

The Celts: Where did they come from, where did they go?

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June 10, 2015

Celts in the time of Caesar

In his campaign memoir *Commentarii De Bello Gallico* [58-49 BCE], Caesar refers the people inhabiting most of what is now France as "...those who in their own language are called Celts, in our language Gauls." If this were all we knew about the Celts, they would seem to be just one of many western European tribes, hemmed in by the Germans and Belgians to the north, the Narbonnes and Aquitanians to the south, and in the process of being conquered by the Romans. But we now know, from linguistic and archaeological evidence that the Celts were a group of people who ranged in the centuries before Caesar all the way from the British Isles to Galatia (in modern Turkey), and from the Rhine in the north to southwest Iberia. And we know of their rich culture, their metallurgical expertise, their weaving of tartans, their magnificent jewelry and decorative arts, their bardic songs and harps, and (regrettably, in the opinion of some) the bagpipe!



Where did these people come from, and what became of them? To shed some light on this question, let's look at modern DNA and linguistic evidence.

Celtic Languages

One clear link between the Celtic peoples of the past and present is their languages. Indo-European in origin, their languages are distinct from Latin, Germanic and Norse tongues, the three main components of modern European languages.

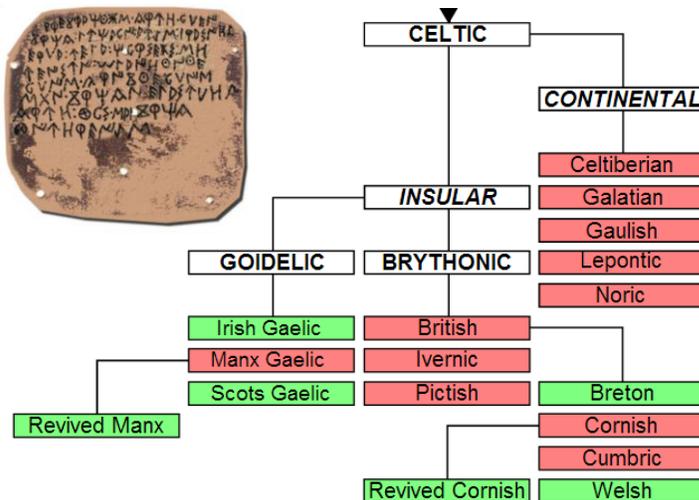


Fig. 1 - A possible phylogeny of the Celtic languages.¹ Continental, Brythonic, and Scots-Irish branches mirror the presumed history of the speakers of these languages. The Luzaga Plaque (inset) contains Celtiberian writing.²

	Welsh	Irish	Breton
Welsh	0	0.87	0.62
Irish	0.87	0	0.9
Breton	0.62	0.9	0

	English	Dutch	German
English	0	0.5	0.5
Dutch	0.5	0	0.25
German	0.5	0.25	0

Table 1 – Lexical distances between three modern Celtic languages and three modern Germanic languages. Note the greater separation between Celtic languages as compared to Germanic languages.³

The large lexical distances between Irish and the other Celtic languages implies a long-ago separation between the peoples of Ireland and Britain, and the relatively recent separation of Breton from the Brythonic languages, on a similar time scale to the separation of English and German from their common linguistic ancestor. This is consistent with the theory that Brittany was settled by refugees from the British Isles fleeing the Anglo-Saxon invasions ca. 450 CE.

But beyond this, linguistic analysis cannot really tell us much about the early Celtic peoples. To study them further, we need to turn to modern genetic analysis.

The Settlement of Europe as viewed with mitochondrial DNA

European hunter-gatherers began to move north from their ice-age refugia during the Holocene Epoch (starting ~12,000 years ago) to populate north-western Europe and the British Isles. The next wave of European population began about 9000-7000 years ago, with the movement of agriculturalists from Anatolia into Europe. The final wave was 4500 years ago when people descended from the Pontic Steppes, bringing with them horses, two-wheeled carts and chariots. In fact, these people, the Yamnaya, introduced the spoked wheel to Europe and rapidly established themselves as a dominant force on the continent. Many linguists credit them with the introduction of Indo-European language. Fig. 2 illustrates these two major settlement waves: Anatolian and Yamnaya.

So the Celtic peoples of the Hallstatt culture (800-500 BCE), and their proto-Celtic ancestors were surely products of these three settlement waves, and their genetics would have reflected this fact. Recently, the technology for accurately genotyping ancient human remains has enabled us to get a picture of what ancient European DNA was like. Let's start with mitochondrial DNA, the kind passed to children from their mothers only.

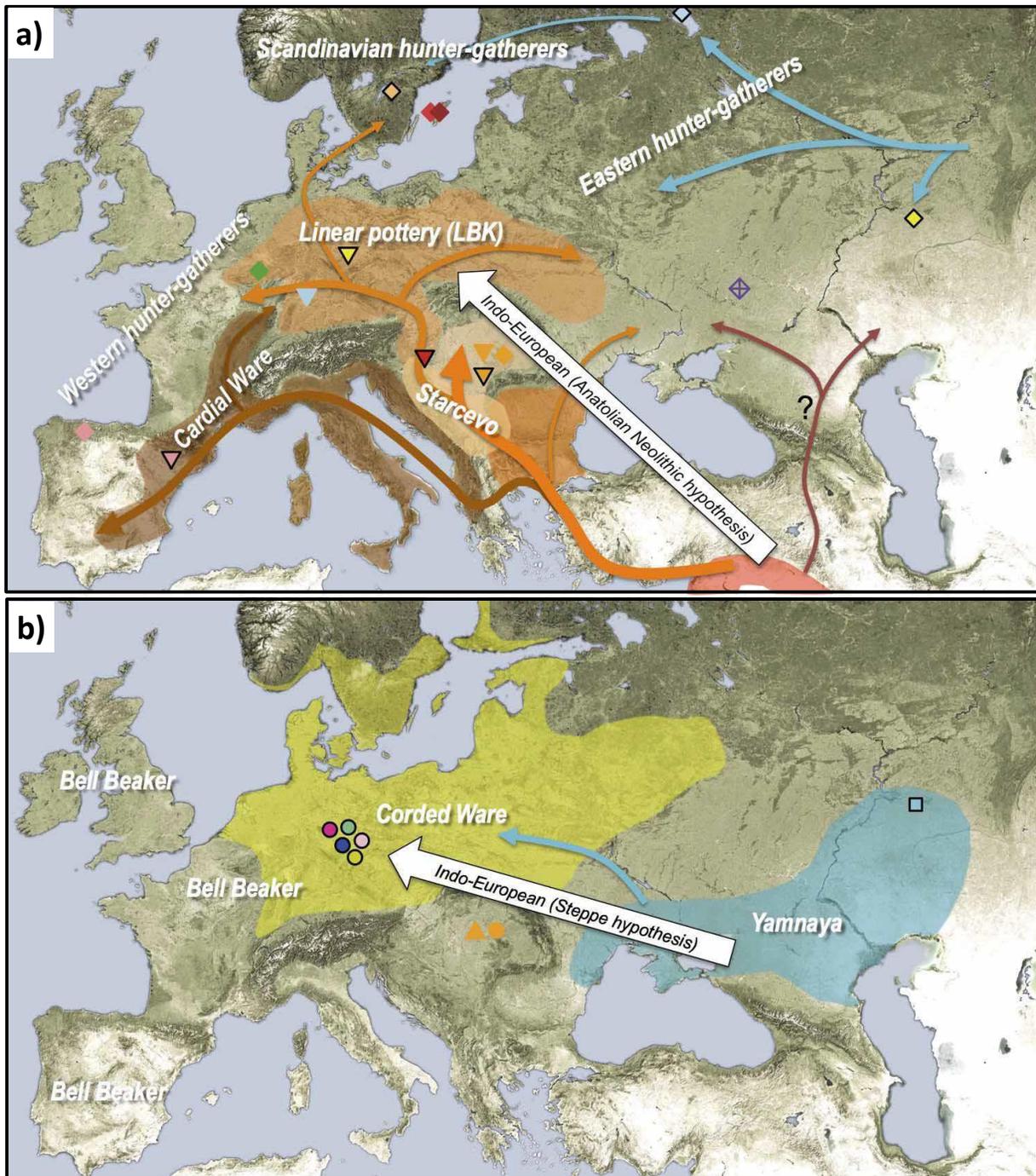


Fig 2 – Settlement of Europe from the East.⁴ About 9000 – 7000 years ago, Anatolian farmers settled in Europe, introducing agriculture to the continent which was then sparsely occupied by hunter-gatherers, with whom they interbred (a). Starting about 4500 years ago, the Yamnaya people of the Pontic steppes brought horses, two-wheeled chariots, and their DNA to Europe. Experts disagree as to which of these settlement waves introduced Indo-European language to Europe. The Celtic people and modern Europeans, both speakers of Indo-European languages, are for the most part descended from these two settlement waves, a fact attested to by DNA evidence.

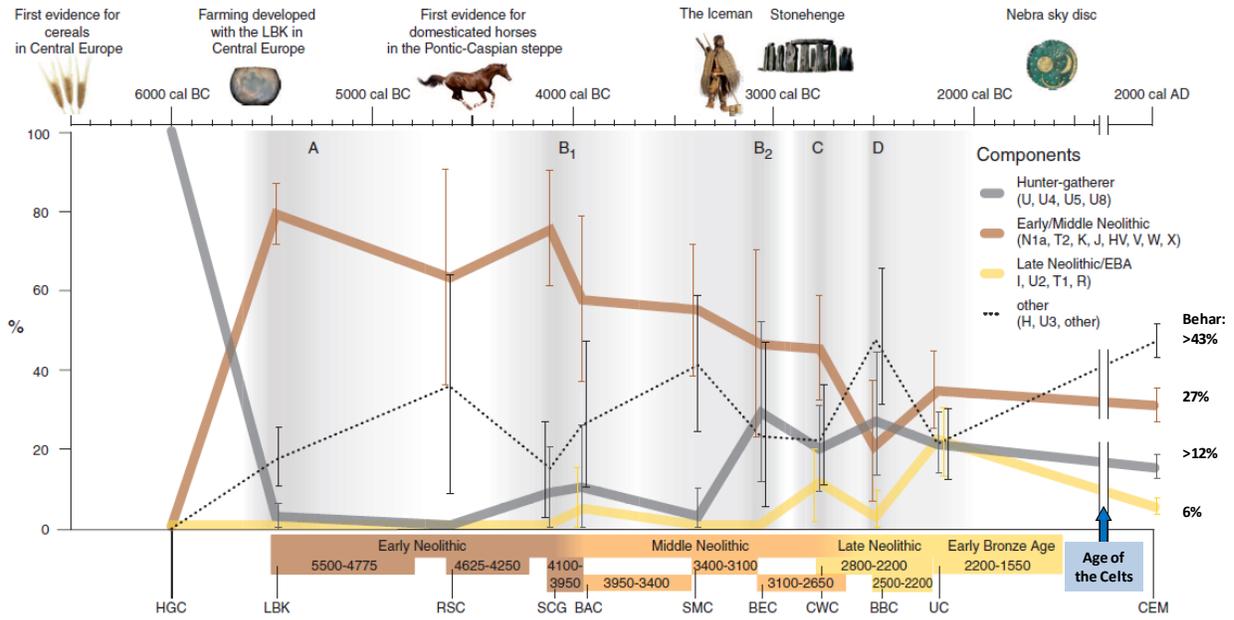


Fig. 3 – Mitochondrial DNA in European prehistory [After Brandt (2013)]. In modern Europe, all but 6% of mtDNA – the type passed through mothers to their children – has been present since Neolithic times, long before the arrival of the Yamnaya settlers from the steppes.⁵ By interpolation, it appears that Celts – both ancient and modern – would have similar mtDNA profiles as modern Europeans, who carry inheritance from Hunter-gatherers, Anatolian farmers and Yamnaya horsemen.⁶

Mitochondrial DNA studies of both ancient skeletons and modern humans shows us that Europeans in the age of the Celts had very similar mtDNA to modern Europeans. Furthermore, although mtDNA frequencies of occurrence show some variation across Europe, there is no pattern of mitochondrial haplogroups that offers us any insight into their geographic origin, and no concentrations that might be associated with a “Celtic” mitochondrial haplotype. On the basis of mtDNA, Celts and modern Europeans seem indistinguishable.

European Settlement as viewed with Autosomal DNA

The most recent academic publication on ancient and modern European DNA⁷ analyzes the admixture of autosomal DNA from ancient skeletons and modern Europeans. By comparing autosomal SNP sequences found in ancient hunter-gatherers, Early-Neolithic farmers, and Yamnaya with both modern Europeans and ancient European skeletal remains, the authors have generated a genetic profile showing the precursors of both ancient and modern Europeans. In Fig. 4a, we see that European skeletons from earlier than 2500 BCE are mostly descended from Neolithic agriculturalists, with some admixture of the early hunter-gatherers. At 2500 BCE, the Yamnaya come on the scene. Five skeletons from central Germany dated to that period are mostly Yamnaya, and appear to have been only recently mixed with the then-indigenous European population. Through the late Neolithic, Bronze and Iron ages up to 1100 BCE (at the early days of the ancient Celts) the Yamnaya component moves toward about 50%.

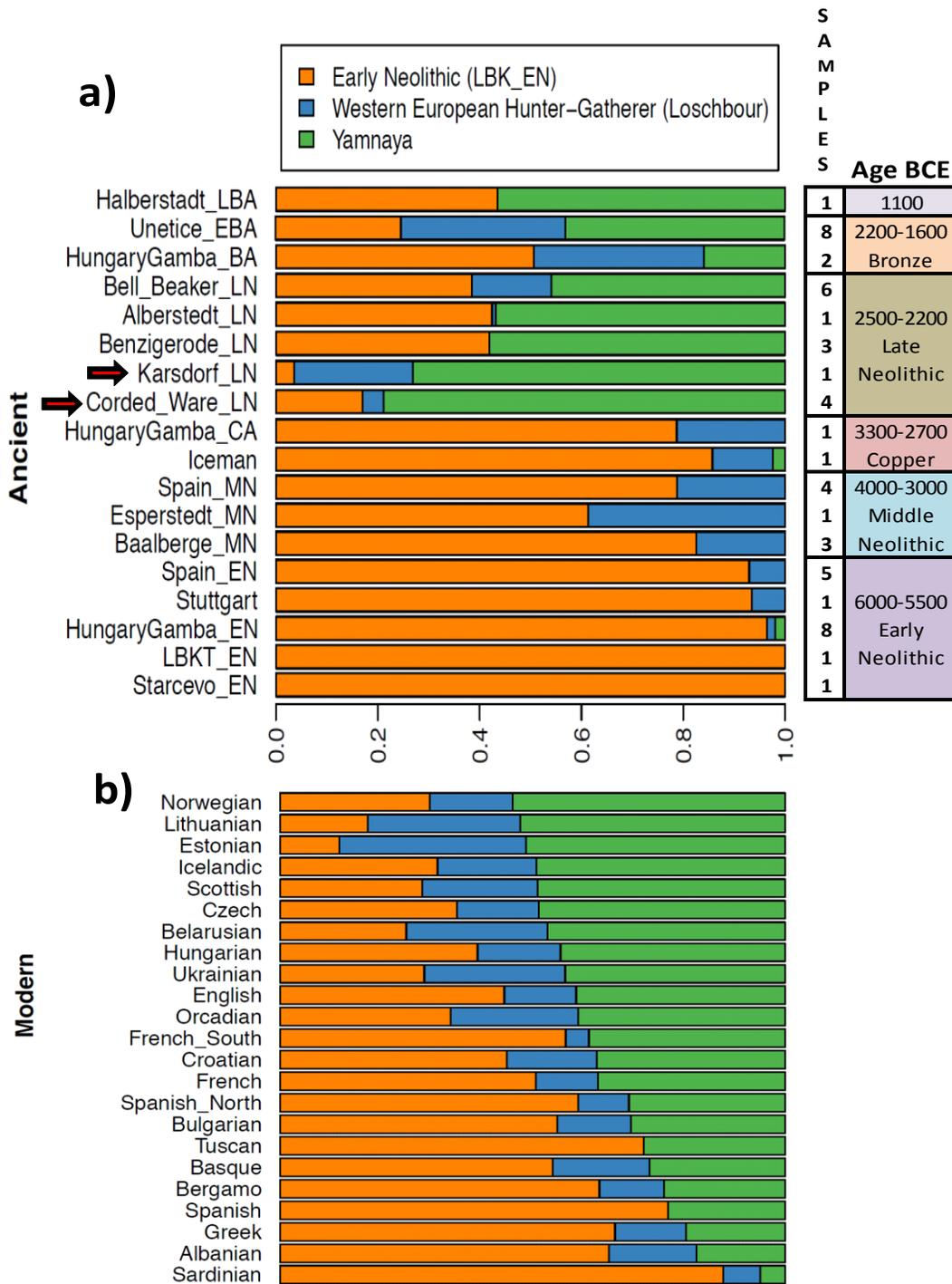


Fig 4 – Admixture analysis of genomic sequences from ancient skeletons (a) shows that prior to 2700 BCE, Europeans were descended mostly from Anatolian farmers who settled Europe between 7000 and 5000 BCE (orange), and partly from earlier European hunter-gatherers (blue). After 2500 BCE the situation changed dramatically, with a large influx of Yamnaya settlers from the Pontic Steppes (green). In five skeletons discovered in Germany (red arrows), the Yamnaya component was the largest. Most modern Europeans (b) are 20% - 50% descended from the Yamnaya, with a pronounced north-south gradient to the admixture. Note that the average Yamnaya component in modern Europeans is about 40%, slightly lower than in ancient European skeletons. The Celts probably had a similar admixture of hunter-gatherer, Anatolian farmer, and Yamnaya as do the modern northern Europeans. [After Haak et al, 2015]

So what can this admixture analysis tell us about the Celts? Unfortunately, not much. Early Europeans interbred to such an extent that this kind of analysis could not tell us the difference between a pure Celt and, say, a pure German. So we turn next to analysis of the Y-chromosome, the marker passed from father to son undiluted, though not un-mutated, through the generations.

Y-Chromosome Analysis of the Europeans

The study of Y chromosome Single Nucleotide Polymorphisms (SNPs) and their arrangement into haplogroups within the European population is of great interest to both academic and amateur investigators. Thousands of amateurs have submitted DNA samples for Y-SNP analysis and have banded together in volunteer groups to seek patterns that might illuminate their genetic backgrounds. The worldwide database listing Y-SNPs and their haplogroups is in fact an amateur enterprise.⁸ In Fig. 5, I show a portion of the Y chromosome haplogroup tree as it is presently understood, and as it might pertain to the Celts. This tree concentrates on the subclade called R1b, and traces it from the Steppes through to modern Europe.

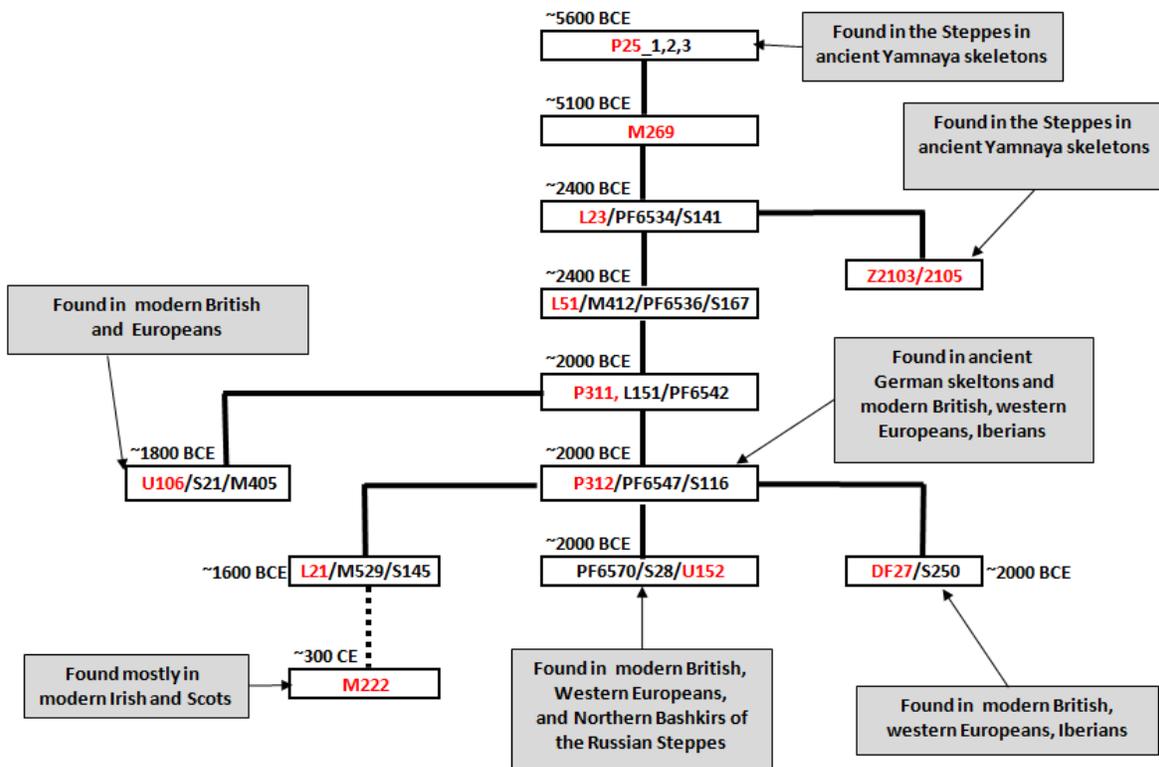


Fig. 5 – Phylogeny of major European Y-Haplogroups. DNA from ancient Yamnaya and German burials documents the connection between Europe and the Pontic Steppes. Haplogroup P312>DF27 was likely found in Celtiberians, and haplogroup P312>K21>...>M222 is found nearly exclusively in Irish and Scots and their American descendants. Surprisingly, a 4000 year old mutation, U152, has been found in both Europeans and Bashkirs of the Russian steppes. [Terminal mutated SNP of haplogroup is listed. Red indicates most commonly-used name for listed SNP.]⁹

Originally found in modern males, several of the Y-chromosome SNP mutations have recently been found in ancient skeletons.¹⁰ Of greatest interest are P25, a mutation believed to have first appeared about 5600 BCE, and P312, a mutation dating to about 2000 BCE and which probably occurred in Europe. P312 was genotyped in the skeletal remains of a man buried between 2296–2206 BCE in central Germany.¹¹ The mitochondrial haplotype of this man was H, the most commonly-found in samples of his era [Fig. 3]. He was one of the six samples portrayed in Fig. 4(a) as Bell_Beaker_LN, a group with about 50% Yamnaya heritage. We focus on the P312 sample because it is the earliest known example which could possibly be a paternal ancestor to at least some Celts.

Figure 6 summarizes the data collected from amateur genealogists who have participated in the Family Tree DNA (FTDNA) Y-Haplogroup projects.¹² Because these participants are over-represented by Americans with British Isles ancestry, the data points representing earliest known ancestors are heavily concentrated in the British Isles, and no pattern emerges there. However, the picture for Continental Europe is fairly clear. The four main European Haplogroups can be imagined to be associated with Iberian (R1b-P312), Germanic (R1b-U106), Nordic (I1), and Slavic (R1a). Each of these haplogroups is present everywhere in Europe to some extent, and all are heavily represented in the British Isles. But R1b-P312 alone seems to be prevalent in Western Europe south of the Rhine, in Gaul and Iberia, homeland of the Celts in the time of Caesar. And although the data does not clearly indicate that all Celts were R1b-P312, it does imply that many of them may have been. The Celtiberians most likely were R1b-P312.

The clearest indication of a Celtic haplotype is M222, associated with a mutation about 300 CE, and found most heavily among the people of Ireland (Fig. 7). This haplogroup is also prevalent in Scotland and the border counties, but not much in England. This would be consistent with the Irish raids on Scotland following the Roman retreat from Britain in about 550 CE. Not surprisingly, M222 is also common in the United States.

Summary for Celtic ancestry in Continental Europe

Recent academic publications give a clear picture of European genetic ancestry: a combination of early indigenous hunter-gatherers, Early Neolithic Farmers from Anatolia, and Late Neolithic invaders from the Pontic Steppes. In both mitochondrial and autosomal DNA, Europeans were, by the age of the Celts, a mixture of these three ancestral groups. But Y-DNA data collected from thousands of amateur volunteers seems to indicate that Celtic men may have been more commonly of the R1b-P312 haplogroup, a group that could possibly be assigned to the Yamnaya people of the Steppes via recent genotyping of ancient skeletons.

To get another take on Celtic DNA ancestry, we need to turn to the greatest reservoir of modern Celtdom: the British Isles.

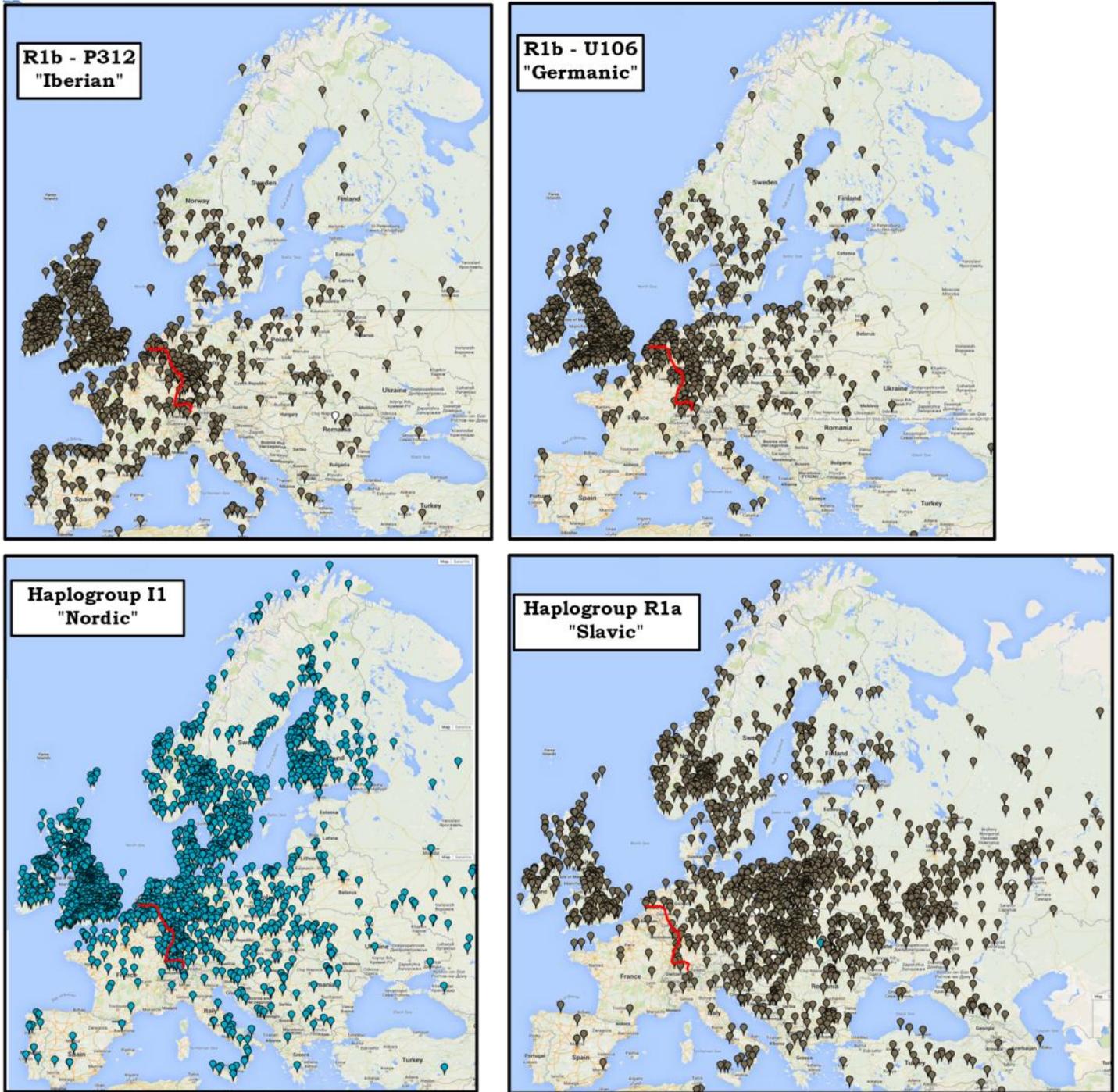


Fig. 6 – Four main Y-haplogroups of Europe, labeled according to the ancestral populations they supposedly represent, though substantial overlap is evident. Points depict the earliest-known ancestors of FTDNA Y-haplogroup project participants per their genealogy-based claims.¹³ Only R1b-P312 has a major ancestral presence below the Rhine River (red line). All haplogroups are heavily represented in the British Isles, though this is over-emphasized owing to the large number of British descendants among North American participants. These data seem to suggest that Celtiberians, and possibly other sub-Rhine Celts, were members of the P312 subclade of haplogroup R1b, which is estimated to have originated in Europe about 4000-4500 years ago.



Fig. 7 – R1b-M222, a subclade of R1b-P312, appears almost exclusively in Ireland, but with some presence in Scotland and, to a much lesser extent, England. Estimated to be 1700 years old, this subclade would have appeared before the Irish raids on Scotland and Wales began (550 CE), which could explain the spread to Britain. This subclade also had significant presence among early settlers in the mid-Atlantic colonies in British America.

Celts in the British Isles

The primary bastion of Celtic culture and ethnic pride today is in the British Isles, among the Scottish, Irish and Welsh and their descendants in North America. But is there any DNA evidence that can differentiate these people from the rest of the British population? It should be noted that the Basques, who even today speak an ancient non-Indo-European language are in fact genetically indistinguishable from their non-Basque neighbors (R1b Y-chromosome haplotype). And despite the attested settlement of Brittany by refugee Brythonic Celts ca. 450 CE, no genetic evidence of a connection to Britain has been found. So cultural differentiation and genetic characteristics do not necessarily correlate.

A recent publication (Leslie, 2015)¹⁴ sheds new light on this question. Using a sophisticated statistical analysis technique called Fine-Scale Analysis (FSA), the authors were able to genetically segment the British population to a degree previously not possible. As shown in Fig. 8, they were able to separate the Scots, Welsh and Cornish from the rest of the British population and from each other. The Scots and Cornish, it turns out, are extremely close to the English. The most separate Celtic group is the residents of North Wales, with South Wales residents midway between them and the English. So here at last is a definite genetic footprint for the Celts: the most remote part of Wales is genetically Celtic.

These authors (including Barry Cunliffe) illustrate the settlement of Britain in Fig. 9. The most surprising part of this map is the complexity of the settlement of Scotland versus the genetic homogeneity of its people (excepting Orkney). The peoples of the border counties of England are genetically Scottish, despite the historical conquests of the Anglo-Saxons, Norwegians and Danes in the area. It seems that the Celts have persevered genetically despite foreign conquest and linguistic assimilation. This raises a basic question: “What determines the characteristics of a people, genetics or culture?” In fact it must be a combination of the two. But as a footprint of ethnic history, language (e.g. Basque) and cultural traditions seem to be every bit as durable as genetics; perhaps even more so.

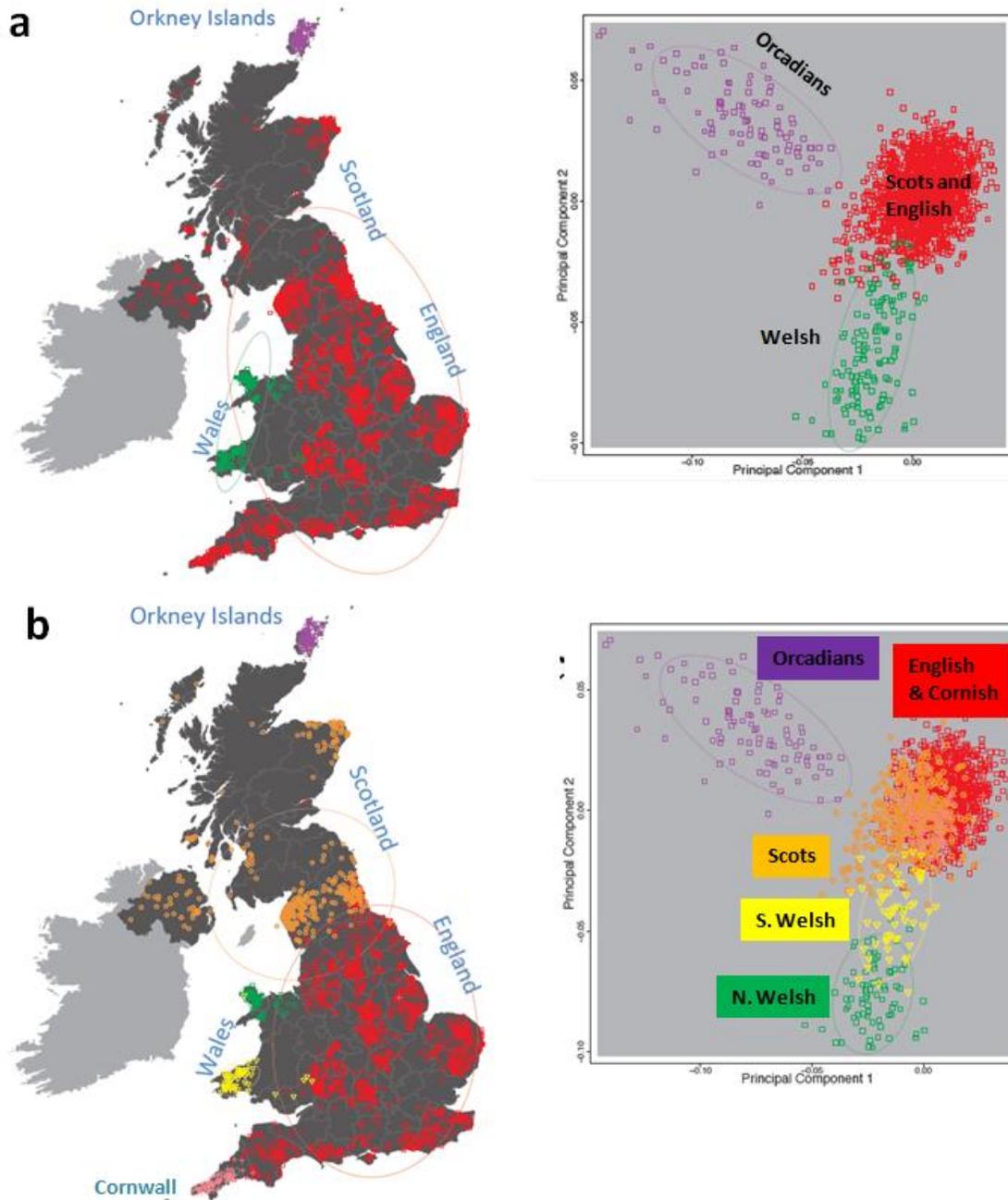


Fig. 8 – (a) Orcadians (Norse origin) and Welsh (Celtic origin), are differentiated from Scots (Celtic origin) and English (Celtic, Anglo-Saxon and Scandinavian) using both fine scale analysis (FSA) and principal component analysis - a form of genetic map illustrating genetic separation (PCA). In (b), finer division of the data with FSA reveals differentiation between English and Scots, despite the overlap of these populations in PCA, and between northern and southern Welsh. Cornish can be separated from English with FSA but not PCA, indicating that the Cornish people, who once spoke a Celtic language, are now more Anglo-Saxon than Celtic.

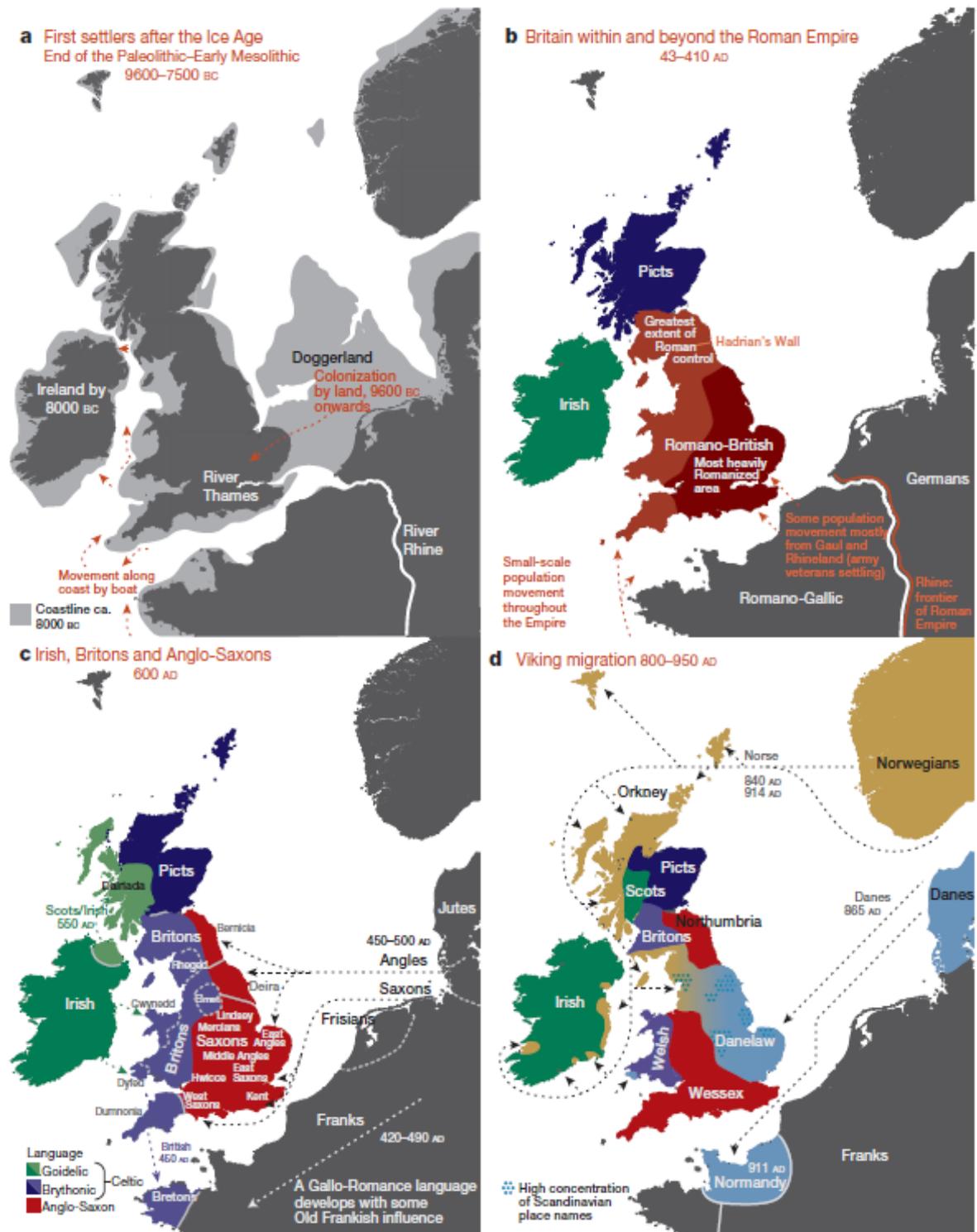


Fig 9 – The peopling of Britain according to British authors (Leslie 2015). Britain was settled by hunter-gatherers from western Europe (a) before it was settled by agriculturalists. Britain and Ireland were settled by relatives of the continental Celts before Roman times (b). The Anglo-Saxon invasion (c) settled the eastern portion of Britain by 600 CE (c), with Celtic Britons settling in Armorica (modern Brittany) in 450 CE. Irish Celts invaded Scotland about 550 CE in what was probably the last Celtic expansion. Subsequent Viking settlements are shown in (d).

Conclusion

So where did the Celts come from and where did they go? Autosomal admixture and mitochondrial DNA analyses indicate that the continental Celts of old were descended, as were most Europeans, from early hunter-gatherers, Anatolian farmers, and horsemen from the Pontic steppes. Y chromosome analysis hints at the possibility – but does not prove - that Celtic men were descended from the R1b-P312 common ancestor, a man who lived some 4500 years ago in Europe and who spawned a descendant whose skeleton has been unearthed and identified in Germany. The likelihood is that Celts were more of a tribal and cultural group rather than a genetic isolate. Most likely, the continental Celts blended in with Germanic, Nordic and Frankish tribes to produce the modern Europeans: distinct culturally, but not much genetically.

However, modern Celts in Britain are genetically distinct from Anglo-Saxon and Scandinavian Britons, but vary substantially between the Scottish, Welsh and Cornish branches. They comprise the best answer to the question “Where did the Celts go?” Answer: Western British Isles and North America.

References

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 - ² The Luzaga Plaque showing Celtiberian script: http://en.wikipedia.org/wiki/Celtiberian_language. Accessed April 30, 2015
 - ³ Lexical distances computed from 200-word Swadesh lists compiled by Maurizio Serva: <http://univaq.it/~serva/languages/languages.html> Accessed April 30, 2015
 - ⁴ Haak, W. et al., “Massive migration from the steppe was a source for Indo-European languages in Europe,” *Nature* (2015) **522**, 207-211, doi:10.1038/nature14317
 - ⁵ Brandt, G. et al., “Ancient DNA Reveals Key Stages in the Formation of Central European Mitochondrial Diversity,” *Science*, vol. 342, pp. 257-261, 11 October, 2013.
 - ⁶ Behar, D., “The Genetic Structure of the Jewish People (Slide 32),” Lecture at Stanford University, October 11, 2012. Behar’s data shown here refers to non-Ashkenazi Europeans.
 - ⁷ Haak, W. et al., “Massive migration from the steppe was a source for Indo-European languages in Europe,” *Nature* (2015) **522**, 207-211, doi:10.1038/nature14317
 - ⁸ The International society of Genetic Genealogy (ISOGG) maintains and yearly updates the Y chromosome haplogroup tree. <http://www.isogg.org/tree/>
 - ⁹ Age of haplogroups was estimated using the statistical variance of Y-STRs, combined with published mutation rates. An average interval of 30 years per male generation was assumed.
 - ¹⁰ Haak, W. et al., “Massive migration from the steppe was a source for Indo-European languages in Europe,” *Nature* (2015) **522**, 207-211, doi:10.1038/nature14317
 - ¹¹ Haak et al. Sample I0806: SI-2, pg. 16, SI-3 pg. 33, SI-4 pp. 39-41. A 50 year old male found at Quedlinburg VII.
 - ¹² <https://www.familytreedna.com/groups/r-1b/about/background>
 - ¹³ These are men of European descent living mostly in Europe and North America. Numbers of participants are: R1b-312, 2100; R1b-U106, 2000; I1, 4600; R1a, 3000. Accessed April 30, 2015.
 - ¹⁴ Leslie, S. et al., “The fine-scale genetic structure of the British population,” *Nature*, 19 March 2015, pg. 309.