

# Ancient DNA in Europe

Report to the R-U106 group

November 2017 edition

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## Contents

<b>Part 2: Ancient DNA and migrations around the U106 origin</b>	<b>2</b>
Introduction to ancient DNA testing	2
Ancient DNA results	3
<i>40000-8000 BC</i>	3
<i>8000-6000 BC</i>	4
<i>6000-5250 BC</i>	5
<i>5250-4500 BC</i>	6
<i>4500-3400 BC</i>	7
<i>3400-2925 BC</i>	8
<i>2925-2550 BC</i>	9
<i>2550-2140 BC</i>	10
<i>2140-1950 BC</i>	11
<i>1950-1500 BC</i>	12

# Ancient DNA

DNA extracted from archaeological remains are an invaluable source of the distribution of haplogroups in ancient and prehistoric times, and in recording the clades that had formed by those people's deaths. They provide a method to validate the ages of nodes in the haplotree, and they provide information we can use to deduce the migrations of people in these ancient times.

This document focusses on ancient DNA results in Europe between until 1500 BC, after which few useful samples are available. These cover a wide range of periods, from the first modern humans to inhabit Europe, to the arrival of R-L11 into Europe (circa 3000 BC), and the spread of R-L11 that broadly defines the current haplogroup distributions today. The maps on the following pages show these ancient DNA results, broken up by period, to highlight the differences between them.

The ancient DNA records used to provide the following maps come from Jean Manco's database:

<http://www.ancestraljourneys.org/ancientdna.shtml>

## PROBLEMS WITH ANCIENT DNA

There are many difficulties in testing ancient DNA, related to both the preservation of the sample and possible contamination since that person's death, including by the archaeologists and scientists handling the remains. At the time of writing (November 2017), extracting and sequencing DNA from some 45,000-year-old remains has been achieved, and analysis of 5,000-year-old remains is becoming routine. However, the quality of the results is still much lower than commercial tests and depends strongly on the state of preservation. Typically, a modern sequencing test might reach a few dozen good-quality reads on the same base pair. If you find the same allele (A,C,G,T) at that base pair (nearly) every time, it gives you confidence that you have the correct one. With ancient DNA, you are lucky to get one or two reads, though calls are usually only made when a higher number of good-quality reads is reached (say 5x).

This means that the effective coverage of ancient DNA is very variable, and doesn't cover every SNP that a standard sequencing test would. Only in a small proportion of samples is the DNA of sufficiently good quality to call novel variants from the test, and often only broad haplogroups (e.g. "R1b") are published. Several dedicated individuals process the publicly-available raw results from these tests to extract further known SNPs. These results often remain tentative, and may still only identify a test as, e.g. R1b-M269, rather than some more recent variant, but we have to do the best with what we have.

The problems associated with ancient DNA are summarised in the review article by Kivisild (2017):

<https://link.springer.com/article/10.1007/s00439-017-1773-z>

## ASSOCIATING ANCIENT DNA WITH ARCHEAOLOGICAL CULTURES

What we get from ancient DNA is a sequence of called variants present in the genes of a single man. Normally, there is enough information to tie that man to a particular culture that lived at that time. Today, an entire culture cannot be adequately represented by a single person, or a single family. There is no particular reason to think that it was any different in pre-historic times. Any ancient culture is therefore going to be a mixture of haplogroups.

However, each culture will have a *different* admixture of haplogroups, so tracking the ancient migrations of our ancestors requires tracking how these haplogroup admixtures change over geographical space and over time. Over ancient timescales, this is a case of looking at the ratio of haplogroup I to G, I to R, G to R, etc. In more modern times, we need to look at the ratio of more contemporary haplogroups, like R-U106 to R-P312, etc. The most important thing, where possible, is to look at the spread of contemporaneous haplogroups, to maximise the fraction of that haplogroup within that culture.

The sparse sampling of ancient DNA means that we do not get a complete picture of a haplogroup's distribution. For example, if a culture is sampled by a single haplogroup I individual, that doesn't mean the rest of the culture was haplogroup I. Similarly, if there are three or four R-P312 results from a culture, but no R-U106 results, that doesn't mean that R-U106 is not there, merely that it is likely to be present at a much lower percentage. It's also important to remember that ancient DNA often only samples burials of the elite classes (there are many exceptions). This may mean that we only sample a few ruling families, while the bulk of ancient peoples go unrecorded because they didn't warrant a high-status burial (e.g. a large tumulus), where their remains would be well-preserved and easily identifiable. Sequencing of results from battlefields, etc., can help rectify this, but there will remain a class bias in our results, particularly in (post-)Neolithic cultures.

As with all datasets, our knowledge improves as more ancient DNA is sequenced. True sequencing of ancient DNA has only really been possible in the last handful of years, so we are only starting to get a real picture of how different haplogroups populated Europe. This is a fast-evolving field, with potentially game-changing discoveries being made every few months..

## ANCIENT U106 RESULTS

While this document is intended to be fairly general, it is made for the R-U106 group. There have only been two confirmed U106+ burials discovered in time period we consider here (up to 1500 BC). The first is RISE98, who was found buried in the southernmost tip of Sweden, and appears to have lived at some point during the latter centuries of the third millennium BC, coming from the Swedish Battle Axe culture, seemingly a descendant culture of the western Corded Ware Culture. The second is at De Tuithoorn, north of Amsterdam, and appears to represent a transition population between the subsiding Bell Beaker Culture and a culture of the Nordvestblock.

This lack of ancient R-U106 is partly expected. Most ancient burials in northern, western and central Europe around 3000-2000 BC are R-P312. The top of the R-P312 tree branches much faster than R-U106, indicating a faster population spread. However, this doesn't entirely account for the lack of observed R-U106. It seems likely that R-U106 exists in a region that is not well sampled during the period 2500-2000 BC. It may be holed up somewhere like the southern Baltic coast, where few testers have been sampled.

After 2000 BC, the only currently (November 2017) confirmed U106+ burials are from a Roman-era cemetery in York, one of which is R-DF98 and one of which is R-DF96. It is likely that these burials represent gladiators from within Roman Britain. The isotopic analysis of the R-DF96 burial suggests that he came from a more mountainous region. The paper's authors posit Wales, but other areas of the British Isles (e.g. southern Scotland) remain possible. Only one of the burials mentioned in that paper shows isotopic and autosomal DNA evidence from coming from outside the British Isles.

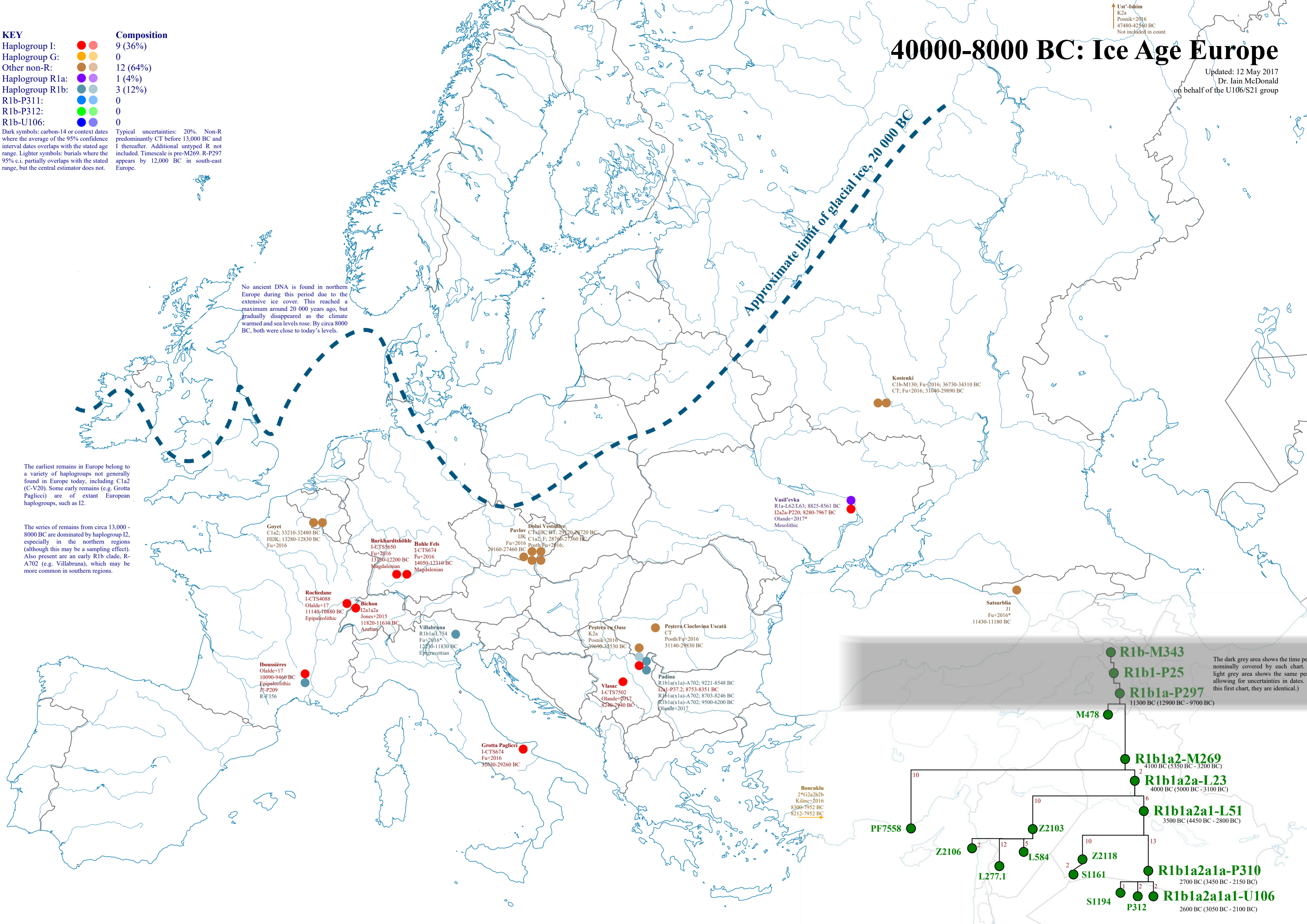
# 40000-8000 BC: Ice Age Europe

Updated: 12 May 2017  
 Dr. Iain McDonald  
 on behalf of the U106/S21 group

KEY	Composition
Haplogroup I:	9 (36%)
Haplogroup G:	0
Other non-R:	12 (64%)
Haplogroup R1a:	1 (4%)
Haplogroup R1b:	3 (12%)
R1b-P311:	0
R1b-P312:	0
R1b-U106:	0

Dark symbols: carbon-14 or context dates where the average of the 95% confidence interval dates overlaps with the stated age range. Lighter symbols: burials where the 95% c.i. partially overlaps with the stated range, but the central estimator does not.

Typical uncertainties: 20%. Non-R predominantly CT before 13,000 BC and I thereafter. Additional untyped R not included. Timescale is pre-M269. R-P297 appears by 12,000 BC in south-east Europe.



No ancient DNA is found in northern Europe during this period due to the extensive ice cover. This reached a maximum around 20 000 years ago, but gradually disappeared as the climate warmed and sea levels rose. By circa 8000 BC, both were close to today's levels.

The earliest remains in Europe belong to a variety of haplogroups not generally found in Europe today, including C1a2 (C-V20). Some early remains (e.g. Grotta Paglicci) are of extant European haplogroups, such as I2.

The series of remains from circa 13,000 - 8000 BC are dominated by haplogroup I2, especially in the northern regions (although this may be a sampling effect). Also present are an early R1b clade, R-A702 (e.g. Villabruna), which may be more common in southern regions.

**Kostenki**  
 C1b-M130; Fu+2016; 36730-34310 BC  
 CT; Fu+2016; 31040-29890 BC

**Vasil'evka**  
 R1a-L62/L63; 8825-8561 BC  
 I2a2a-P220; 8280-7967 BC  
 Olande+2017\*  
 Mesolithic

**Goyet**  
 C1a2; 33210-32480 BC  
 HDK; 13280-12830 BC  
 Fu+2016

**Burkhardtshöhle**  
 I-CTS5650  
 Fu+2016  
 13790-12200 BC  
 Magdalenian

**Hohle Fels**  
 I-CTS674  
 Fu+2016  
 14050-12310 BC  
 Magdalenian

**Dolni Vestonice**  
 CTxJK; BT; 29120-28720 BC  
 IJK  
 C1a2; F; 28760-27360 BC  
 Fu+2016  
 Posth; Fu+2016;

**Rochedane**  
 I-CTS4088  
 Olalde+17  
 11140-10880 BC  
 Epipaleolithic

**Bichon**  
 I2a1a2a  
 Jones+2015  
 11820-11610 BC  
 Azilian

**Villabruna**  
 R1b1a-L754  
 Fu+2016\*  
 12230-11830 BC  
 Epigravettian

**Peștera cu Oase**  
 K2a  
 Posth; Fu+2016  
 39690-35530 BC

**Peștera Cioclovina Uscată**  
 CT  
 Posth; Fu+2016  
 31140-29830 BC

**Satsurblia**  
 J1  
 Fu+2016\*  
 11430-11180 BC

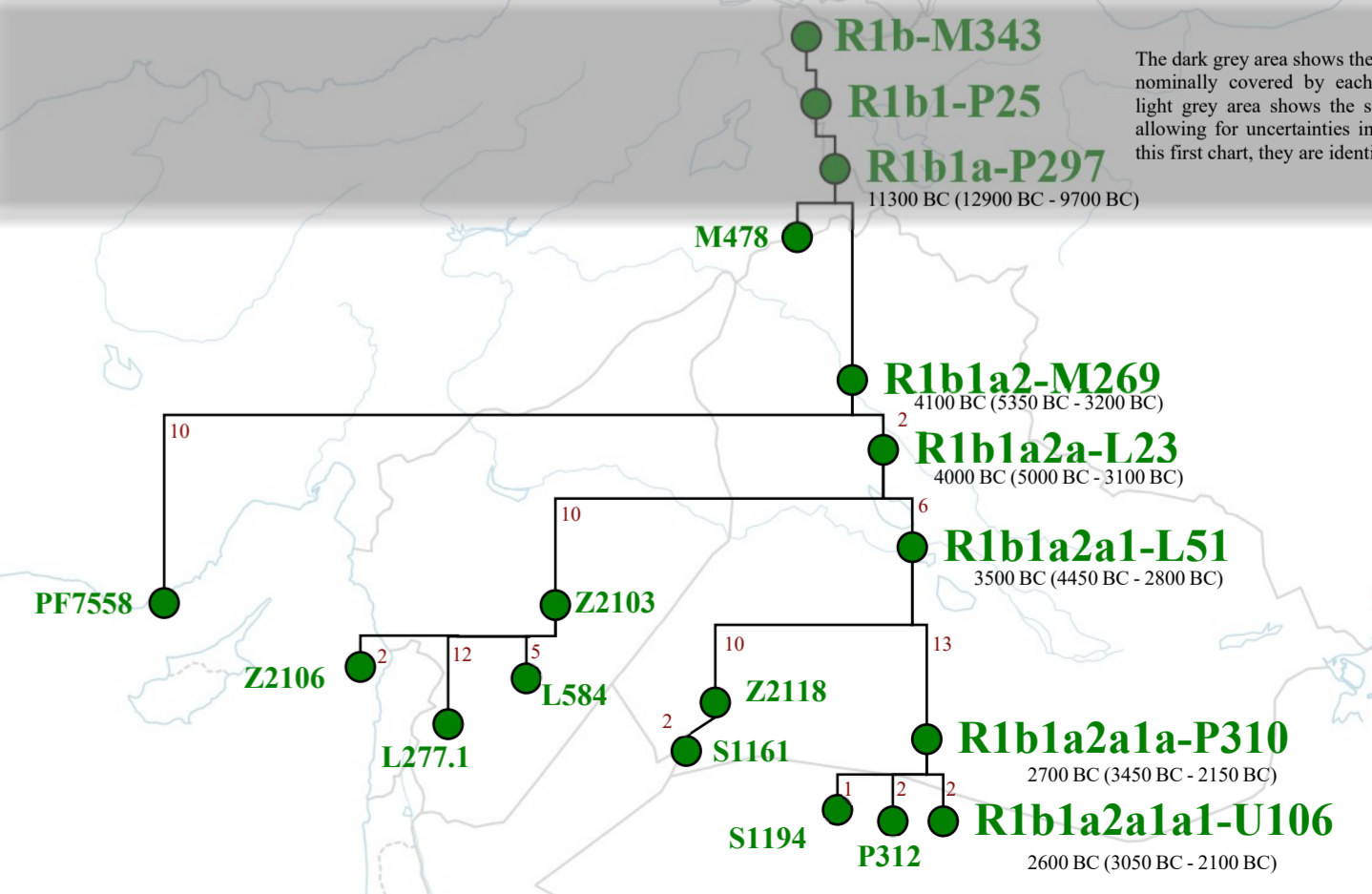
**Ibousières**  
 Olalde+17  
 10090-9460 BC  
 Epipaleolithic  
 R-P209  
 R-F356

**Vlasac**  
 I-CTS7502  
 Olande+2017  
 8248-7940 BC

**Padina**  
 R1b1a(x1a)-A702; 9221-8548 BC  
 I2a1-P37.2; 8753-8351 BC  
 R1b1a(x1a)-A702; 8703-8246 BC  
 R1b1a(x1a)-A702; 9500-6200 BC  
 Olande+2017

**Grotta Paglicci**  
 I-CTS674  
 Fu+2016  
 32630-29260 BC

**Boneculu**  
 2\*G2a2b2b  
 Kilinc+2016  
 8300-7952 BC  
 8212-7952 BC



The dark grey area shows the time period nominally covered by each chart. Light grey area shows the same period allowing for uncertainties in dates. In this first chart, they are identical.

# 8000-6000 BC: The Neolithic revolution

Updated: 17 May 2017  
 Dr. Iain McDonald  
 on behalf of the U106/S21 group

KEY	W/C Eur	Fmr. USSR	Balkans	Anatolia
Haplogroup I:	3 (100%)	0	9 (56%)	3 (16%)
Haplogroup G:	0	0	1 (6%)	9 (47%)
Other non-R:	0	1 (33%)	0	7 (37%)
Haplogroup R1a:	0	1 (33%)	0	0
Haplogroup R1b:	0	1 (33%)	6 (38%)	0
R1b-P311:	0	0	0	0
R1b-P312:	0	0	0	0
R1b-U106:	0	0	0	0

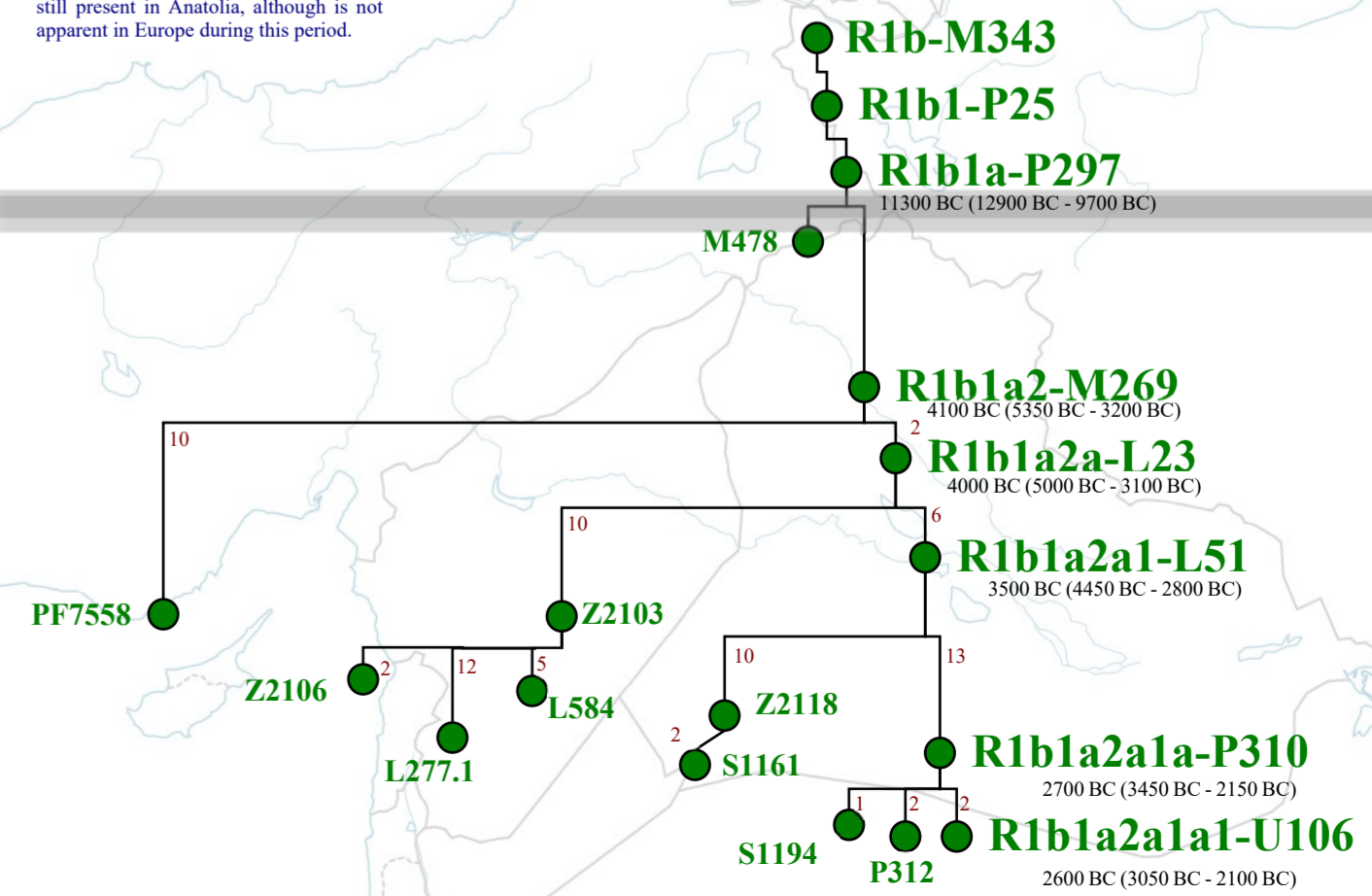
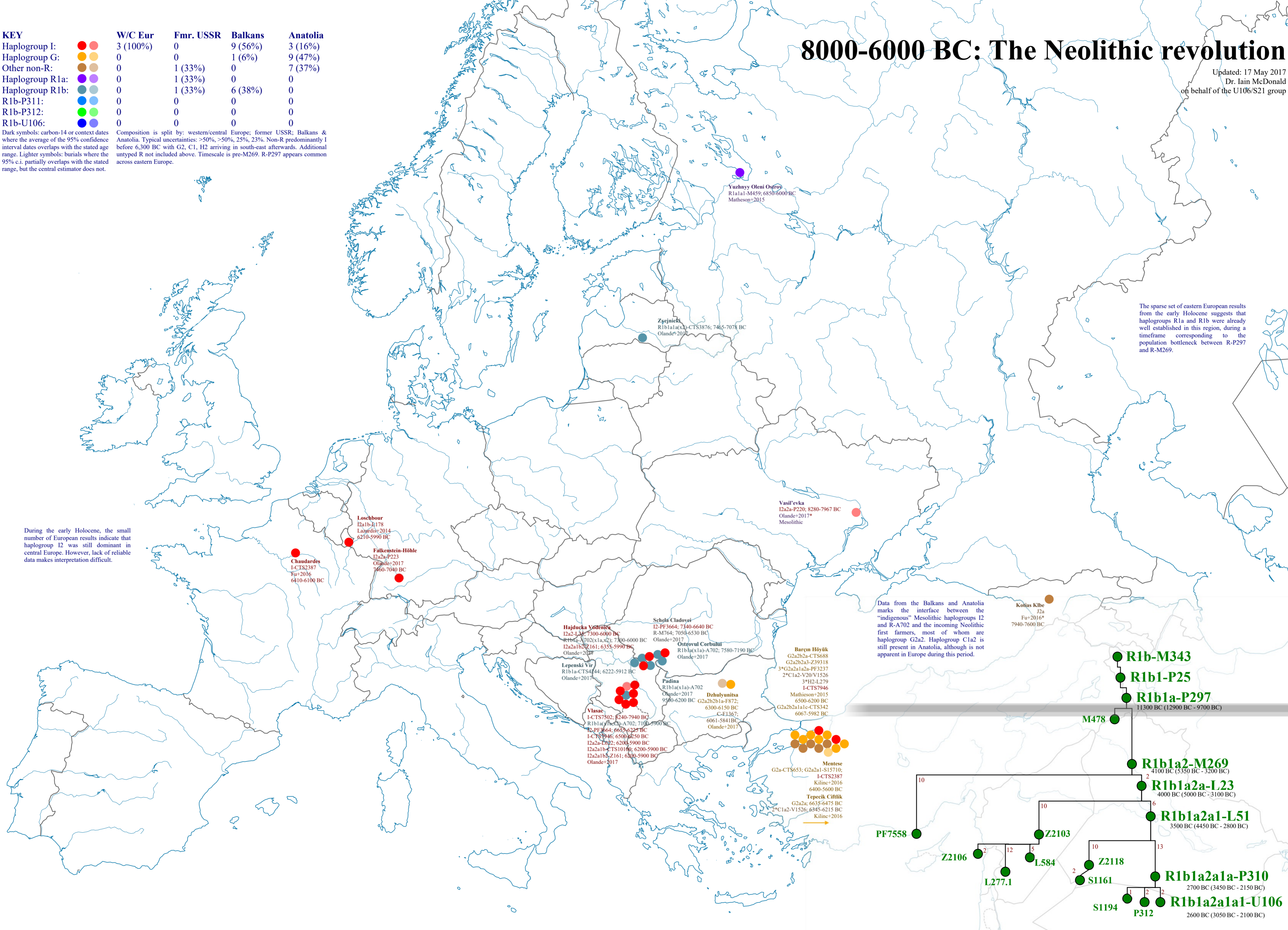
Dark symbols: carbon-14 or context dates where the average of the 95% confidence interval dates overlaps with the stated age range. Lighter symbols: burials where the 95% c.i. partially overlaps with the stated range, but the central estimator does not.

Composition is split by: western/central Europe; former USSR; Balkans & Anatolia. Typical uncertainties: >50%, >50%, 25%, 23%. Non-R predominantly I before 6,300 BC with G2, C1, H2 arriving in south-east afterwards. Additional untyped R not included above. Timescale is pre-M269. R-P297 appears common across eastern Europe.

During the early Holocene, the small number of European results indicate that haplogroup I2 was still dominant in central Europe. However, lack of reliable data makes interpretation difficult.

The sparse set of eastern European results from the early Holocene suggests that haplogroups R1a and R1b were already well established in this region, during a timeframe corresponding to the population bottleneck between R-P297 and R-M269.

Data from the Balkans and Anatolia marks the interface between the "indigenous" Mesolithic haplogroups I2 and R-A702 and the incoming Neolithic first farmers, most of whom are haplogroup G2a2. Haplogroup C1a2 is still present in Anatolia, although is not apparent in Europe during this period.



# 6500-5250 BC: Farmers in the Balkans

Updated: 17 May 2017  
 Dr. Iain McDonald  
 on behalf of the U106/S21 group

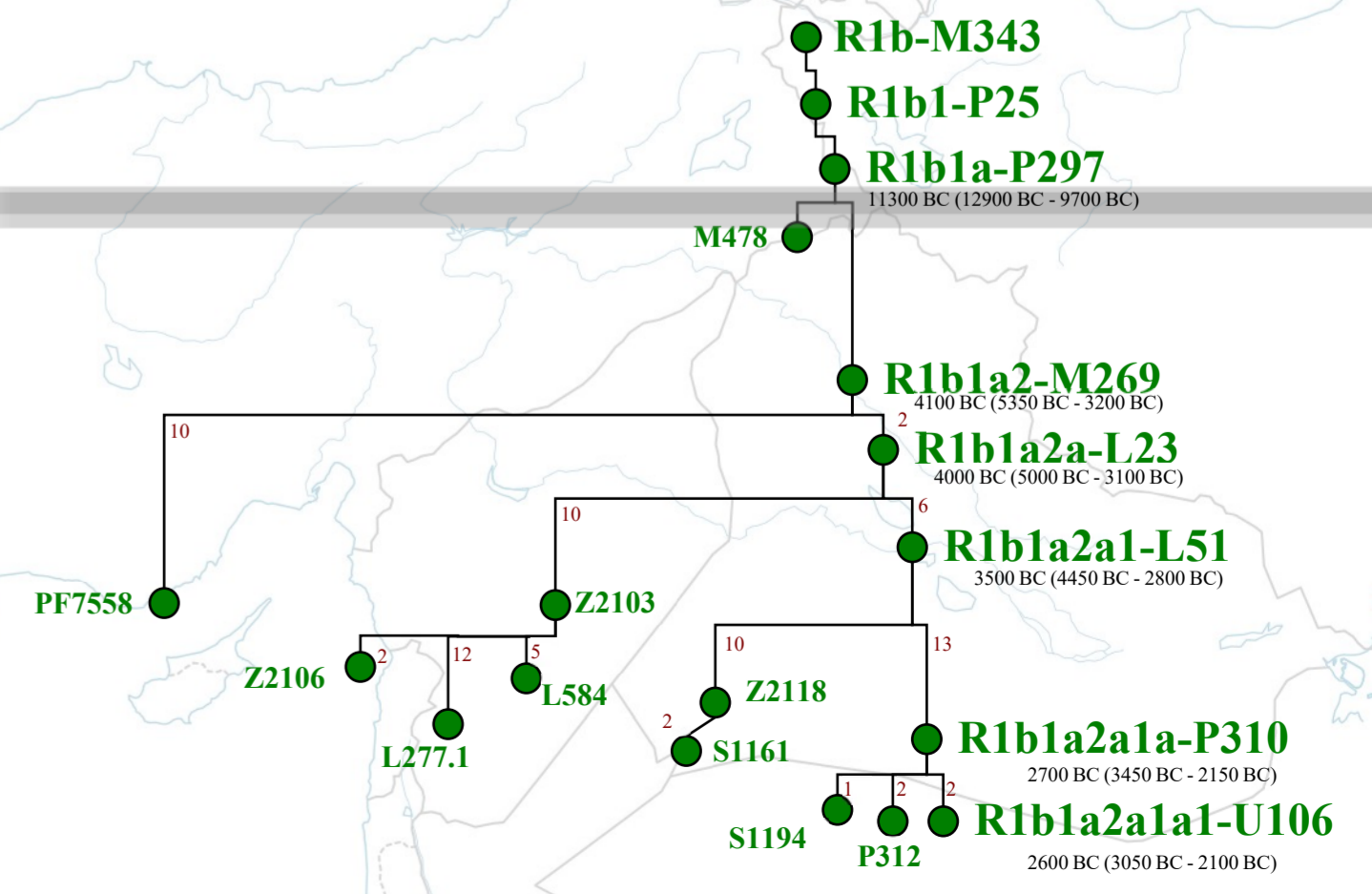
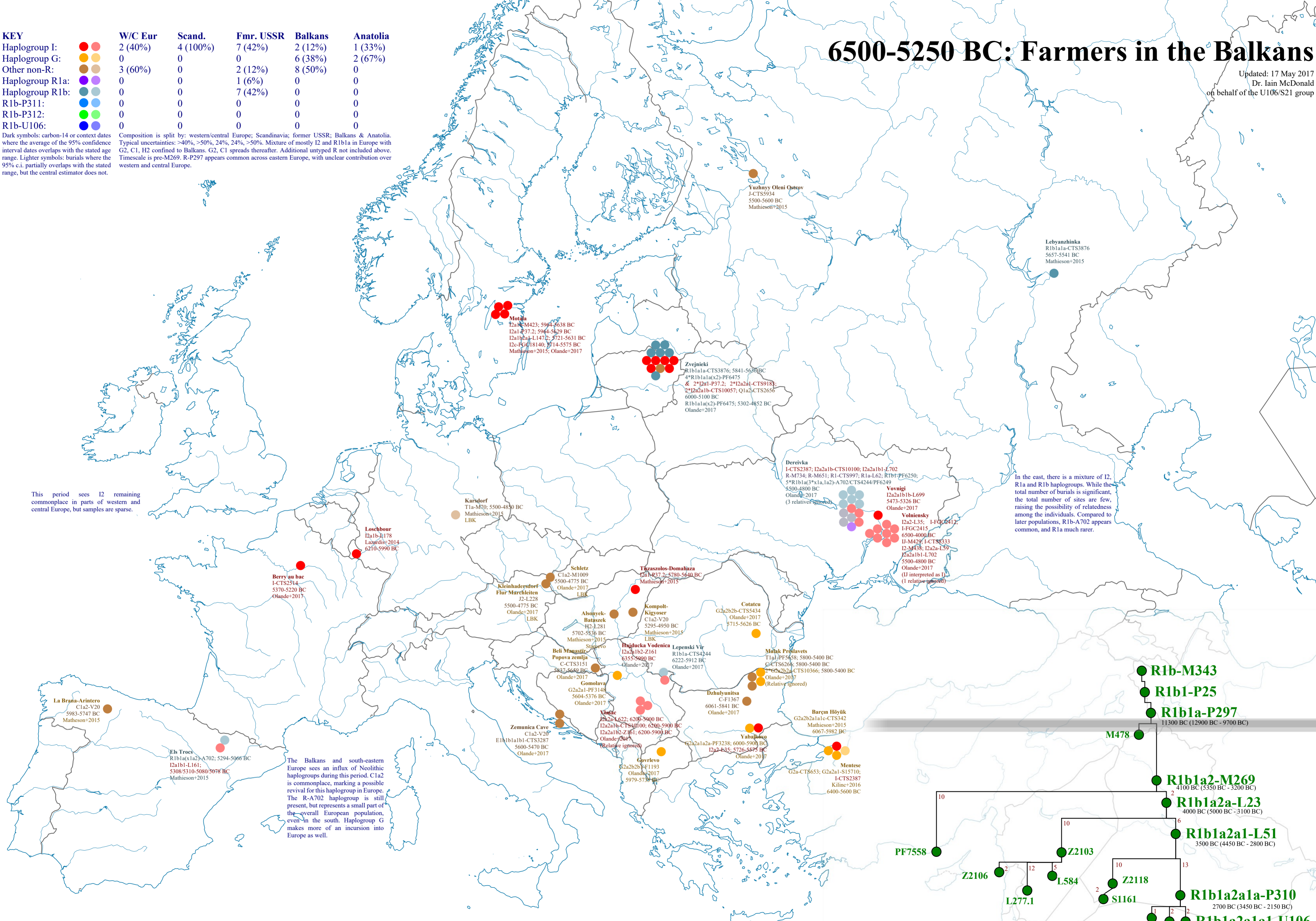
KEY	W/C Eur	Scand.	Fmr. USSR	Balkans	Anatolia
Haplogroup I:	2 (40%)	4 (100%)	7 (42%)	2 (12%)	1 (33%)
Haplogroup G:	0	0	0	6 (38%)	2 (67%)
Other non-R:	3 (60%)	0	2 (12%)	8 (50%)	0
Haplogroup R1a:	0	0	1 (6%)	0	0
Haplogroup R1b:	0	0	7 (42%)	0	0
R1b-P311:	0	0	0	0	0
R1b-P312:	0	0	0	0	0
R1b-U106:	0	0	0	0	0

Dark symbols: carbon-14 or context dates where the average of the 95% confidence interval dates overlaps with the stated age range. Lighter symbols: burials where the 95% c.i. partially overlaps with the stated range, but the central estimator does not.

Composition is split by: western/central Europe; Scandinavia; former USSR; Balkans & Anatolia. Typical uncertainties: >40%, >50%, 24%, 24%, >50%. Mixture of mostly I2 and R1b1a in Europe with G2, C1, H2 confined to Balkans. G2, C1 spreads thereafter. Additional untyped R not included above. Timescale is pre-M269. R-P297 appears common across eastern Europe, with unclear contribution over western and central Europe.

This period sees I2 remaining commonplace in parts of western and central Europe, but samples are sparse.

In the east, there is a mixture of I2, R1a and R1b haplogroups. While the total number of burials is significant, the total number of sites are few, raising the possibility of relatedness among the individuals. Compared to later populations, R1b-A702 appears common, and R1a much rarer.



The Balkans and south-eastern Europe sees an influx of Neolithic haplogroups during this period. C1a2 is commonplace, marking a possible revival for this haplogroup in Europe. The R-A702 haplogroup is still present, but represents a small part of the overall European population, even in the south. Haplogroup G makes more of an incursion into Europe as well.

# 5250-4500 BC: Farmers in Europe

Updated: 23 May 2017  
 Dr. Iain McDonald  
 on behalf of the U106/S21 group

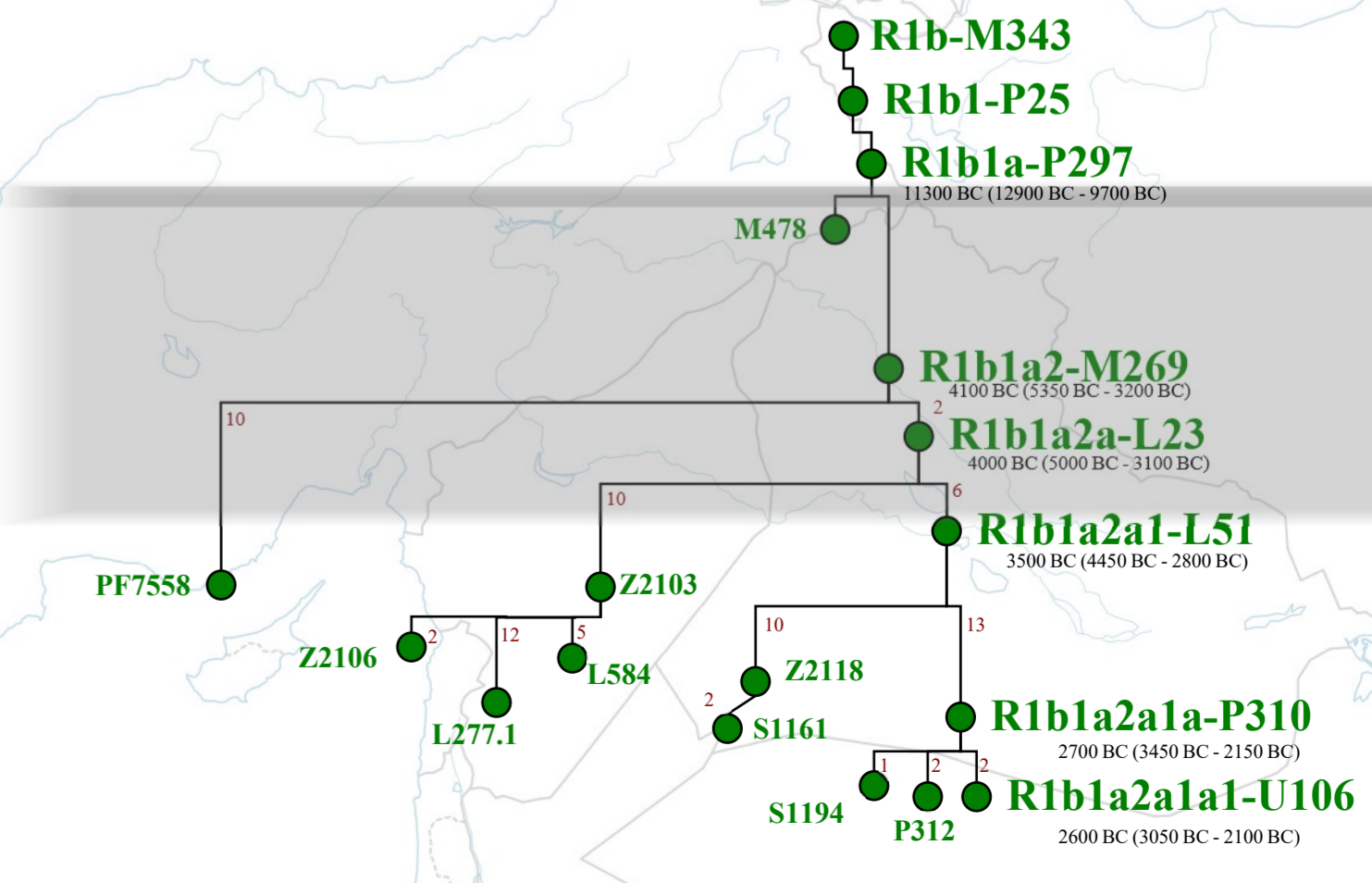
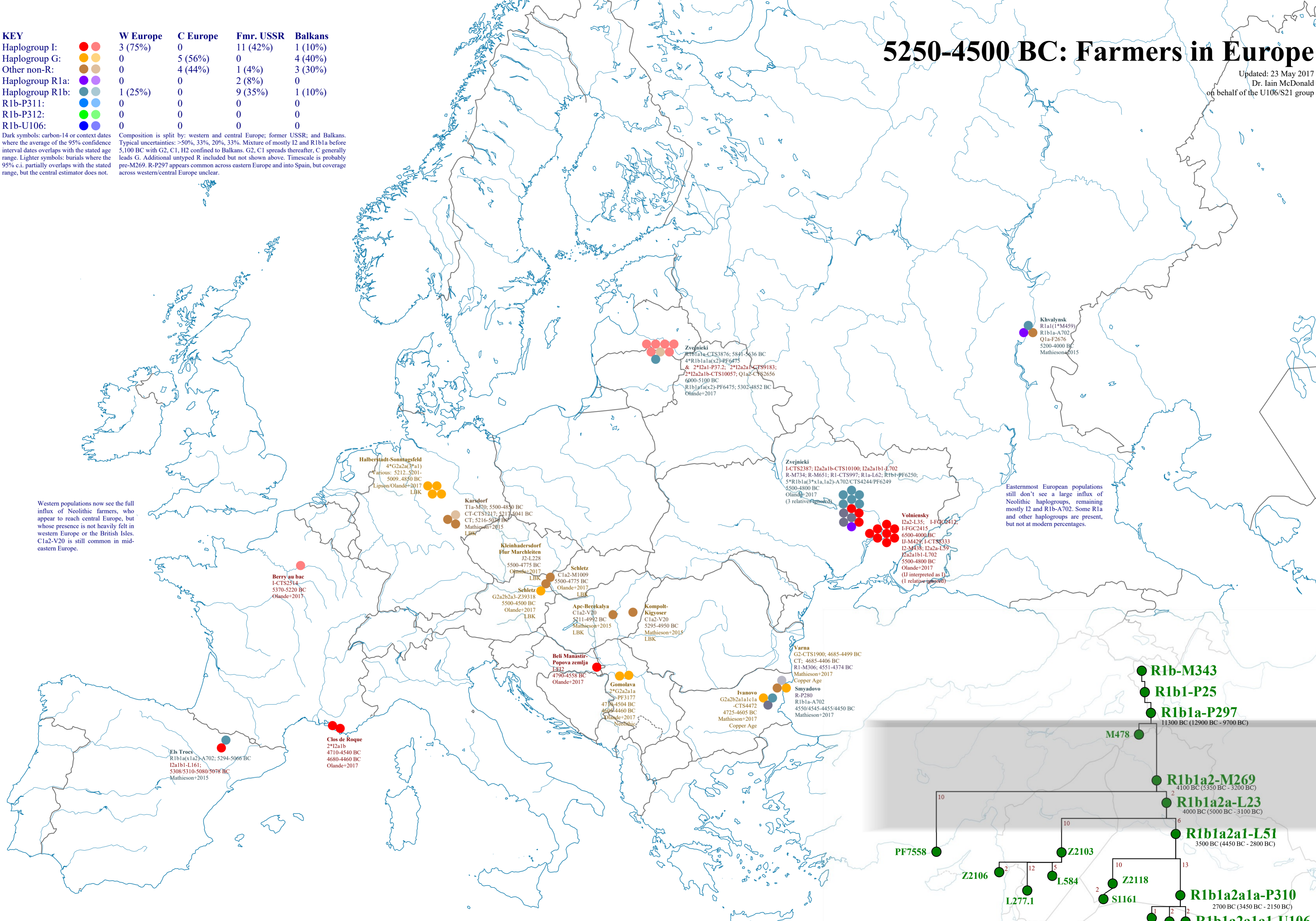
KEY	W Europe	C Europe	Fmr. USSR	Balkans
Haplogroup I:	3 (75%)	0	11 (42%)	1 (10%)
Haplogroup G:	0	5 (56%)	0	4 (40%)
Other non-R:	0	4 (44%)	1 (4%)	3 (30%)
Haplogroup R1a:	0	0	2 (8%)	0
Haplogroup R1b:	1 (25%)	0	9 (35%)	1 (10%)
R1b-P311:	0	0	0	0
R1b-P312:	0	0	0	0
R1b-U106:	0	0	0	0

Dark symbols: carbon-14 or context dates where the average of the 95% confidence interval dates overlaps with the stated age range. Lighter symbols: burials where the 95% c.i. partially overlaps with the stated range, but the central estimator does not.

Composition is split by: western and central Europe; former USSR; and Balkans. Typical uncertainties: >50%, 33%, 20%, 33%. Mixture of mostly I2 and R1b1a before 5,100 BC with G2, C1, H2 confined to Balkans. G2, C1 spreads thereafter, C generally leads G. Additional untyped R included but not shown above. Timescale is probably pre-M269. R-P297 appears common across eastern Europe and into Spain, but coverage across western/central Europe unclear.

Western populations now see the full influx of Neolithic farmers, who appear to reach central Europe, but whose presence is not heavily felt in western Europe or the British Isles. C1a2-V20 is still common in mid-eastern Europe.

Easternmost European populations still don't see a large influx of Neolithic haplogroups, remaining mostly I2 and R1b-A702. Some R1a and other haplogroups are present, but not at modern percentages.



# 4500-3400 BC: The spread of copper

Updated: 24 May 2017  
 Dr. Iain McDonald  
 on behalf of the U106/S21 group

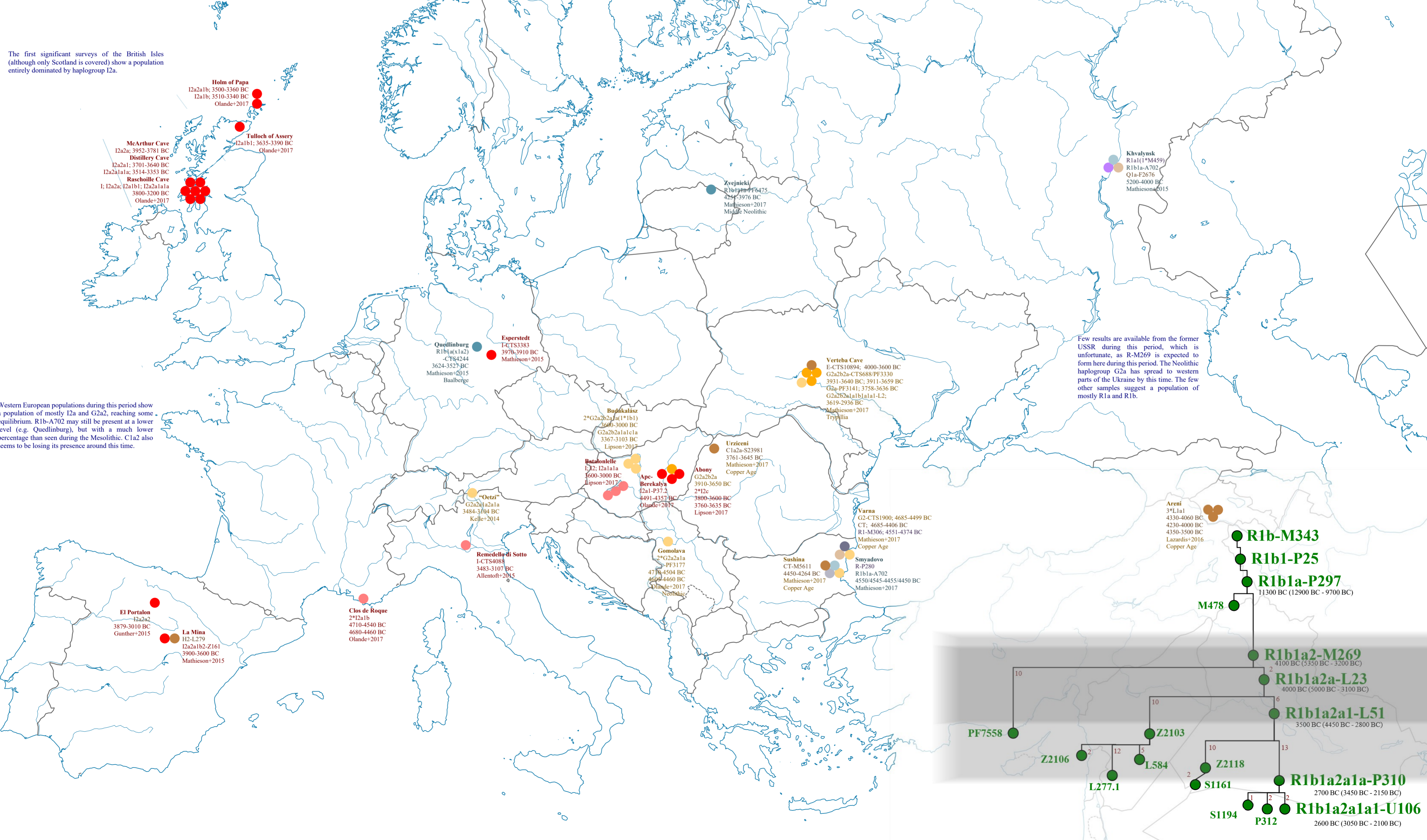
KEY	Brit. Isles	W/C Europe	Fmr. USSR	Balkans
Haplogroup I:	10 (100%)	3 (60%)	0	3 (60%)
Haplogroup G:	0	0	3 (38%)	1 (20%)
Other non-R:	0	1 (20%)	4 (50%)	2 (40%)
Haplogroup R1a:	0	0	0	0
Haplogroup R1b:	0	1 (20%)	1 (13%)	0
R1b-P311:	0	0	0	0
R1b-P312:	0	0	0	0
R1b-U106:	0	0	0	0

Dark symbols: carbon-14 or context dates where the average of the 95% confidence interval dates overlaps with the stated age range. Lighter symbols: burials where the 95% c.i. partially overlaps with the stated range, but the central estimator does not.

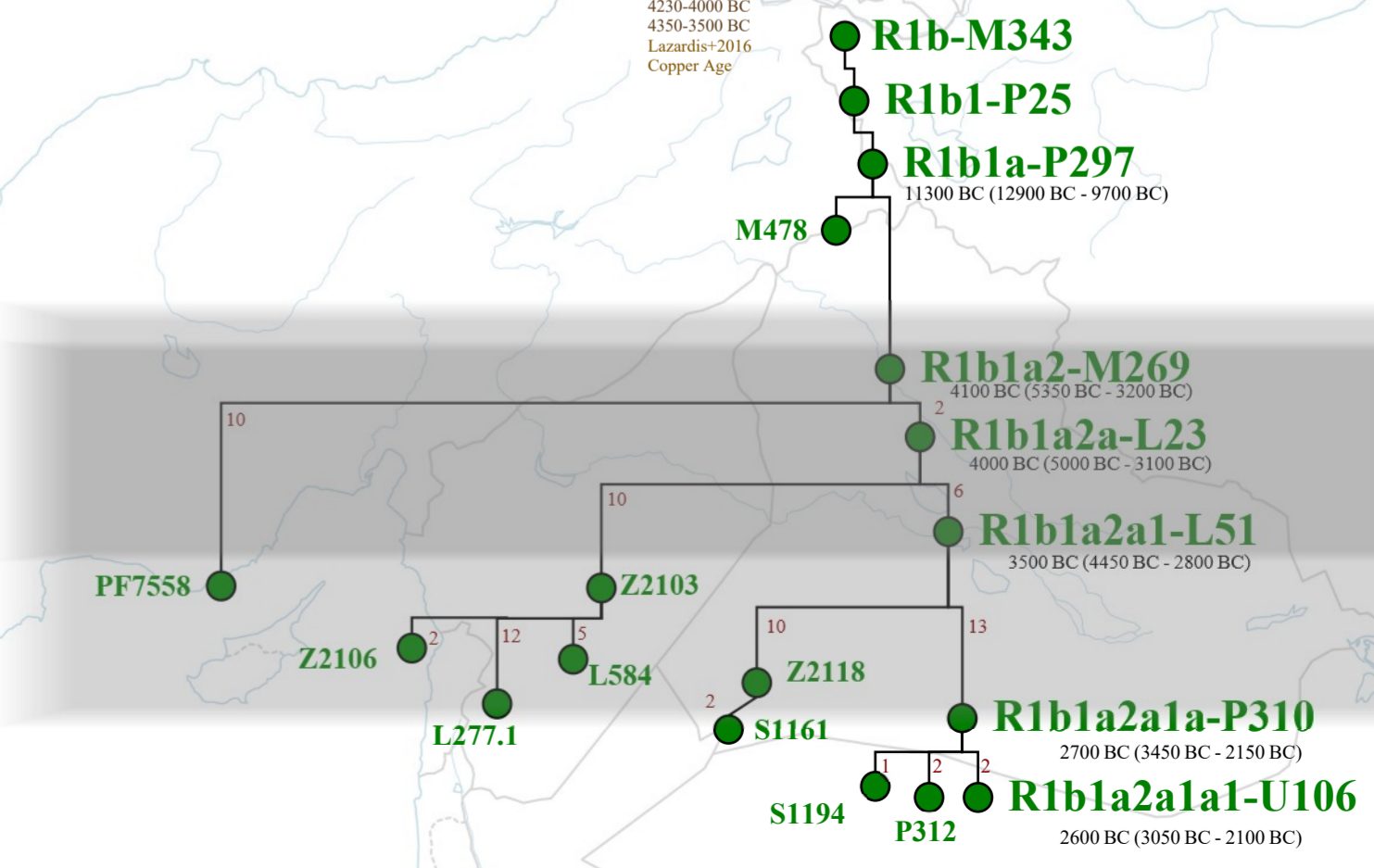
Composition is split by: British Isles; western/central Europe; former USSR; and Balkans. Typical uncertainties: 32%, >45%, 35%, >45%. Fewer burials during this period, possible archaeologically attested population decline. Timescale may be pre-M269. R-P297 still present in northern continental Europe, but notable absence of haplogroup R results overall. Neolithic haplotypes now present in Ukraine. No impact in Scotland.

The first significant surveys of the British Isles (although only Scotland is covered) show a population entirely dominated by haplogroup I2a.

Western European populations during this period show a population of mostly I2a and G2a2, reaching some equilibrium. R1b-A702 may still be present at a lower level (e.g. Quedlinburg), but with a much lower percentage than seen during the Mesolithic. C1a2 also seems to be losing its presence around this time.



Few results are available from the former USSR during this period, which is unfortunate, as R-M269 is expected to form here during this period. The Neolithic haplogroup G2a has spread to western parts of the Ukraine by this time. The few other samples suggest a population of mostly R1a and R1b.



# 3400-2925 BC: The rise of the Yamnaya

Updated: 15 June 2017  
 Dr. Iain McDonald  
 on behalf of the U106/S21 group

KEY	Brit. Isles	W/C Europe	Fmr. USSR	Balkans
Haplogroup I:	9 (100%)	12 (63%)	0	4 (80%)
Haplogroup G:	0	7 (37%)	1 (14%)	0
Other non-R:	0	0	0	1 (20%)
Haplogroup R1a:	0	0	0	0
Haplogroup R1b:	0	1	6 (86%)	0
R1b-P311:	0	0	0	0
R1b-P312:	0	0	0	0
R1b-U106:	0	0	0	0

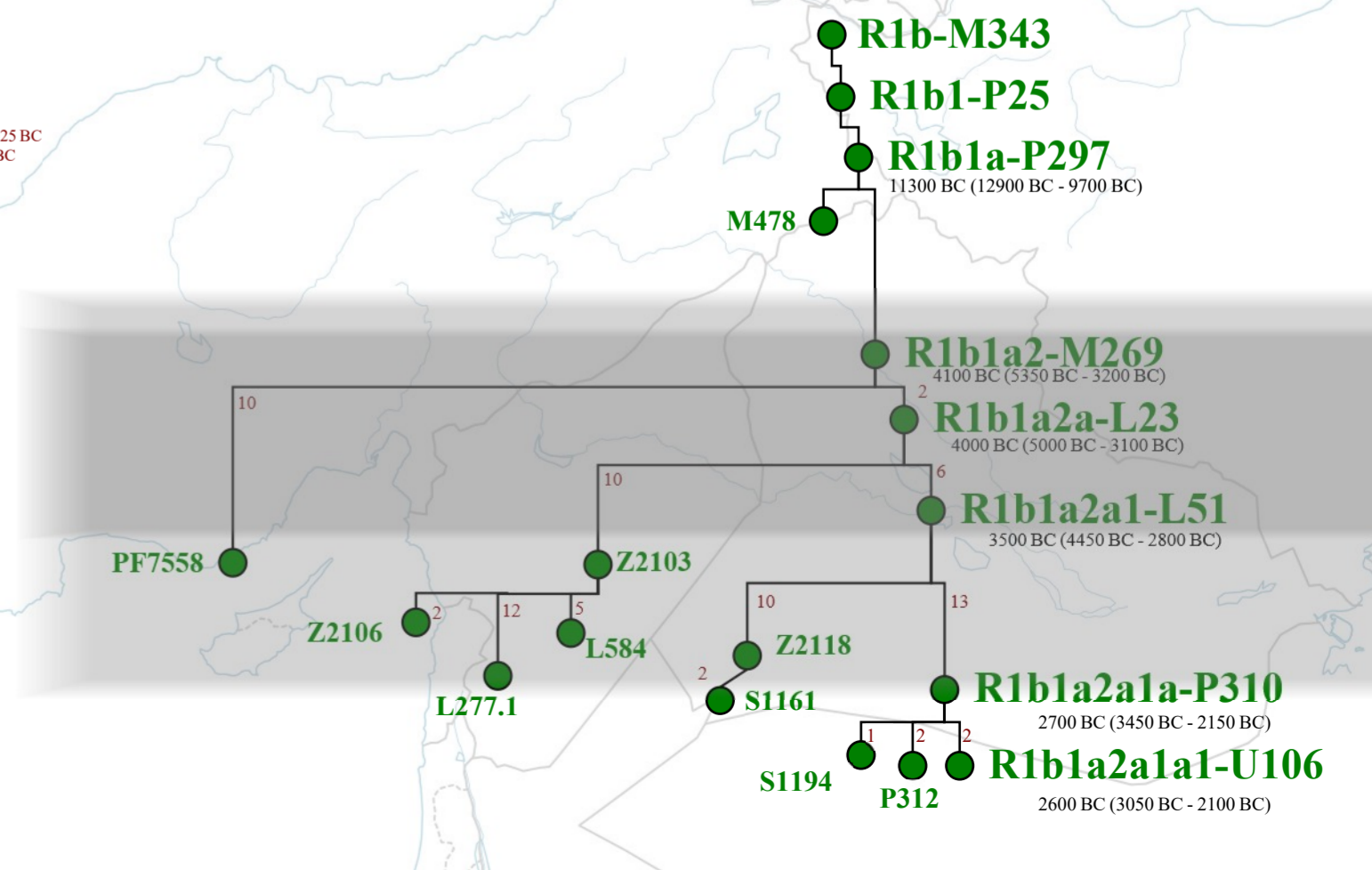
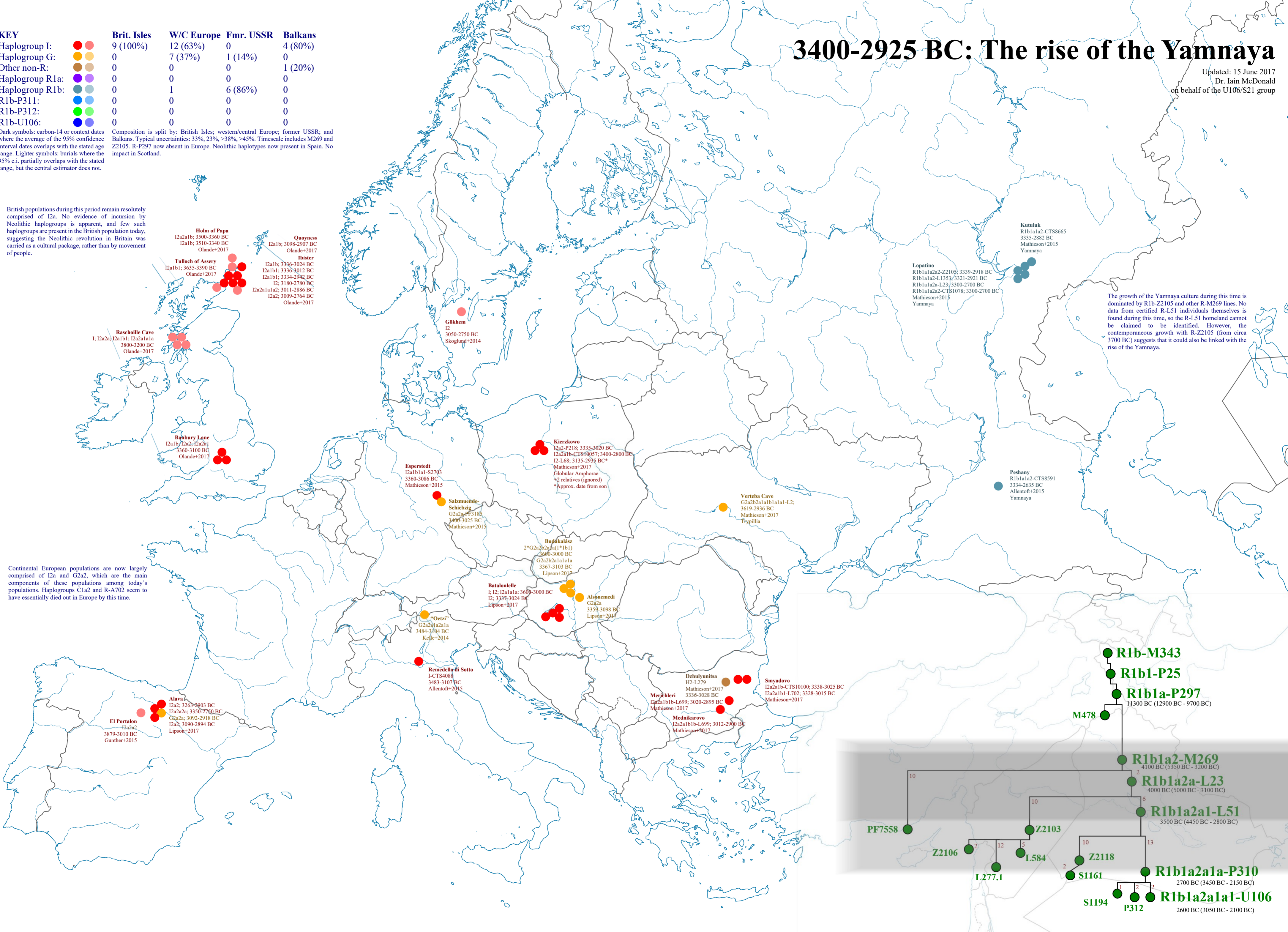
Dark symbols: carbon-14 or context dates where the average of the 95% confidence interval dates overlaps with the stated age range. Lighter symbols: burials where the 95% c.i. partially overlaps with the stated range, but the central estimator does not.

Composition is split by: British Isles; western/central Europe; former USSR; and Balkans. Typical uncertainties: 33%, 23%, >38%, >45%. Timescale includes M269 and Z2105. R-P297 now absent in Europe. Neolithic haplotypes now present in Spain. No impact in Scotland.

British populations during this period remain resolutely comprised of I2a. No evidence of incursion by Neolithic haplogroups is apparent, and few such haplogroups are present in the British population today, suggesting the Neolithic revolution in Britain was carried as a cultural package, rather than by movement of people.

The growth of the Yamnaya culture during this time is dominated by R1b-Z2105 and other R-M269 lines. No data from certified R-L51 individuals themselves is found during this time, so the R-L51 homeland cannot be claimed to be identified. However, the contemporaneous growth with R-Z2105 (from circa 3700 BC) suggests that it could also be linked with the rise of the Yamnaya.

Continental European populations are now largely comprised of I2a and G2a2, which are the main components of these populations among today's populations. Haplogroups C1a2 and R-A702 seem to have essentially died out in Europe by this time.





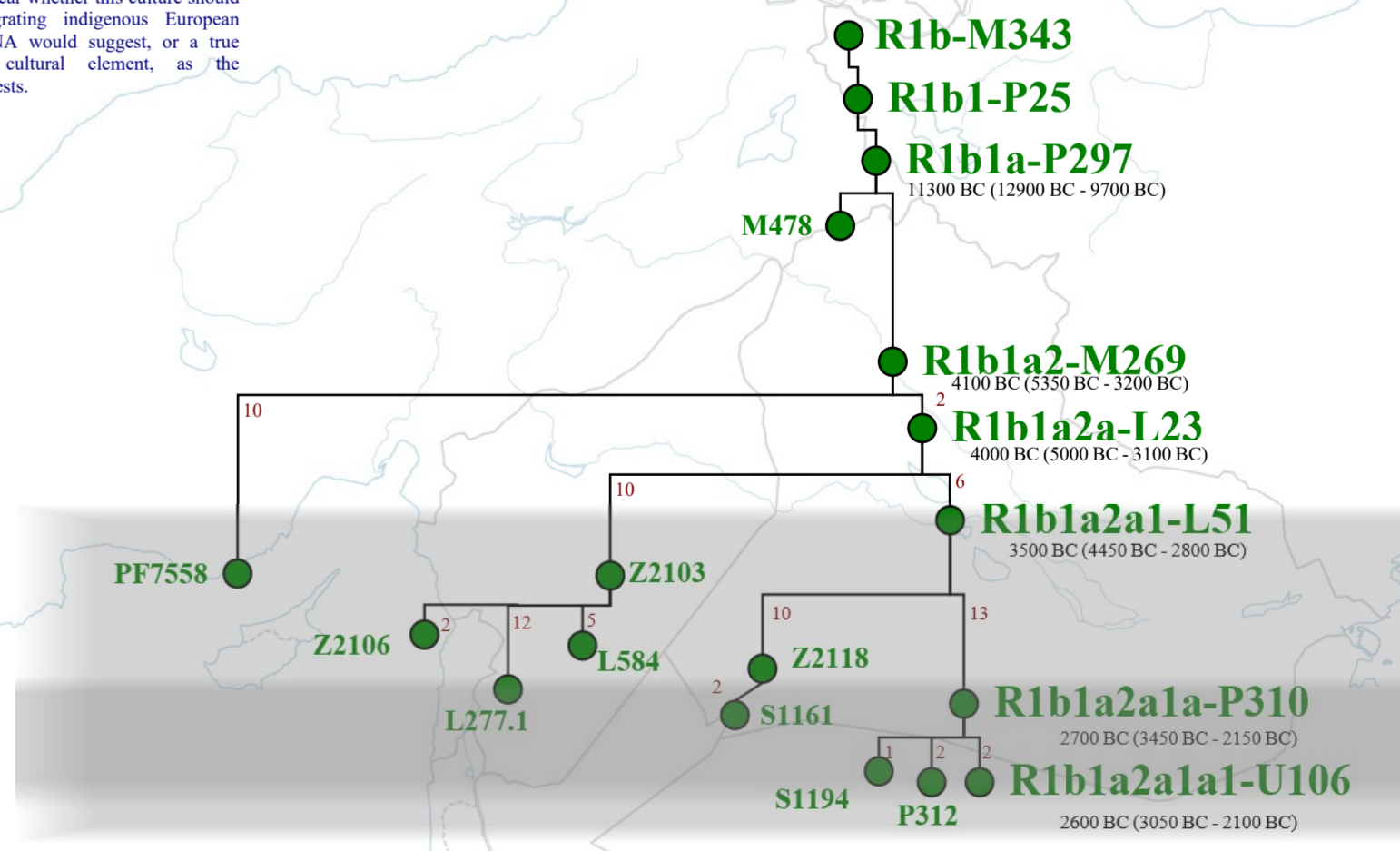
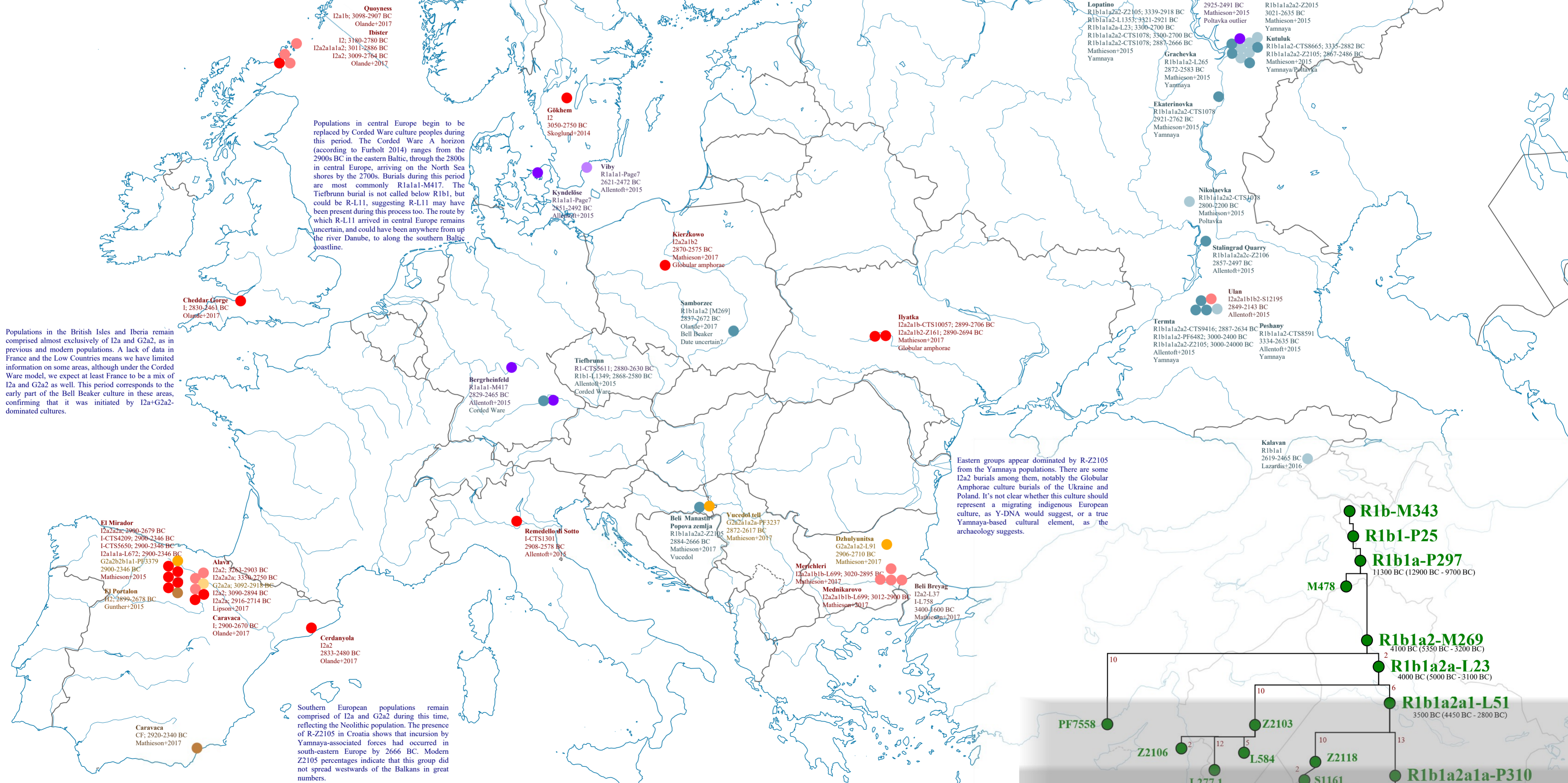
# 2925-2550 BC: The Corded Ware Culture

Updated: 17 July 2017  
 Dr. Iain McDonald  
 on behalf of the U106/S21 group

KEY	Brit. Isles	C. Europe	S. Europe	Fmr. USSR	Balkans
Haplogroup I:	2 (100%)	1 (17%)	9 (82%)	2 (17%)	0
Haplogroup G:	0	0	1 (9%)	0	2 (67%)
Other non-R:	0	0	1 (9%)	0	0
Haplogroup R1a:	0	3 (50%)	0	1 (8%)	0
Haplogroup R1b:	0	2 (33%)	0	9 (75%)	1 (33%)
R1b-P311:	0	0	0	0	0
R1b-P312:	0	0	0	0	0
R1b-U106:	0	0	0	0	0

Dark symbols: carbon-14 or context dates where the average of the 95% confidence interval dates overlaps with the stated age range. Lighter symbols: burials where the 95% c.i. partially overlaps with the stated range, but the central estimator does not. Burials with 95% c.i. starting after 2571 BC and central estimators after 2410 BC are not shown in this case.

Composition is split by: British Isles; central Europe (Denmark, Germany, Poland); southern Europe (Spain, Italy) former USSR (Russia, Ukraine); and Balkans. Typical uncertainties: >70%, >40%, 30%, 29% and >57%. Timescale includes M269 and may include L11. R-M269 appears in Europe by:  
 \* Poland: 2837-2672 BC (M269 or equivalent but see: <http://www.anthrogenica.com/showthread.php?10565/page15>);  
 \* Croatia: 2884-2666 BC (Z2105);  
 \* Germany: possibly 2880-2630 BC (R1); probably 2868-2580 BC (R1b1).



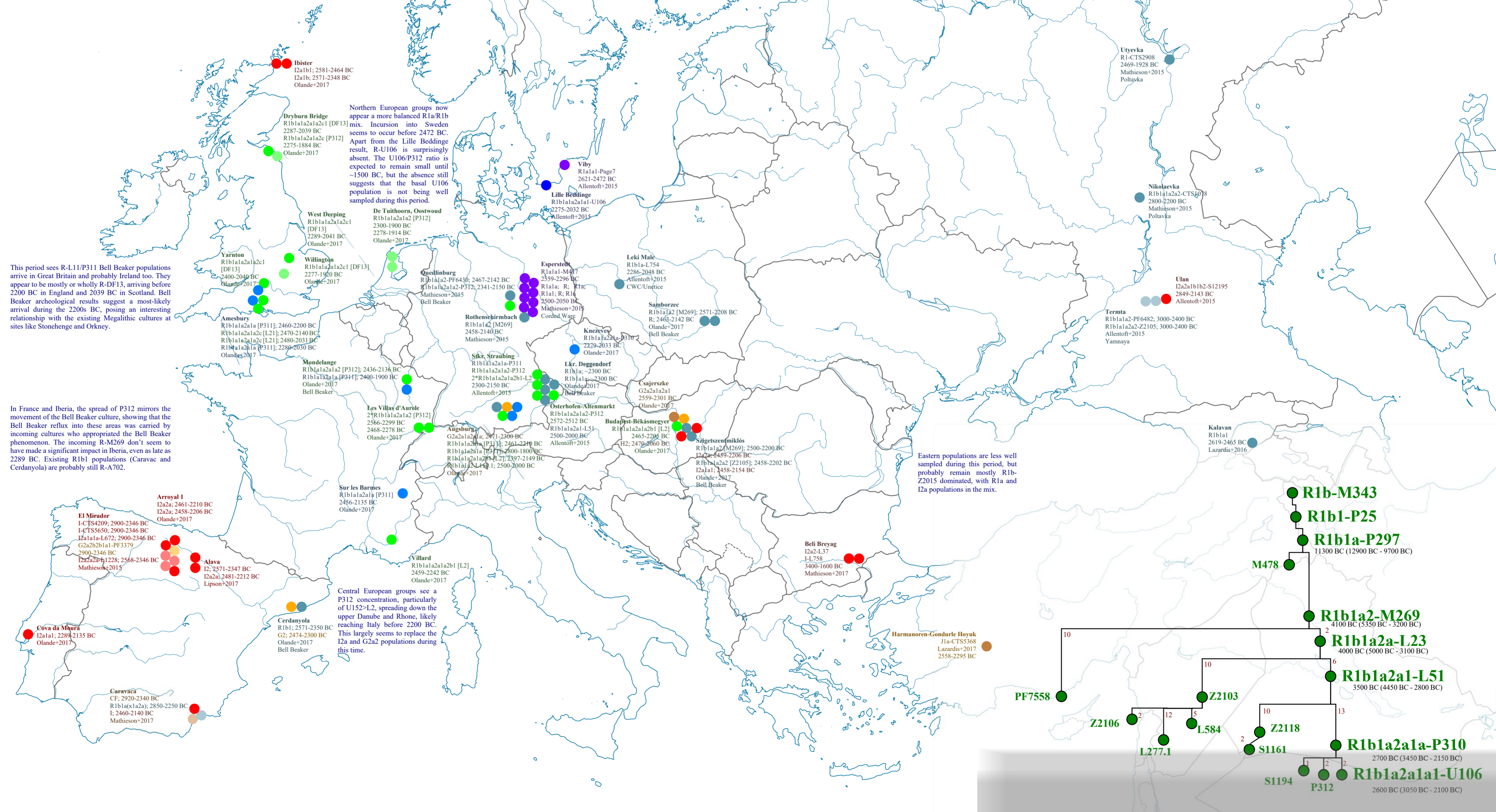
# 2550-2140 BC: The Bell Beaker Culture

Updated: 17 July 2017  
 Dr. Iain McDonald  
 on behalf of the U106/S21 group

KEY	Brit. Isles	Iberia	C. Europe	Scandinavia	S.E. Europe	Fmr USSR
Haplogroup I:	2 (22%)	7 (78%)	0	0	4 (44%)	1 (25%)
Haplogroup G:	0	1 (11%)	1 (3%)	0	1 (11%)	0
Other non-R:	0	0	0	0	1 (11%)	0
Haplogroup R1a:	0	0	8 (24%)	1 (50%)	0	1 (25%)
Haplogroup R1b:	0	1 (11%)	10 (29%)	0	2 (22%)	2 (50%)
R1b-P311:	2 (22%)	0	5 (15%)	0	0	0
R1b-P312:	5 (56%)	0	10 (29%)	0	1 (11%)	0
R1b-U106:	0	0	0	1 (50%)	0	0

Dark symbols: carbon-14 or context dates where the average of the 95% confidence interval dates overlaps with the stated age range. Lighter symbols: burials where the 95% c.i. partially overlaps with the stated range, but the central estimator does not. Burials with 95% c.i. ceasing before 2460 BC and central estimators before 2645 BC, or beginning after 2210 BC are not shown in this case.

Composition is split by: British Isles; Spain/Portugal; western/central Europe from France to Poland, Austria to the Netherlands; Scandinavia (southern Sweden); Hungary and the Balkans; and the former USSR. Typical uncertainties: 33%, 33%, 17%, >50%.  
 \* Poland: 2837-2672 BC (M269 or equivalent);  
 \* Croatia: 2884-2666 BC (Z2105);  
 \* Germany: possibly 2880-2630 BC (R1); probably 2868-2580 BC (R1b1);  
 \* France: 2566-2299 BC (P312);  
 \* Hungary: 2465-2205 BC (L2);  
 \* England: 2460-2200 BC (P311);  
 \* Scotland: 2287-2039 BC (DF13);  
 \* Sweden: 2275-2032 BC (U106);  
 \* Netherlands: 2278-1914 BC (P312).

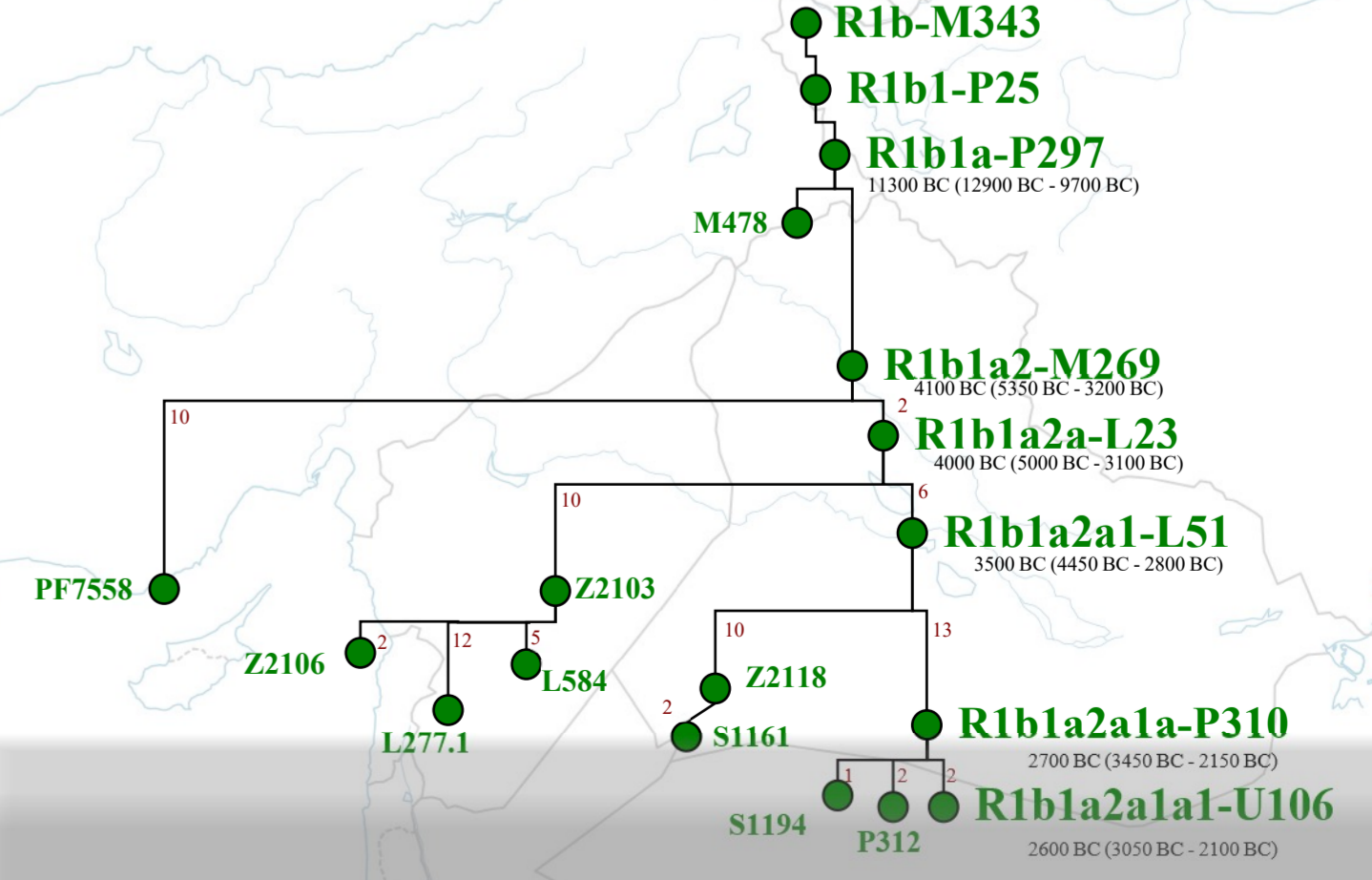


This period sees R-L11/P311 Bell Beaker populations arrive in Great Britain and probably Ireland too. They appear to be mostly or wholly R-DF13, arriving before 2200 BC in England and 2039 BC in Scotland. Bell Beaker archaeological results suggest a most-likely arrival during the 2200s BC, posing an interesting relationship with the existing Megalithic cultures at sites like Stonehenge and Orkney.

Northern European groups now appear a more balanced R1a/R1b mix. Incursion into Sweden seems to occur before 2472 BC. Apart from the Lille Beddinge result, R-U106 is surprisingly absent. The U106/P312 ratio is expected to remain small until ~1500 BC, but the absence still suggests that the basal U106 population is not being well sampled during this period.

In France and Iberia, the spread of P312 mirrors the movement of the Bell Beaker culture, showing that the Bell Beaker reflux into these areas was carried by incoming cultures who appropriated the Bell Beaker phenomenon. The incoming R-M269 don't seem to have made a significant impact in Iberia, even as late as 2289 BC. Existing R1b1 populations (Caravaca and Cerdanyola) are probably still R-A702.

Eastern populations are less well sampled during this period, but probably remain mostly R1b-Z2105 dominated, with R1a and I2a populations in the mix.



# 2140-1950 BC: Late Bell Beaker

Updated: 27 July 2017  
 Dr. Iain McDonald  
 on behalf of the U106/S21 group

KEY	Brit. Isles	C. Europe	Fmr USSR
Haplogroup I:	1 (10%)	3 (37%)	0
Haplogroup G:	0	0	0
Other non-R:	0	0	0
Haplogroup R1a:	0	0	1 (100%)
Haplogroup R1b:	0	0	0
R1b-P311:	2 (20%)	0	0
R1b-P312:	7 (70%)	5 (63%)	0
R1b-U106:	0	0	0

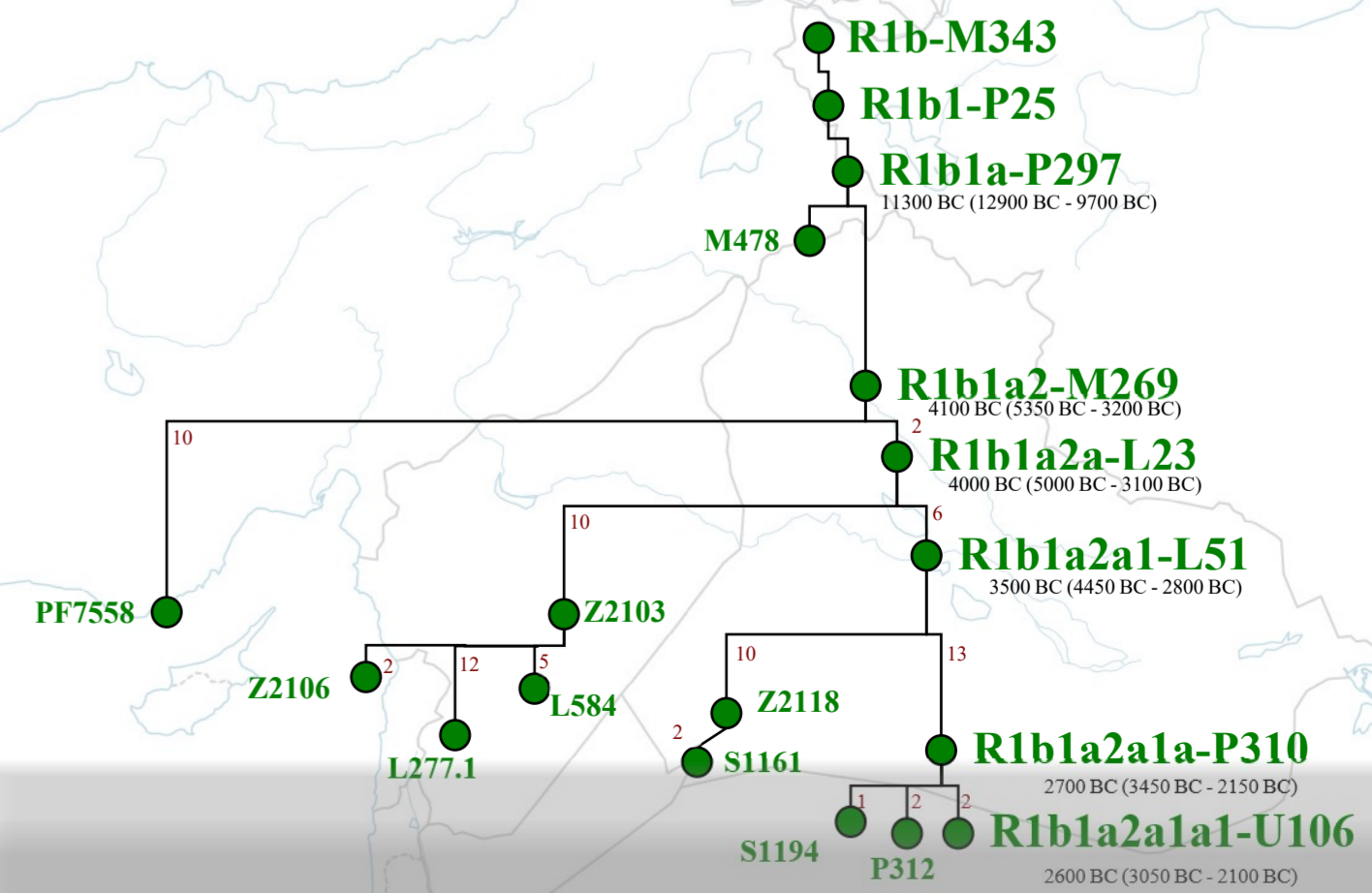
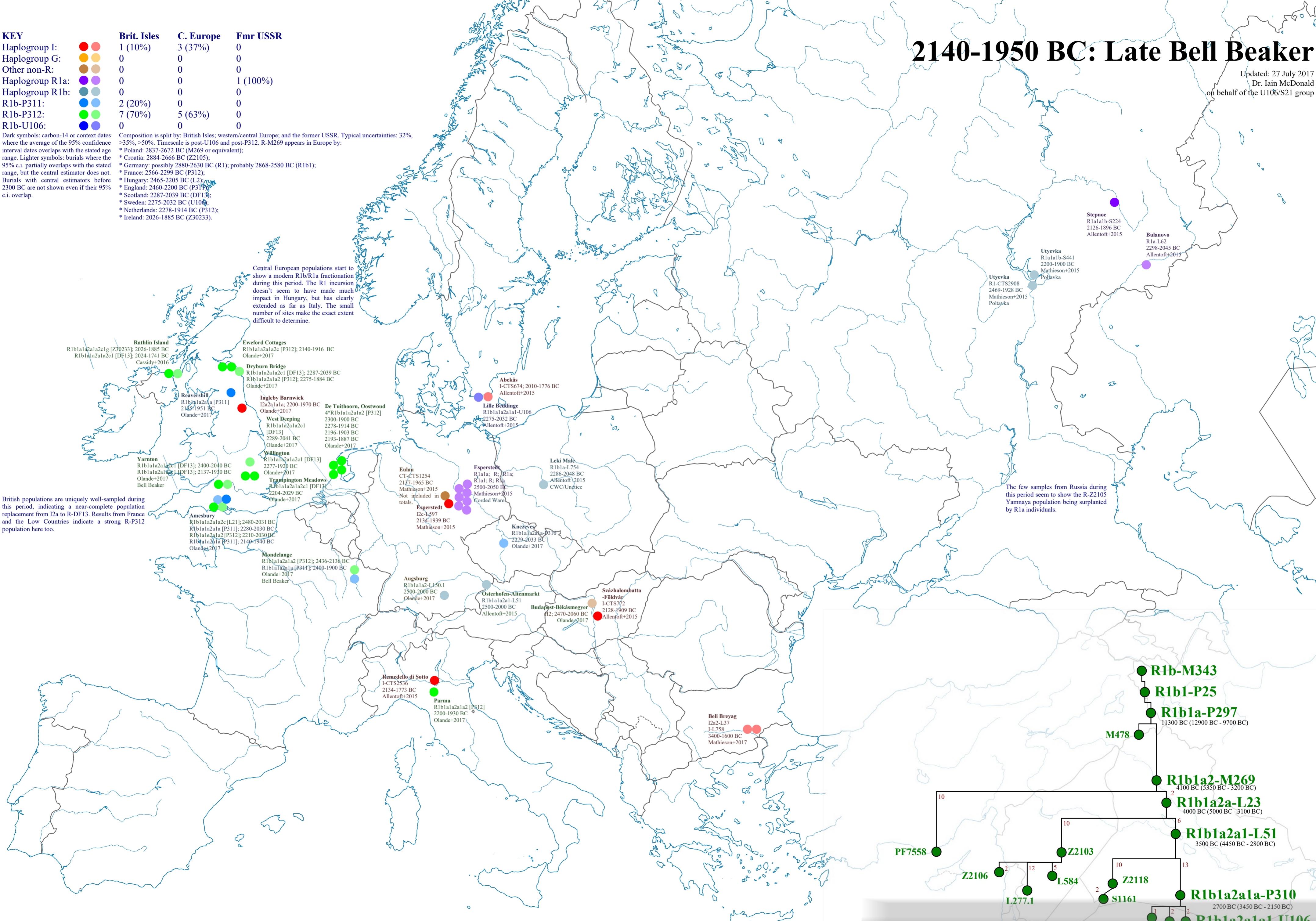
Dark symbols: carbon-14 or context dates where the average of the 95% confidence interval dates overlaps with the stated age range. Lighter symbols: burials where the 95% c.i. partially overlaps with the stated range, but the central estimator does not. Burials with central estimators before 2300 BC are not shown even if their 95% c.i. overlap.

Composition is split by: British Isles; western/central Europe; and the former USSR. Typical uncertainties: 32%, >35%, >50%. Timescale is post-U106 and post-P312. R-M269 appears in Europe by:  
 \* Poland: 2837-2672 BC (M269 or equivalent);  
 \* Croatia: 2884-2666 BC (Z2105);  
 \* Germany: possibly 2880-2630 BC (R1); probably 2868-2580 BC (R1b1);  
 \* France: 2566-2299 BC (P312);  
 \* Hungary: 2465-2205 BC (L2);  
 \* England: 2460-2200 BC (P311);  
 \* Scotland: 2287-2039 BC (DF13);  
 \* Sweden: 2275-2032 BC (U106);  
 \* Netherlands: 2278-1914 BC (P312);  
 \* Ireland: 2026-1885 BC (Z30233).

Central European populations start to show a modern R1b/R1a fractionation during this period. The R1 incursion doesn't seem to have made much impact in Hungary, but has clearly extended as far as Italy. The small number of sites make the exact extent difficult to determine.

The few samples from Russia during this period seem to show the R-Z2105 Yamnaya population being supplanted by R1a individuals.

British populations are uniquely well-sampled during this period, indicating a near-complete population replacement from I2a to R-DF13. Results from France and the Low Countries indicate a strong R-P312 population here too.



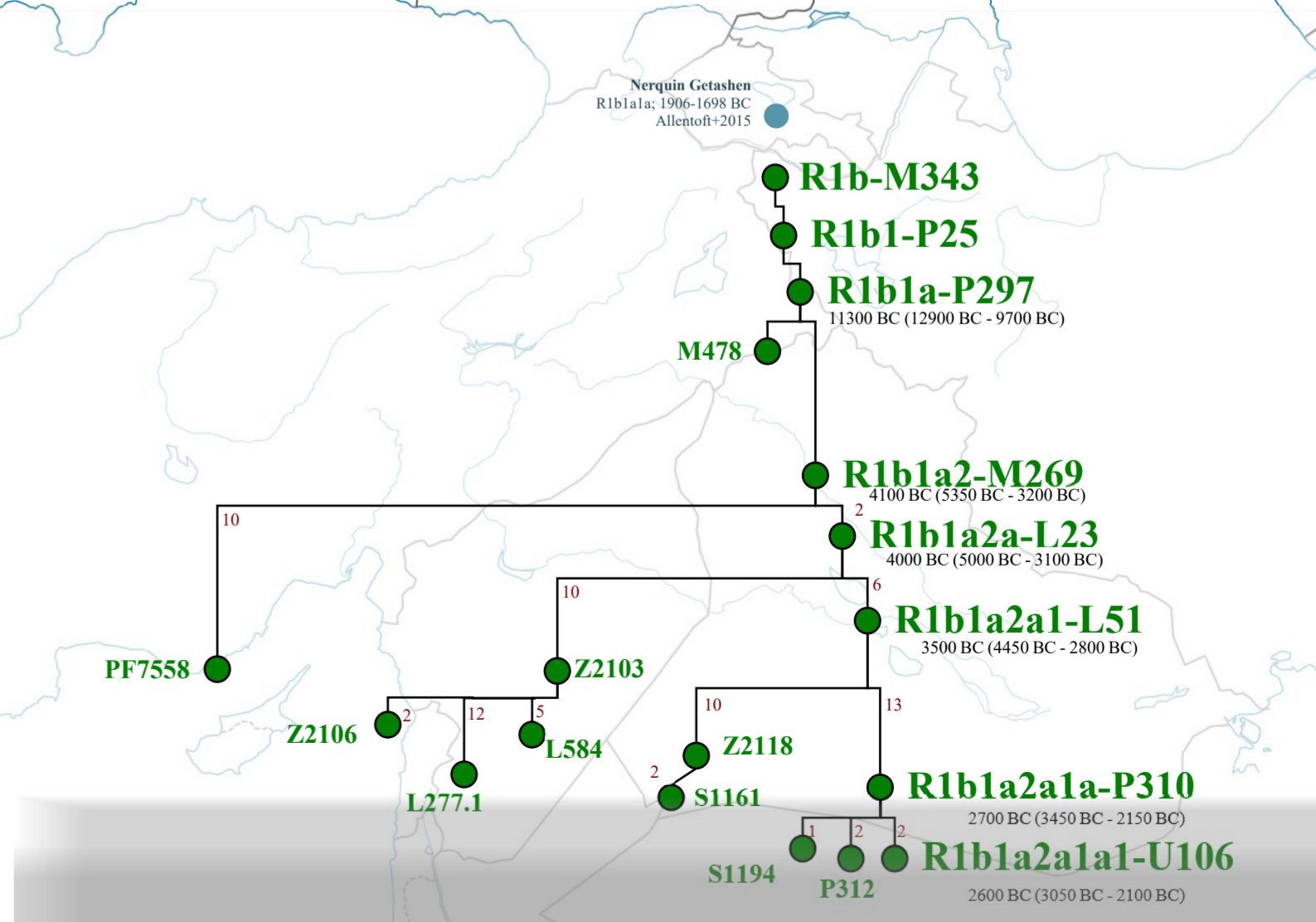
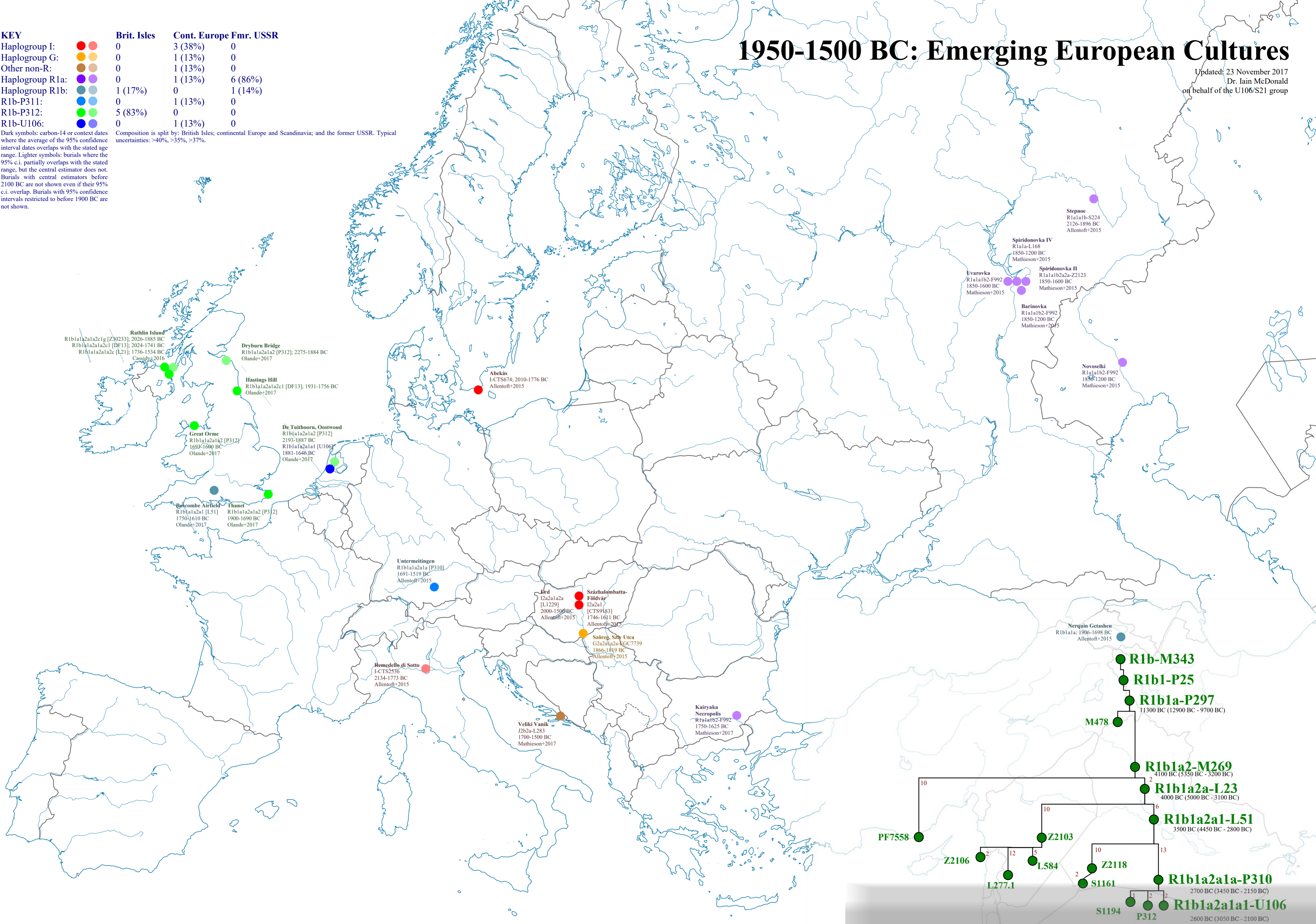
# 1950-1500 BC: Emerging European Cultures

Updated: 23 November 2017  
 Dr. Iain McDonald  
 on behalf of the U106/S21 group

KEY	Brit. Isles	Cont. Europe	Fmr. USSR
Haplogroup I:	0	3 (38%)	0
Haplogroup G:	0	1 (13%)	0
Other non-R:	0	1 (13%)	0
Haplogroup R1a:	0	1 (13%)	6 (86%)
Haplogroup R1b:	1 (17%)	0	1 (14%)
R1b-P311:	0	1 (13%)	0
R1b-P312:	5 (83%)	0	0
R1b-U106:	0	1 (13%)	0

Dark symbols: carbon-14 or context dates where the average of the 95% confidence interval dates overlaps with the stated age range. Lighter symbols: burials where the 95% c.i. partially overlaps with the stated range, but the central estimator does not. Burials with central estimators before 2100 BC are not shown even if their 95% c.i. overlap. Burials with 95% confidence intervals restricted to before 1900 BC are not shown.

Composition is split by: British Isles; continental Europe and Scandinavia; and the former USSR. Typical uncertainties: >40%, >35%, >37%.



**Rathlin Island**  
 R1b1a1a2a2c1g [Z30233]; 2026-1885 BC  
 R1b1a1a2a2c1 [DF13]; 2024-1741 BC  
 R1b1a1a2a2c [L21]; 1736-1534 BC  
 Cassidy+2016

**Dryburn Bridge**  
 R1b1a1a2a1a2 [P312]; 2275-1884 BC  
 Olande+2017

**Hastings Hill**  
 R1b1a1a2a2c1 [DF13]; 1931-1756 BC  
 Olande+2017

**Great Orme**  
 R1b1a1a2a1a2 [P312]  
 1693-1600 BC  
 Olande+2017

**De Tuithoorn, Oostwoud**  
 R1b1a1a2a1a2 [P312]  
 2193-1887 BC  
 R1b1a1a2a1a1 [U106]  
 1881-1646 BC  
 Olande+2017

**Bakcombe Airfield**  
 R1b1a1a2a1 [L51]  
 1750-1610 BC  
 Olande+2017

**Thanet**  
 R1b1a1a2a1a2 [P312]  
 1900-1690 BC  
 Olande+2017

**Abekás**  
 I-CTS674; 2010-1776 BC  
 Allentoft+2015

**Untermeitingen**  
 R1b1a1a2a1a [P310]  
 1691-1519 BC  
 Allentoft+2015

**Jód**  
 I2a2a1a2a [L1229]  
 2000-1500 BC  
 Allentoft+2015

**Százhalombatta-Földvár**  
 I2a2a1 [CTS9183]  
 1746-1611 BC  
 Allentoft+2015

**Szöreg, Szig Utca**  
 G2a2a1a2a-KGC7739  
 1866-1819 BC  
 Allentoft+2015

**Remedello di Sotto**  
 I-CTS2356  
 2134-1773 BC  
 Allentoft+2015

**Veliki Vanik**  
 J2b2a-L283  
 1700-1500 BC  
 Mathieson+2017

**Kairyaka Necropolis**  
 R1a1a1b2-F992  
 1750-1625 BC  
 Mathieson+2017

**Stepnoe**  
 R1a1a1b-S224  
 2126-1896 BC  
 Allentoft+2015

**Spiridonovka IV**  
 R1a1a-L168  
 1850-1200 BC  
 Mathieson+2015

**Uvarovka**  
 R1a1a1b2-F992  
 1850-1600 BC  
 Mathieson+2015

**Spiridonovka II**  
 R1a1a1b2a2a-Z2123  
 1850-1600 BC  
 Mathieson+2015

**Barinovka**  
 R1a1a1b2-F992  
 1850-1200 BC  
 Mathieson+2015

**Novoselki**  
 R1a1a1b2-F992  
 1850-1200 BC  
 Mathieson+2015

**Nerquin Getashen**  
 R1b1a1a; 1906-1698 BC  
 Allentoft+2015

**R1b-M343**  
**R1b1-P25**  
**R1b1a-P297**  
 11300 BC (12900 BC - 9700 BC)

M478

**R1b1a2-M269**  
 4100 BC (5350 BC - 3200 BC)  
**R1b1a2a-L23**  
 4000 BC (5000 BC - 3100 BC)

**R1b1a2a1-L51**  
 3500 BC (4450 BC - 2800 BC)

PF7558

Z2106

Z2103

L277.1

L584

Z2118

S1161

**R1b1a2a1a-P310**  
 2700 BC (3450 BC - 2150 BC)

S1194

**R1b1a2a1a-U106**  
 2600 BC (3050 BC - 2100 BC)

P312