe/Austria-Hungary	913	4.5%		41
Poland	242	4.1%		10
Netherlands	87	3.4%		3
Iberia	840	2.9%		24
Denmark + South Sweden	284	2.1%		6
Ireland	99	2.0%		2
Ukraine	504	1.0%		5
Balkans	1254	1.0%		12
Levant	376	0.5%		2
Turkey	644	0.5%		3
Finno-Permians + Tatars	903	0.2%		2
Russian + Belarussian	1359	0.2%		3
Caucasus	1365	0.0%		0
North Africa	528	0.0%		0

The most recent study to include S28/U152 is that of [Busby et al., 2011](#). It has a larger dataset which includes the above Myres data. There is a vast storehouse of information in this study (note the supplementary material), however once again S28/U152 is not broken down into sub-categories.

**[Are there any subgroupings of S28 / U152?](#)** In the most recent revision of the Chromosome Consortium, R-U152 is being placed as R1b1b2a2g on the new [phylogenetic tree](#). What follows is a listing of all known SNPs downstream of U152.

1) Apparent Private or “Family” SNPs:

- a) Two subclades have been identified in the new tree, which were thought at one time to be phylogenetically equivalent to U152 (in other words



sister clades to R-U152). These are M126-R1b1b2h1, and M160-R1b1b2h2. There have been a number of academic studies using these latter two markers, and they have been tested extensively in the commercial sphere but have not been observed beyond the original study in which they were published. Underhill et al. (2000) tested a sample of 60 “Europeans” and found 1 who was M126+, and 3 who were M160+. In closely examining the data, it appears that all of these individuals were Italians. It would, however, appear that these two markers may in fact be “private SNPs” and unlikely to be seen again except in the same area or with the same families tested in the original study.

- b) An individual from the Shetland Islands was found to have “private” or “family” SNP which EthnoAncestry termed S44. It is unknown at this time how widespread this mutation is since it has been tested in very few individuals.
- c) It was reported that the individual whose ancestors were Ashkenazi from Latvia also has a private SNP as determined by Thomas Krahn at FTDNA who has labeled this SNP L4 and is associated with DYS492=14. The SNP has been found in four or more Ashkenazi males with different surnames and whose ancestors come from different Eastern European countries. All have the distinctive DYS385a,b=14,14 motif.
- d) Thomas Krahn at FTDNA also identified another SNP in the flanking regions of the amplicon (primer of circa 200 base pairs) used to detect the U152 SNP. This individual is from Lincolnshire, England. Considering the number of people tested for U152 at this point, it would appear that L3 may be a private SNP.
- e) In the process of testing four men with the deCODEme test, one, of Northern Italian ancestry (U152+, L2+, L20+) is M228+. This SNP has been reported in African Pygmies with haplogroup B, so this is some sort of parallel mutational event. It is probably private but only further testing can ascertain the frequency.
- f) Sims and Ballantyne (2008), while studying the Y-SNP M222, observed that one individual who was U152+ had a SNP situated close to the M222 marker. Sixteen other individuals who were U152+ were tested for this SNP, but were ancestral. Hence although the authors have placed the SNP in the phylogenetic category of R-U152, this may be premature since only 6.3% of their sample of R-U152 have this SNP – one person of a total of 16 – which suggests that the SNP may be in the “private” or “family” category.
- g) SNPs such as the above continue to be identified.

## 2) Possible SNPs of Wider Phylogenetic Significance:

The first category of U152 males are those who test negative for all non private downstream SNPs and so are R-U152\*. This group can be parsed into two groups by the STR marker DYS492. As a rule, those who are ancestral U152 will either have 12 or 14 repeats.

Of the three newly discovered SNPs being offered by FTDNA for those who are U152+, one is **L2 / S139 or rs#2566671** which was discovered via 23ANDme testing of a U152 individual. The first person to be identified as being L2 / S139+ (via 23andME testing) was Luc VanBraekel (of Belgian descent). Family Tree DNA then began testing this marker and a group of us (including DKF) were in the next “batch” to learn that they were positive on this marker.

Thanks to 23andMe testing another SNP within (downstream of) L2 / S139 has been found. It is **L20 / S144 or rs#7063305**. David K. Faux was the first to be designated as having a mutation at this location and Giuseppe Belgieri (of Italian Alpine descent) was the second – both via 23andME testing (and ironically they have the lowest genetic distance of those tested). A study is presently being conducted by Steve Gilbert and David Faux, with the present geographical distribution of the members of this haplogroup being plotted on a map, and then attempting to relate the findings to early historical migrations. To date the best interpretation appears to be that the description of the Roman author Livy fits the data. In other words about 600 AD the precincts of the Celtic Bituriges Cubi were overcrowded and the King Ambigatus sent his sister’s sons Segovesus and Belovesus to lead the excess population eastward, the former toward the Hercynian Forest in Germany and the latter into Italy.

EA is offering both of these markers via their “Custom Select” (S139 and S144); and FTDNA are now offering both within their “Advanced Menu”.

A [chart](#) showing the relationship of all of the known SNPs below M269 has been created by Thomas Krahn. It illustrates how L2 and L20 as well as the private SNPs fit within the phylogenetic categorization. These can be visualized via the website of Richard Rocca by [clicking here](#).

Dale Bricker has made a [prediction](#), largely hinging on whether the value of DYS456 is 15 (L20 / S144 positive) or 16,17 (L20 / S144 negative); and in relation of the marker 1BOF7 (8 repeats for U152\* and 10 repeats for L2+). It will be a while before we are able to assess the validity of this interesting hypothesis, largely due to few having ordered 1BOF7.

The following statistics (expressed in percentages) pertaining to the percentages of each of these groups comes from the FTDNA R-U152 database of Charles Kerchner and Tibor Feher with N = 169:

**U152\* with DYS492 = 12:** 25%

**U152\* with DYS492 = 14:** 10%

**L2\*:** 46%

**L20:** 17%

L4: 2%

When the results of more individuals who are R-U152 are available via the deCODEme and 23ANDme testing, it is possible that further subgroups will become apparent when individuals are compared on SNPs which fall within the broad R-M269 category.

There is at present almost no difference in the modal scores of 67 marker Y-STR (short tandem repeat – the typical markers used in genetic genealogy) haplotypes between R-M269\* (“Western Variety”), R-P312\*, and the non-Frisian grouping of R-U106. However, it appears that within R-U152 there is a bimodal distribution for one marker, DYS492 with 12 predominating (and being the ancestral variety in most other R-M269 clades), but with about 10% having a score of 14 on this allele, but one third among those with ancestry in Germany. It is anticipated that at some point the 12 / 14 split will show a more specific meaningful geographic distribution, but at present nothing can be offered beyond limited speculation.

***Has anything been written about what the data appears to tell in the way of geographic distribution patterns or a connection with any cultural groups?*** In 2007 David K. Faux first wrote a two part manuscript (continually updated) purporting to tell the “[story of U152 as a La Tene marker](#)”. This study compares the archaeological, historical, and linguistic data with the genetic Y-chromosome data. There is a remarkable overlap between the regions known to have been aboriginal to the Hallstatt and La Tene Central European Celts, or areas where there is documented expansion (largely in the early 6<sup>th</sup> and 4<sup>th</sup> Centuries BC) which took peoples from the Alpine regions such as Switzerland and Austria (plus eastern Gaul, Southern Germany) as far west as Central Spain (possibly circa 7<sup>th</sup> Century), and north to and outpost in Jutland and nearby areas in Norway and Sweden, scattered as far east as Anatolia and Western Ukraine (by the 3<sup>rd</sup> Century BC), and Britain (between the 3<sup>rd</sup> and 1<sup>st</sup> Centuries BC). A recent finding of R-U152,L2+ in a Kipchak tribesman from Kazakhstan may relate to the incursions of this group into Ukraine and Hungary in the Middle Ages and eastward migration when the empire collapsed. [A recent publication](#) by Martin Ballauf is even more extensive, being 417 pages in length, in German (supplemented with many maps and charts), focusing on the link between the Alpine cultures and S28 / U152. Three studies by David K. Faux relate specifically to Britain. The first explores the possible connection between the [Cimbri tribes of Denmark, the Danelaw, and R-U152](#). A second focuses on the [Angle tribe of Schleswig, the Angle Kingdoms of England, and R-U152](#). Another referring specifically to the possibility of a connection between the [Belgae tribes of the Continent, the southern part of England, and R-U152](#). These could for example be the Belgae who settled in England before the time of Caesar, the Normans, or the Flemings.

**UPDATE:**

As of 2011 the author has turned over responsibility for updating information on U152 to trusted colleagues Tibor Feher (Administrator of FTDNA's U152 Project), Steve Gilbert and Richard Rocca. Please see the latter's website <http://www.U152.org> for further information.

David K. Faux, Ph.D., C. Psych. (Retired)

R-U152, S139 / L2+, S144 / L20+ (S28 as tested by EthnoAncestry in 2005; and U152 as tested by FTDNA and deCODEme, as well as L2 and L20+ by FTDNA in 2008, and all three tested via 23andMe in 2008).

Seal Beach, California and Caledonia, Ontario

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