Haplotypes of R1b1a2-P312 and related subclades: origin and “ages” of most recent common ancestors

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SUMMARY

A detailed analysis of a 2299 of 67 marker haplotype dataset provided by Michael Walsh, administrator of R1b1a2-L21 site http://www.familytreedna.com/public/RL21/default.aspx?section=yresults has allowed to identify base (ancestral) 67 marker haplotypes and timespans to their common ancestors as follows:

<table>
<thead>
<tr>
<th>Haplotype</th>
<th>Loci</th>
<th>Time span (ybp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>R1b1a2</td>
<td>L265, M269, M520, S3, S10, S13, S17</td>
<td>~7000 ybp</td>
</tr>
<tr>
<td>R1b1a2a</td>
<td>L23/S141, L49.1</td>
<td>~6200 ybp</td>
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<tr>
<td>R1b1a2ala1a</td>
<td>L51/M412/S167</td>
<td>5300±700 ybp</td>
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<tr>
<td>R1b1a2ala1</td>
<td>L11, P310, P311</td>
<td>~4800 ybp (in Europe)</td>
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<tr>
<td>R1b1a2ala1a</td>
<td>M405/S21/U106</td>
<td>4175±430 ybp</td>
</tr>
<tr>
<td>null mutation U106</td>
<td></td>
<td>3325±450 ybp</td>
</tr>
<tr>
<td>R1b1a2ala1b</td>
<td>P312/S116</td>
<td>~4800 ybp</td>
</tr>
<tr>
<td>null mutation P312</td>
<td></td>
<td>3575±400 ybp</td>
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<tr>
<td>R1b1a2ala1b1</td>
<td>[L63]</td>
<td>~1800 ybp</td>
</tr>
<tr>
<td>R1b1a2ala1b2</td>
<td>M153</td>
<td>~3640 ybp</td>
</tr>
<tr>
<td>R1b1a2ala1b3</td>
<td>S28/U152</td>
<td>4125±450 ybp</td>
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<td>null mutation U152</td>
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<td>3525±460 ybp</td>
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<td>R1b1a2ala1b3c</td>
<td>L2/S139</td>
<td>4025±410 ybp</td>
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<td>R1b1a2ala1b3c1</td>
<td>L20</td>
<td>3650±400 ybp</td>
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<tr>
<td>R1b1a2ala1b3d</td>
<td>L4/S178</td>
<td>1275±290 ybp</td>
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<td>R1b1a2ala1b4</td>
<td>L21/M529/S145</td>
<td>3750±380 ybp</td>
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<td>null mutation L21</td>
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<td>3025±460 ybp</td>
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<tr>
<td>null mutation L21</td>
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<td>1500±325 ybp</td>
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<td>R1b1a2ala1b4b</td>
<td>M222</td>
<td>1450±160 ybp</td>
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<td>R1b1a2ala1b4c</td>
<td>L144</td>
<td>~4000 ybp</td>
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<tr>
<td>R1b1a2ala1b4f</td>
<td>L159.2</td>
<td>1775±200 ybp</td>
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<td>R1b1a2ala1b4g</td>
<td>L193</td>
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<td>R1b1a2ala1b4h</td>
<td>L226</td>
<td>1500±170 ybp</td>
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<tr>
<td>R1b1a2ala1b4i</td>
<td>P314.2</td>
<td>2225±300 ybp</td>
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<td>L176.2/S179.2</td>
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<td>null mutation SRY</td>
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<td>R1b1a2ala1b5b</td>
<td>L165/S68</td>
<td>~3000 ybp</td>
</tr>
<tr>
<td>R1b1a2ala1b6</td>
<td>L238/S182</td>
<td>~1000 ybp</td>
</tr>
</tbody>
</table>

1 In Asia
2 4575±380 ybp (a different dataset)
3 3800±380 (a different dataset)
A geographical/regional distribution of R1b1a2-P312 and it’s the largest subclade P312-L21 was analyzed. The Bell Beaker movements from the Iberian Peninsula up North, North-East and to the Isles from 4800 years before present (ybp) and upward provides the best fit with the data of DNA genealogy.

**Introduction**

This article continues a series of studies on DNA genealogy of bearers of R1b haplogroup, published in the Proceedings of the Russian Academy of DNA Genealogy and other editions, such as (ISSN 1942-7484), a complete list is given in [http://aklyosov.home.comcast.net](http://aklyosov.home.comcast.net), the list below is a short version in order from the latest publications down to some earliest ones):


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HISTORY OF R1b HAPLOGROUP from Central Asia to Europe

Appearance of R1b in Central Asia (Altai, Xinjiang, North-Western China), its ancient migrations to Europe; Bashkirs, Caucasian people, Anatolia, Sumer, North Africa, Iberia, the Basques, continental Europe, British Isles), Bell Beakers as R1b1a2 -P312 and -U106 and their upstream (L51, L11/L151/P310/P311) and downstream subclades in Europe, and non-Bell Beakers R1b1a2-M269, -L23, and their downstream subclades in Europe

It was shown in a series of more than 30 papers (Klyosov, 2008-2011, see above and the list of references below) that haplogroup R1b1, as well as its brother
haplogroup R1a1, arose in Central Asia (Southern Siberia or adjacent regions, such as Altai, Xinjiang, North-Western China). R1a arose around 21,000 years before present (ybp), R1b arose next, about 16,000 ybp. Since the very slow (with respect to mutations) 22 marker European R1a1-M17 base (aka deduced ancestral) haplotype [DYS 426, 388, 392, 455, 454, 438, 531, 578, 395S1a, 395S1b, 590, 641, 472, 425, 594, 436, 490, 450, 617, 568, 640, 492]

12 12 11 – 11 11 – 11 8 17 17 8 10 8 12 10 12 8 12 11 11 12  (R1a)

and R1b1a2-M269 base 22 marker haplotype

12 12 13 – 11 11 – 12 – 11 9 15 16 8 10 8 12 10 12 12 8 12 11 11 12  (R1b1a2)

differ by 7 mutations, as marked above (Klyosov, 2011a), which gives 7/0.006 = 1167 generations without correction for back mutations, or 1380 generations with the correction (the correction factor in this particular case equals 1.187), that is 34,600 years between their common ancestors, THEIR common ancestor lived approximately (34600+5000+7000)/2 = 23,300 years before present. This is a common ancestor of R1 haplogroup. Here 0.0060 is the mutation rate constant for the 22 marker haplotype (in mutation/haplotype/generation of 25 years) [Klyosov, 2011b].

Indeed, if the R1 common ancestor lived 23,300 ybp, then the R1a1M17 base haplotype on the Russian Plain appeared (2,300 + 16,000) = 18,300 years after the R1 appearance, and the R1b1b2-M269 arose (7,300 + 9,000) = 16,300 years after the R1 appearance, hence, the difference between the two base haplotypes above equals to (18,300 + 16,300) = 34,600 years, exactly as the two 22 marker base haplotypes show as the seven mutation difference between them.

After haplogroup R1 arose about 23,000 years ago, and its downstream R1b arose in Central Asia 16,000 ago, the latter had migrated across North Kazakhstan (including the later Botai archaeological culture, 6500-5500 ybp), through the territory of the present-day Bashkirs (13-11-8 thousand ybp), established Seroglazovo archaeological culture (13-11 thousand ybp) and then Middle Volga Basin archaeological cultures (Srednevolga culture 87 thousand ybp; Samara culture 7 thousand ybp; Srednestog culture 7500-5500 ybp; Khvalyn culture 7-6 thousand ybp, Kama culture 7-5 thousand ybp), that is the cultures which then were (tentatively) named “Pre-Kurgan cultures”; R1b1a2-M269 subclade arose around 7,000 ybp, and then R1b1a2-L23, around 6,500 ybp. Both of them came to the Caucasus region around 6,500-6,000 yps, and possibly earlier. Those R1b1b2 spoke non-IndoEuropean language(s), which can be vaguely traced now under various names. Some call them ProtoTurkic language, some Sino-Caucasian language, some call them the Erbin language (because of R1b haplogroup of their
bearers), some call them Western Caucasian or North-Western Caucasian languages, some call them the Basque language, and find some similarities between the Caucasian and Basque languages, etc.

In fact, those similarities do exist, albeit in a rather weak form because thousands of years passed since then. Still now most of R1b1a2 haplotypes on the Caucasus (in Armenia, Dagestan, Georgia) belong to the ancient L23 subclade (with a common ancestor of around 6,000 ybp), and have a characteristic DYS393=12 allele, unlike DYS393=13 in most of European R1b1b2 haplotypes.

From the Caucasus, R1b1a2-L23 and R1b1a2-M269 bearers went South over the mountains, to Anatolia (a common ancestor of 6,000 ybp), and then split into three major routes. One went further South, to Tigris and Euphrates Rivers, and became the Sumers. Many present-day Assyrians, descendants of ancient Sumers, still have their R1b1a2 haplotypes. Another went westward, across Asia Minor, and came to Europe, to the Balkans and Mediterranean Sea region around 4500 ybp. The third group went across Northern Africa and Egypt (and, incidentally, might have left some R1b1b2 Pharaohs there) to the Atlantic and went across Gibraltar to the Iberian Peninsula around 4800 ybp. They became the Bell Beakers, and moved up North into the continental Europe. The Bell Beaker culture in Europe had lasted between about 4000 and 3800 ybp.

R1b1a2 bearers came to the Pyrenees, apparently, as mainly L51/M412 and/or L11/L151/P310 subclades, and soon split there into U106 and P312 downstream subclades, which went to the continental Europe as said Bell Beakers of downstream subclades, among them U198, U152, L2, L20, L4, L21, M222, L226, SRY2627, etc. They left the Basques behind, which still maintain the ancient Erbin (R1b) language, similar in kind with some Caucasian languages, and with the Sumer language, and having some elements of Proto-Turkic languages back to Asia and further to Siberia.

Until the beginning of the 1st millennium BC the R1b1a2 language in Europe was predominantly (or only) non-Indo-European (IE). There is not a single solid evidence of otherwise, that R1b1a2 in Europe spoke IE language before the 1st millennium BC. Celtic language, as well as “Proto-Celtic” language, for instance, is placed by linguists not earlier than 800–900 BC, and all more earlier placements are typically groundless. At the same time, we know that it were R1a1 bearers who brought their IE language to India around 3500 ybp, and it is being dated in Europe to at least 6,000 ybp. There were no R1b1a2 in Europe those times. It must have been R1a1 bearers who spoke proto-IE language(s) in Europe 6,000 ybp and some earlier.
Roots of the Bell Beakers can be traced back by comparing 67 marker base haplotypes of their present-day descendants of “parallel” subclades U106 and P312:


(U106)


(P312)

There are six mutational differences between them (shown in bold in the U106 base haplotypes), which corresponds to 6/0.12 = 50 \rightarrow 53 “conditional” generations (25 year per generation), that is, 1,325 year time span between their common ancestors. The sign \rightarrow means a correction for back mutations (see below). Since a common ancestor of U106 and P312 lived 4175±430 ybp and 4100±415 ybp respectively (see below, also 3950±400 ybp, Klyosov, 2010a, which is practically the same figure within the margin of error), THEIR common ancestor lived \((1325+4175+4100)/2 = 4800\) years ago. This fits to the Bell Beakers timing quite well.

Project description

In this article we consider subclade R1b1a2-P312 and its downstream subclades based on the list of 2299 67 marker P312 haplotypes, provided by Michael Walsh, administrator of R1b1a2-L21 site http://www.familytreedna.com/public/R L21/default.aspx?section=yresults

A haplogroup/subclade tree is given above (see Summary) for R1b1a2-P312 upstream and downstream subclades which are considered in this paper. The nomenclature is that described at http://www.isogg.org/tree/ISOGG_HapgrpR.html, May 2011.

Haplotype analysis Methodology

The essence of the methodology employed in this study is as follows:
(a) to build a haplotype tree and to resolve lineages/branches,
(b) to calculate each branch separately and to identify a timespan to a nearest common ancestor for each one,
(c) to identify a timespan to a common ancestor, if any, for all the branches altogether,
(d) to make calculations with a correction for back mutations, if a timespan is longer than 23 “conditional” generations (25 years each, that is 575 years in 23 “generations”),
(e) to compare calculations for 25, 37, and 67-marker haplotypes, to make sure that the calculations are compatible for all the three haplotype formats,
(f) to verify the data obtained with the logarithmic method (when possible), which does not need mutation counting,
(g) to use calibrated mutation rates and calibrated generation lengths,
(h) to use calibrated mutation rates which are verified with father-son pair massive experiments,
(i) to provide margins of error to all results, for their realistic evaluations.

All the above items are illustrated in the text below those some of them are omitted in order not to make to text too detailed. A few, which need more detailed explanations, are described in this section.

**Analysis of mutations and their rates.** Principal methodology was described in (Klyosov, 2009a,b). Haplotype trees were constructed using PHYLIP, the Phylogeny Inference Package program, as was explained in detail in (Klyosov, 2009a and references therein). A “comb” around the wheel (a “trunk”), in haplotype trees identifies “base” haplotypes, identical to each other and carrying no mutations compared to their ancestral haplotypes. They typically are observed in 12- and 25 marker haplotype trees, but not in 67 marker trees (where all haplotypes are typically mutated compared with their ancestral haplotypes).

The farther the haplotypes lay from the trunk (the wheel), the more mutations they carry compared to the base haplotype, hence, the older the respective branch.

The “base” haplotypes are the ancestral haplotypes in an ideal case. However, since those haplotypes often are deduced ones, it would be inaccurate to call them “ancestral”. Hence, we call them “base” haplotypes.

Timespans to the most recent common ancestor were calculated using both “logarithmic” and “linear” approaches. The logarithmic method is based on the assumption (which largely or practically always holds true) that a transition of the base haplotypes into mutated ones is described by the first-order kinetics:

\[ N = Ae^{kt}, \]

that is
\[ \ln(N/A) = kt \]

where:

\[ \begin{align*}
N & = \text{a total number of haplotypes in a set,} \\
A & = \text{a number of unchanged (identical, not mutated) base haplotypes in the set,} \\
k & = \text{an average mutation rate,} \\
t & = \text{a number of generations to a common ancestor.}
\end{align*} \]

One can see the logarithmic method does not consider mutations in haplotypes; only mutated and non-mutated (base) haplotypes are considered.

Mutation-counting methods are all based on accumulation of mutations in haplotypes over time. They include the “linear”, “quadratic” (ASD) and “permutational” methods (Klyosov, 2009a). In this paper the “linear” method is largely employed, in which a total number of mutations in a set of haplotypes is counted, an average number of mutations per marker is calculated, a correction for back mutations is introduced, either numerically, or using a handy table (Klyosov, 2009a), and a time span to a common ancestor is calculated, either using the table, or applying the respective mutation rates.

It is important that the TSCA (time span to a common ancestor) values obtained by using the linear method and the logarithmic method should be equal to each other within margin of error. It means that the accumulation of mutations in the base (ancestral) haplotype in the course of the TSCA has followed the first order kinetics. In practical terms it means that the dataset indeed has a common ancestor, it represents a lineage, not a mix of different lineages descending from various common ancestors. If the apparent TSCA obtained by the linear and the logarithmic methods significantly differ from each other (beyond the margin of error), those TSCAs both are “phantom” ones, they are both incorrect.

Average mutation rates employed in this paper, are (Klyosov, 2009a) with some corrections made later (Klyosov and Rozhanskii, 2010):

For 12 marker haplotypes – 0.022 mutations per haplotype, 0.00183 mutations per marker,
for 25 marker haplotypes – 0.046 mutations per haplotype, 0.00183 mutations per marker,
for 37 marker haplotypes – 0.090 mutations per haplotype, 0.00243 mutations per marker,
for 67 marker haplotypes – 0.12 mutations per haplotype, 0.00179 mutations per marker.
For 49 marker haplotypes (see below) – 0.080 mutations per haplotype, 0.00163 mutations per marker. The lowest mutation rate constant in this case is the result of removal from the marker panel of 8 markers sensitive to recLOH mutations, null mutations, and other complications.

These mutation rates were calibrated employing 25 years per generation. This is a fixed mathematical figure, not an actual length of generations, which is a “floating” value, depending on many factors, including cultural, demographical, economical, and largely varied between ancient times and today. Time spans to a common ancestor were calculated typically employing all 67 marker haplotypes, and/or sometimes the first 25 and/or 37 markers haplotypes, and, when possible, the data were compared to each other. Margins of error for time spans to common ancestors are calculated as described in (Klyosov, 2009a).

There are many confusions in the literature regarding mutation rate constants. Some authors claim that 25 years per generation is incorrect, and suggest different time spans per generations, typically between 20 and 35 years per generation, citing some arbitrarily chosen examples from recent genealogies. However, it is impossible to know if those generation lengths stay the same down through millennia. On the contrary, it would be hard to imagine that. Generation length is a “floating” factor, and depends on times, cultures, historical situations, etc. Therefore in our approach we do not use any arbitrarily chosen generation length. Since DNA genealogy obtains only a product <kt> (as a ratio of a number of mutations divided by a number of haplotypes or markers in the dataset), where k in the mutation rate and t is a number of generations, we can (and should) set a generation length based on an actual number of years for the calibration example. For instance, an earlier dataset for R1a1 Donald Clan (“Red Subgroup”) contained 44 mutations in 68 of 12 marker haplotypes, and 69 mutations in 60 of 25 marker haplotypes. In a recent update (2010) there were 64 mutations in 125 of 12 marker haplotypes and 166 mutations in 124 of 25 marker haplotypes. Since we know that the common ancestor of the group, John Lord of the Isles, lived (in the context of this study) 650 years ago (he died in 1386, that is 624 years ago), we can make it 26 generations of 25 years each. In other words, we calibrate the mutation rate constant setting it at the mathematical value of 25 years per generation. We could have set it for 13 generations of 50 years each, it would not change a thing. There will be 650 years anyway. Just a mutation rate constant would be twice as high.

Let us see how we do it. For the four dataset for the “Red Subgroup”, setting 26 generations to the common ancestor, we obtain:

12 marker haplotypes (an earlier and a recent count of mutations and haplotypes):
44/68/26 = 0.025±0.005 mutations per haplotype per generation (of 25 years)

64/125/26 = 0.020±0.003 mut/hapl/gen

One can see that these mutation rate constants are the same within the margins of error. The subsequent detailed studies with many datasets set the mutation rate constant as 0.022±0.001 mut/hapl/gen

25 marker haplotypes:

69/60/26 = 0.044±0.007 mutations per haplotype per generation (of 25 years)

166/124/26 = 0.051±0.006 mut/hapl/gen

One can see that these mutation rate constants are the same within the margins of error. The subsequent detailed studies with many datasets set the mutation rate constant as 0.046±0.002 mut/hapl/gen

One has to be careful, though, with those kinds of calibration. The latest (May, 2011) inspection of the Donald R1a1 haplotype series (the Red group) revealed that the Association sharply increased their database, recruiting many haplotypes which are obviously derived from “older” ancestors and have non-proportionally many mutations. For example, in May 2011 the “Red Group” contained 148 of 12 and 25 marker haplotypes, which have 98 and 260 mutations, and 102 of 67 marker haplotypes, which have 454 mutations from their base haplotypes. It gives:

98/148/0.022 = 30 generations from their apparent “common ancestor”, which is likely a phantom one.

260/148/0.046 = 38 generations (!) from their (certainly) phantom “common ancestor”, which allegedly lived 38→40 generations, that is 1000 years back. It is as many as 14 generation older than Lord John of the Isles.

454/102/0.12 = 37→38 generations, that is 950 years back.

The confusions regarding mutation rate constants in the literature continue. Some authors claim that only father-son pair studies can give the right value for mutation rate constants. This, of course, is the most objective approach, when done with a good statistics, that is with thousands and thousands of pairs. However, there is one serious caveat—data would be obtained in mutations per a generation only, hence, again the issue of how many years per generation
should be employed is left unresolved. Again, we need a calibration with actual historical data, that is come back to our approach.

Here is an example. A massive study of almost two thousand of father-son pairs (Ballantyne et al, 2010) revealed 48 mutations in the first 12 markers and 102 mutations in the first 25 markers (unfortunately, 37 and 67 marker haplotypes have not been studied in full, many markers were missing) in $1727 \pm 49$ and $1704 \pm 86$ pairs, respectively. This gives mutation rate constants as $0.028 \pm 0.005$ and $0.060 \pm 0.009$ for 12 marker and 25 marker haplotypes, respectively. Another way of calculations, per (extrapolated) 10,000 father-son pairs and for each marker gave practically the same values, $0.0277 \pm 0.0049$ and $0.0595 \pm 0.0084$ mutations per haplotype per generation. They are exactly the same values as the mutation rate constants employed in our study, but for 32 years per generation, not for 25 years, used in our study. In practical terms, it does not make any difference, except statistics in the Ballantyne et al study was still not very good. For example, even with almost 2000 father-son pairs, a number of mutations in the first 12 marker haplotypes was, respectively, 3, 2, 7, 5, 3, 6, 0, 0, 6, 9, 1, 6. In the following 13 markers it was 14, 4, 0, 0, 3, 2, 0, 19, 12 (some markers were combined in the cited study). Hence, margin of error for those data was rather wide, namely $\pm 14\%$ and $\pm 10\%$, respectively, only for a number of mutations observed in the cited study.

Being applied for said Clan Donald “Red Subgroup”, the father-son pair mutation rate constants give:

12 marker haplotypes:

$44/68/0.028 = 23$ generations

$64/125/0.028 = 18$ generations

25 marker haplotypes:

$69/60/0.060 = 19$ generation

$166/124/0.060 = 22$ generations

An average number of generations is $20.5 \pm 2.4$, that is $656 \pm 77$ years to a common ancestor of the “Red Subgroup” of R1a1 individuals, at 32 years per generation.

As one can see, for a practical application of father-son data and the respective mutation constants, it is necessary to calibrate the data.
The principal conclusion is that the mutation rate constants used in this study and listed above, are appropriate and do not contradict with father-son mutational studies.

**Null mutations and recLOH mutations**

In case of null mutations they were counted as one mutation compared to the respective base haplotype. However, null mutation haplotypes typically form their separate branch on the haplotype tree. In that case there is no need to count null mutations, since all haplotypes in the branch and their base haplotype all contain the null mutation.

In case of recLOH mutations they were counted as one mutation regardless how large was a gap between the base allele and a resulting recLOH allele. For example, if the majority of haplotypes in a dataset having one common ancestor (that is verified using the haplotype tree along with the logarithmic method compared with the linear method, see above) have 19-21 in their YCAII loci, and some haplotypes contain 19-19 or 21-21, it is counted each as one mutation, not two. If the base DYS464 alleles are 15-15-17-17, then 15-17-17-17 or 15-15-18-18, is counted as one mutation, not two. If the base DYS385 alleles are 11-14, then 11-11 is counted as one mutation, not three. The same goes for 1414 in these loci. 12-13 in these loci is counted as two mutations as well. In many cases recLOH or no recLOH mutations give the same result, such as 9-9 or 10-10 in DYS459 with its (typically) base 9-10, it would be one mutation anyway, recLOH or no recLOH.

**Correction for back (reverse) mutations**

Essentially, when a mutation happens, and they happen now and then, they can equally happen "up" or "down", e.g. from the ancestral 17 to either 18 or 16 (in a descendant). If it mutates to, say, 18, the next move (after 550 generations on average for 25 marker haplotypes or 460 generations for 67 marker haplotypes) can be to 17 or 19, equally probable.

If it mutates back to 17, to the ancestral allele, this would be the "back mutation", and one cannot see it, looking at the resulting haplotype. It was 17 in the ancestral haplotype, and it went 17-> 18 ---> 17, that is 17 again. How do we know that ANY allele in a present day haplotype is not back mutated?

In fact, we do not know. However, we can calculate a probability of such an event in all the 67 alleles in a 67 marker haplotype, or in a haplotype of any
format. Those back mutations actually slow down the OBSERVED mutations. We observe, say, 125 mutations in a dataset, and we calculate that in fact there were 137 mutations. This is a correction for back mutations.

There are two principal ways to introduce a correction for back mutation into the calculations. One way is to use the following formula (Adamov & Klyosov, 2008; Klyosov, 2009a)

$$\lambda = \frac{\lambda_{obs}}{2}(1 + \exp(\lambda_{obs}))$$

where:

$\lambda_{obs} = \text{observed average number of mutations per marker in a dataset (or in a branch, if the dataset contains several branches/lineages),}$

$\lambda = \text{average number of mutations per marker corrected for back mutations}$

The above formula is applicable for completely symmetrical pattern of mutations, that is for equal number of mutations “up” and “down” from the base (ancestral) haplotype. For asymmetrical series of haplotypes (rather, for mutations in the dataset) a degree of asymmetry should be calculated and a slightly more complicated formula (Klyosov, 2009a) should be used; however, this additional factor is, as a rule, not very significant, and typically fits into a margin of error of calculations.

Let us consider an example, in which a dataset of 100 of 25 marker haplotypes contains 400 mutations from the base haplotype. Then 400/100x25 = 0.160 mutations per marker. At the mutation rate of 0.002 it would give 0.160/0.002 = 80 generations, that is 80x25 = 2,000 years to a common ancestor. However, as it was mentioned above, with 24 generations and deeper in time one should introduce a correction for back mutations. At 80 generations it is almost two centuries. Here is how it works:

$$\lambda = \frac{0.160}{2}(1 + \exp(0.160)) = \frac{0.160}{2}(1+1.174) = 0.174$$

0.174/0.002 = 87 generations, that is 87x25 = 2,175 years to a common ancestor.

Another way is to use the handy Table (Klyosov, 2009a), which provides two columns of data – one without a correction for back mutations, second for the corrected value. For our example it shows that 80 generations, not corrected for
back mutation, corresponds to 87 generations after the correction is made. It is exactly the same value of 87 generations calculated above using the mathematical formula.

As an example of the logarithmic method with a correction for back mutations, let us consider a series of 750 of 19 marker Basque and Iberian R1b1 haplotypes (Adams et al, 2009) containing 16 of identical, that is base haplotypes in the series. It gives $\ln(750/16)/0.0285 = 135$ generations without a correction for back mutations. The correction Table described above immediately gives $135 \Rightarrow 156$ generations (corrected), that is $156 \times 25 = 3900$ years to a common ancestor of the Basque and Iberian haplotypes, predominantly subclade R1b1b2-P312*. This is within the margin of error with the timespan to a common ancestor of Basque and Iberian haplotypes calculated using the linear method (Klyosov, 2009a).

**49 marker haplotypes**

Some calculations below have been done using 49 marker haplotypes, which represent a 67 marker panel from which 18 markers were removed due to their inclinations to recLOH mutations, null mutations and other complications. Removed markers were DYS385a;b; DYS3892; DYS459a;b; DYS464a,b,c,d; YCAIa,b; CDYa,b; DYS395S1a,b; DYS425; DYS413a,b. The mutation rate constant for the 49 marker panel was equal to 0.08 mutation/haplotype/generation, that is 0.00163 mutation/marker/generation of 25 years. 102 haplotypes of the Clan Donald (R1a1 “Red Group”) series in the 49 marker format fit that mutation rate constant within 10% of its value.

**Haplotype analysis. Actual 67 marker haplotypes**

A series of 2299 of 67 marker haplotypes which is considered in this paper, is too “heavy” for a contemporary personal computer to be calculated altogether into a haplotype tree. Typically, 1100–1300 haplotypes in the 67-marker format is a limit for composing of haplotype trees when PHYLIP program is employed. Therefore, the haplotypes were considered by their subclades.

As a first approximation the logarithmic method was used. The whole series of 2299 of 67 marker haplotypes contained 154 of 12 marker base haplotypes

13 24 14 11 11 14 12 12 12 13 13 29

which gives $\ln(2299/154)/0.022 = 123 \Rightarrow 141$ generations, that is approximately 3525 years to a common ancestor of all 2299 haplotypes.
The same series contained seven base 25 marker haplotypes

13 24 14 11 14 12 12 13 13 29 - 17 9 10 11 25 15 19 29 15 15 17 17

which gives \[\ln(2299/7)/0.046 = 126 \rightarrow 145\] generations, that is approximately 3625 years to a common ancestor. This is a quite a reasonable value for the P312 subclade, which typically varies from 3600 to 400 ybp for various series of haplotypes.

It should be noted that these two series of 12 and 25 marker base haplotypes obtained using the logarithmic method, gave a difference of only four generations, or less than 3% between each other, and generally fit into a typical range of TSCA (timespans to common ancestors) for P312 subclade. This shows that all 2099 of 67 marker haplotypes are derived - with a good probability - from one common ancestor.

Among those 154 base (presumably ancestral and other statistically accidental fits) 12 marker haplotypes there were:

- 26 haplotypes from England (8.1%)
- 26 from Ireland (4.5%)
- 19 from Scotland (7.0%)
- 8 from Germany (7.8%)
- 6 from Spain (10.2%), Wales (9.4%), France (6.5%) each
- 2 from Denmark, Czech, Finland, Netherlands each
- 1 from Sweden, Switzerland, Greece, Luxembourg, Poland, Portugal,
  and 43 did not have a geographical assignment.

Among seven 25 marker base haplotypes, four were from Scotland, two from Ireland, and one from England.

Statistics with 25 marker haplotypes is not too good to make any meaningful conclusion, however, the highest amount of base 12 marker haplotypes in Spain might be indicative regarding the origin of P312 in Europe (see above). The highest amount of P312* haplotypes is found also in Iberia (Myres et al, 2009).

**R1b1a2-P312 and its six immediate downstream subclades**

Here is how all six immediate downstream subclades are represented in the 2099 67 marker haplotype dataset (without including their downstream subclades):
With inclusion of some downstream subclades, L176.2 would add L165 (9 haplotypes) and SRY2627 (141 haplotypes) and with its total 155 haplotypes takes 6.7% of all, close to that in U152. However, L21 would add 462 haplotypes of its downstream subclades M222, L144, L159, L193, L226, and P314 and with 1486 haplotypes takes 65% of all, two-thirds of the dataset.

**L21 haplotypes**

L21 is one of six immediate downstream subclades of R1b1a2-P312 (see the chart above). However, it is the most populous among them all.

Fig. 1 shows a tree of 1024 of 67 marker haplotypes R1b1a2-L21, downstream of P312. Of those the first 220 haplotypes (numbers 1-220) were marked as L21, 701 haplotypes (221-922) were marked L21*, the last 102 haplotypes (923-1024) were marked L21**. All the three marked groups were scattered around the tree.

According to Michael Walsh, asterisk in a subclade index shows that it was confirmed that a haplotype is ancestral for the major downstream SNPs. For example, P312* is P312+ L21- U152- SRY2627- M222- M153-. However, since L21 was not always included in some early testing packages, P312* can in those cases be P312+ L21+.

The whole tree has the following base haplotype:

```
13 24 14 11 11 14 12 12 12 13 13 29 - 17 9 10 11 11 25 15 19 29 15 15 17 17 -
11 11 19 23 16 15 18 17 36 38 12 12 - 11 9 15 16 8 10 10 10 10 12 23 23 1610 12 12
15 8 12 22 20 13 12 11 13 11 12 12 (L21, 3750±380 ybp)
```

This haplotype differs by only one mutation (shown in bold in DYS 456) compared with the parent P312 base haplotype (see above). To be exact, in 1024 of L21 haplotypes an average allele in DYS456 was 15.71, that is close to 16. This places apart common ancestors of P312 and L21 by 1/0.12 = 8 generations only, that is by 200 years, That is, if P312 arose 4100 ybp, L21 should arose approximately 3900 ybp.

Let’s check it.
All 1024 haplotypes of R1b1a2-L21 have 16,056 mutations from the base haplotype shown above. It gives 16056/1024/0.12 = 131 \rightarrow 150 generations, that is 3750±380 years from the common ancestor of L21 subclade. This value is the same as that (3750 ybp) calculated from a mutational difference from the P312 and L21 base haplotypes.

Those 1024 haplotypes have 4 base 25 marker haplotypes, which gives $\ln(1024/4)/0.046 = 121 \rightarrow 138$ generations, that is approximately 3450 years to the common ancestors. These values, 3750±380 ybp obtained by the “linear” method and 3450 ybp by the logarithmic method are the same within the margin of error.

**A small branch of 108 haplotypes within L21 subclade**

Fig. 1 reveals one clearly separate branch within L21 subclade, at 7 o’clock, containing 108 haplotypes, with the base haplotype

13 24 14 10 11 14 12 12 12 13 13 30 – 18 9 10 11 11 25 15 19 30 15 15 17 17 –
11 12 19 24 16 15 18 17 37 38 12 12 – 12 9 15 16 8 10 10 8 10 10 12 22 23 16 10 12 12
15 8 11 22 20 13 12 11 13 11 11 12 12
Fig. 1. 67 marker haplotype tree of 1024 haplotypes of R1b1a2-P312-L21. A list of haplotypes were provided by Michael Walsh, administrator of R1b1a2-L21 site

This branch composed as a separate tree is shown in Fig. 2.
Fig. 2. 67 marker haplotype tree of 108 haplotypes of R1b1a2-L21 which form a distinct branch in Fig. 1 at 7 o’clock. The tree contains 24 haplotypes marked as L21 (numbers 94 and 100-122), 76 haplotypes marked as L21* (between 242 and 596), and 8 haplotypes marked as L21** (973-980). Those groups did not form any distinct sub-branches.

The base haplotype shown above differs by 10 mutations from the L21 base haplotypes (shown above in bold). Surprisingly, it is seemingly not identified as yet subclade of L21. Its 108 haplotypes contain 798 mutations, which gives 798/108/0.12 = 62 → 66 generations, that is 1650±175 years to a common ancestor of the branch. It is a middle of the † millenniumAD.

It is not the M222 base haplotype

with a common ancestor of 1450±160 ybp (Klyosov, 2010a,b), and with 22 mutations (shown in bold) between the base haplotype of M222 and that of the unidentified subclade above. Those 22 mutations between two 67 marker haplotypes place their common ancestors by 5600 years apart, and put THEIR common ancestor at 4350 ybp. Apparently, it was the “original” L21 common ancestor before his descendants passed the population bottleneck.

It is not the L226 (Irish Type III) base haplotype


with a common ancestor of 1450±290 ybp (Klyosov, 2010b), and with 20 mutations (shown in bold) between the base haplotype of L226 and that of the unidentified subclade above. Those 20 mutations between two 67 marker haplotypes place their common ancestors by 500 years apart, and put THEIR common ancestor at 4050 ybp. Again, it was apparently the “original” L21 common ancestor before his descendants passed the population bottleneck.

Despite L222 (R1b1a2a1-b4b) and L226 (R1b1a2a1-b4h) were ruled out, there are still at least seven subclades, downstream of L21 which could be considered for this new branch with a common ancestor of 1650±175 ybp. Those are M37 (-b4a), P66 (-b4c), L96 (-b4d), L144/L195 (-b4e), L159.2 (-b4f), L193 (-b4g), P314.2 (-b4i). Its assignment remains to be established.

Since the 1024 haplotype series of L21 contained 108 haplotypes of some younger, downstream branch, with a common ancestor of 1650±175 ybp, this admixture could distort the TSCA value for L21, making it higher or lower, depending on specifics of the admixture. However, since the admixture adds only about 10% of all the haplotypes, the distortion might be negligible. Let us examine it.

When the 108 haplotypes of the “young branch” were subtracted from the 1024 L21 haplotypes, the base haplotypes stayed the same, and 14,278 mutations were found from it in the remaining 916 haplotypes. It gave 14278/916/0.12 = 130 → 149 generations, that is 3725 years to a common ancestor, which is practically equal to 3750 years for the initial 1024 haplotypes. One can see that in this particular case the reduction of the number of haplotypes in the series (from 1024 to 916, by 10.6%) was only a little lower than the reduction of a number of mutations (from 16,056 to 14,278, by 11.1%), hence, there was practically no distortion in the TSCA.
L21 null mutation in a series of haplotypes

Null mutations happen in various markers, however, DYS425 is probably the most subjected to null mutations in the 67 marker panel. Null mutation is not, of course, a complete elimination of the marker altogether. It just shows that an allele in this marker cannot be determined by the same method (the same primer) as that successfully employed with other populations of haplotypes. A null mutation is inherited, that is transmitted onto haplotype of a descendant. Hence, it is a "marker" by itself.

Fig. 3. 67 marker haplotype tree of 46 haplotypes of R1b1a2-L21 null mutation series. Haplotypes numbered between 73 and 220 (15 haplotypes total) belong to L21, 283-918 (27 haplotypes total) belong to L21*, haplotypes 953, 965, 1023 and 1024 belong to L21**. There are 24 Ireland haplotypes, five Scotland, four England, one Wales, Spain and Sweden each, the rest are of unknown ancestry.

In the considered dataset of 2299 haplotypes null mutations occur in the L21 subclade (46 null mutated haplotypes), U152 (seven haplotypes), SRY2627 (six
haplotypes), L20 and P312 (three haplotypes in each), L193 and M222 (one haplotype in each).

Fig. 3 shows a haplotype tree of null mutated haplotypes of L21 subclade. The branch of six haplotypes on the right-hand side is obviously the most ancient one. Its base haplotype differs by 5 mutations from that of L21 parent subclade (deviations from L21 are remarked below):

```
13 24 14 11 11 14 12 12 12 13 13 30 - 17 9 10 11 11 25 15 19 29 15 15 16 17 -
11 11 19 23 15 15 18 18 36 38 12 12 - 11 9 15 16 8 10 10 8 10 100 23 23 16 10 12 12
15 8 12 22 20 13 12 11 13 11 11 12 12 (L21 null DYS425, 3025±460 ybp)
```

All six haplotypes contain 78 mutations from the above base haplotype, which gives 78/6/0.12 = 108 → 121 generations, that is 3025±460 years from a common ancestor. Five mutations between L21 and L21-null base haplotypes results in 5/0.12 = 42 → 44 generations, that is 1100 “lateral” years between the common ancestors. It indicates that THEIR common ancestor lived approximately (1100+3750+3025)/2 = 3940 years ago. It is in a vicinity of 4050 ybp for the common ancestor for L21, which was described above as “it was apparently the “original” L21 common ancestor before his descendants passed the population bottleneck”.

Therefore, it very likely that the L21-null branch split from the initial L21 common ancestor at the very beginning (time-wise) of the subclade.

Let us verify it with the more recent branches in Fig. 3.

Immediately at the foot of the just described old branch there is a small branch of four haplotypes. Still, they provide us with 268 markers (67x4). The base haplotype of the branch is as follows (mutations from the 6 haplotype old branch base haplotype are marked):

```
13 24 14 11 11 15 12 12 12 13 13 29 - 17 9 10 11 11 25 15 19 28 15 15 17 17 -
11 11 19 23 15 15 18 19 36 38 12 12 - 11 9 15 16 8 10 10 8 10 10 9 0 22 23 16 10 12 12
15 8 12 22 20 13 12 11 13 11 11 12 12 (L21 null DYS425, sub-branch, 1500±325 ybp)
```

All four haplotypes contain 27 mutations from the above base haplotype, which gives 27/4/0.12 = 56 → 60 generations, that is 1500±325 years from a common ancestor. 7 mutations (most of them are fractional ones) between the two null
base haplotypes result in 7/0.12 = 58 → 62 generations, that is 1550 “lateral” years between the common ancestors, and place THEIR common ancestor to approximately \((1550+1500+3025)/2 = 3040\) years ago. It is practically equal to the “age” of the older branch (3025 ybp). In other words, the “older” null branch split off L21 lineage, and after more than a thousand years, namely 1500 ybp, split the “younger” null branch.

Two other “young” small branches on the right hand side of the tree one, 6-haplotype branch in the upper part (between haplotypes 914 and 997), with the base haplotype


\(\text{L21 null DYS425, 1050±220 ybp}\)

and another, 5-haplotype branch, in the lower part of the tree (between 208 and 912), with the base haplotype


\(\text{L21 null DYS425, 1100±250 ybp}\)

each has a (different) common ancestor, who both lived only about a thousand years ago: 29/6/0.12 = 40 → 42 generations, that is 1050±220 ybp, and 25/5/0.12 = 42 → 44 generations, that is 1100±250 ybp. They differ by only 4 and 2 mutations (850 and 425 “lateral” years) from the above null-mutated branch of 1500±325 ybp (marked in bold, some mutations are fractional), hence, they are derived from the 1500-ybp null-L21 common ancestor.

The last branch, stretching from the top to the bottom on the left hand side of the tree in Fig. 3, consisting of 25 haplotypes, has the following base haplotype:


\(\text{L21 null DYS425, 1300±170 ybp}\)

All the 25 haplotypes contain 148 mutations, which gives 148/25/0.12 = 49 → 52 generations, that is 1300±170 years from their common ancestor. It is the same null mutated haplotype of 1500±325 ybp common ancestor, within the margins of error of calculations.
We have already established that the 3025±460 ybp and the 1500±325 ybp base haplotypes differ by 7 mutations, which shows that the second one is a downstream from the first one.

Let us take a look at the presumed upstream (1500 ybp) and downstream, younger null mutated base haplotypes.

<table>
<thead>
<tr>
<th>L21 null DYS425, 1500±325 ybp</th>
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<table>
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<th>L21 null DYS425, 1300±170 ybp</th>
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</table>

<table>
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<tr>
<th>L21 null DYS425, 1100±250 ybp</th>
</tr>
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</table>

The above can be summarized as the oldest null mutated L21-DYS425=0 base haplotype split from L21 3025±460 ybp, then the null mutated 1500±325 descendant split, and the latter has derived a series of null mutated lineages with common ancestors of 1300±170, 1100±250 and 1050±220 ybp. It seems that all of them were split in parallel, not consecutively.

Subclades other than L21

R1b1a2-P312* and subclades (M65, M153, L21-M222, L21-L144, L21-159.2, L21-L193, L21-L226, L21-P314.2)

Fig. 4 shows the 67 marker haplotype tree of R1b1a2P312 and its subclades. Its base haplotype is as follows
Fig. 4. 67 marker haplotype tree of 808 haplotypes of R1b1a2-P312 with some subclades. The haplotypes were provided by Michael Walsh, administrator of R1b1a2-L21 site http://www.familytreedna.com/public/RL21/default.aspx?section=yresults)
This base haplotype is very close to that of P312 (see above), and differs by only fractions of mutations. The first 25 alleles contain 5252 mutations from the base haplotype, which gives 5252/808/0.046 = 141 → 164 generations, that is 4100±415 years from a common ancestor.

The whole 808 haplotype dataset contains 39 of 12 marker base haplotypes

13 24 14 11 11 14 12 12 12 13 13 29

This gives ln(808/39)/0.022 = 138 → 161 generations, that is approximately 4025 years from a common ancestor. Since the both methods, the linear and the logarithmic, gave very close TSCAs (4100 and 4025 ybp), it shows that the whole tree was derived from one common ancestor, of the P312 subclade.

P312-M65 subclade

There is only one M65 haplotype (from Wales) in the whole dataset:

13 24 14 11 11 14 12 12 12 14 29 – 17 9 10 11 25 15 19 30 15 15 16 18 –
11 11 19 23 15 15 17 17 38 41 12 12 – 11 9 15 16 8 10 10 8 10 10 12 23 25 16 10 12 12
15 8 11 22 20 13 12 11 13 11 11 12 12 (R1b1a2-P312-M65, ~ 1800 ybp)

Since it is a single haplotype, its mutations (marked above) compared to the base haplotype of the whole tree (see above) may be not statistically justified. Let us take it as a semi-quantitative comparison. 10 mutations between two 67 marker haplotypes correspond to about 2275 years of the mutational evolution. This places a (tentative) common ancestor for the M65 subclade to the beginning of AD, approximately 1800 ybp.

P312-M153 subclade

There are only five haplotypes of this subclade on the tree with 29 mutations from the base haplotype

10 11 19 23 16 15 18 17 35 38 12 12 – 11 9 15 16 8 10 10 8 10 10 12 23 23 16 10 12 12
15 8 12 22 20 13 12 11 13 11 11 12 12 (R1b1a2-M153, ~ 3640 ybp)

and with 4 mutations from the base haplotype of P312. This places a common ancestor of these five M153 haplotypes at 29/5/0.12 = 48 → 51 generations, that is 1275±270 ybp, and with 850 years of a mutational distance from the P312 common ancestor. These figures do not fit, since the P312 common ancestor lived
around 4100 ybp. It seems that those five haplotypes are related to each other, hence, a close time to their common ancestor. Indeed, an analysis of 37 haplotypes of the M153 subclade (Klyosov, 2010c) showed that a common ancestor of those haplotypes lived 2325±340 ybp. With this figure a common ancestor of M153 and P312 lived (2325+4100+850)/2 = 3640 ybp, which is the P312 itself within a margin of error of calculations.

**L21-M222**

312 haplotypes of this subclade take almost the whole right-hand side of the tree in Fig. 4. A detailed analysis of this subclade was performed in (Klyosov, 2010b), and the following base haplotype was determined:


Analysis of 257 haplotypes of this subclade showed that a common ancestor of this subclade lived 1450±160 ybp. 312 of M222 haplotypes in this dataset (of 2299 haplotypes) contained 98 of 12 marker base haplotypes and 25 of 25 marker base haplotypes. This gives ln(312/98)/0.022 = 53 → 56 generations, that is 1400 ybp with 12 marker haplotypes, and ln(312/25)/0.046 = 55 → 58 generations, that is 1450 ybp with 25 marker haplotypes. These figures are practically identical.

**L21-L144**

There are only 7 haplotypes of this subclade among all 2299 haplotypes of R1b1a2-P312 the dataset. Six of them form a rather tight branch (see Fig. 5), with the base haplotype (17-step deviations from the parent L21 base haplotype are marked in bold) [some deviations are fractional]


and one haplotype (number 1 on the tree) very distant from the pack (28 mutations compared to the above base haplotype are marked in bold):

It is of interest that the single L144 haplotype and the tight haplotype branch are equidistant from the parent L21 base haplotype (17 mutations in the both cases, which corresponds to 4150 “lateral” years) but have a huge amount of 28 mutations between them.

Fig. 5. A fragment of the 67 marker haplotype tree of 808 haplotypes of R1b1a2-P312 with some subclades. Haplotypes 1-7 belong to the subclade L21-L144. Six of them are rather closely related to each other, haplotype 1 is remote on the tree. All other haplotypes in this fragment (and all with numbers above 472) belong to subclade P312*. 
Let us figure out why so. The \( \delta \) haplotype pack has 26 mutations from their base haplotype (see above) which gives \( 29/6/0.12 = 36 \rightarrow 37 \) generations, that is \( 925 \pm 200 \) years from their common ancestor. This places a common ancestor of L21 and the tight pack of L144 to approximately 4400 ybp. This somewhat “deeper” than the time when L21 supposedly arose, however, a possible population bottleneck in the L21 subclade and/or margin of error of the calculations might be factors. Still, it suggests that L144 subclade is a direct descendant of L21. The single L144 haplotype with its 17 mutations from the base of L21 places THEIR common ancestors at 3950 ybp, which clearly is L21 itself. 28 mutations between the two L144 places their common ancestor at 4200 ybp, which is again the L21 subclade itself.

In other words, the actual “age” of L21-L144 is close to 4000 years, and not to 925 years, found for just six (obviously closely related) representatives of the L144 subclade.

L21-L159.2

A haplotype tree of 56 haplotypes of this subclade is shown in Fig. 6.

One can notice a separate branch of 16 haplotypes in the upper right hand side of the tree. Still, the tree is derived from one common ancestor.

The upper 16-haplotypes branch has the following base haplotype:

\[
13 \ 24 \ 14 \ 11 \ 11 \ 14 \ 12 \ 12 \ 12 \ 12 \ 14 \ 13 \ 30 \ 17 \ 9 \ 10 \ 11 \ 11 \ 25 \ 15 \ 18 \ 30 \ 15 \ 15 \ 17 \ 17 - \\
11 \ 11 \ 19 \ 23 \ 16 \ 15 \ 18 \ 18 \ 40 \ 40 \ 11 \ 12 - 11 \ 9 \ 15 \ 16 \ 8 \ 10 \ 10 \ 8 \ 10 \ 10 \ 12 \ 23 \ 23 \ 23 \ 17 \ 10 \ 12 \ 12 \\
15 \ 8 \ 12 \ 22 \ 20 \ 14 \ 12 \ 11 \ 13 \ 11 \ 11 \ 11 \ 12 \ 12 \ 12 \ (L21-L159.2, \text{sub-branch1350\pm190 \text{ ybp}})
\]

It differs by 13 mutations (marked above) from its parent L21 base haplotype, and has 97 mutations in the whole branch. It gives \( 97/16/0.12 = 51 \rightarrow 54 \) generations, that is \( 1350 \pm 190 \) years from its common ancestor. 13 mutations from L21 (which corresponds to 3025 “lateral” years between the two ancestor, and places THEIR common ancestor to \( (3025+3750+1350)/2 = 4060 \) ybp. It is the L21 common ancestor within the margin of error.

The rest of the tree (40 haplotypes) has the following base haplotype:

\[
13 \ 24 \ 14 \ 11 \ 11 \ 14 \ 12 \ 12 \ 12 \ 12 \ 14 \ 13 \ 30 \ 17 \ 9 \ 10 \ 11 \ 11 \ 25 \ 15 \ 18 \ 30 \ 15 \ 15 \ 16 \ 17 - \\
11 \ 11 \ 19 \ 23 \ 16 \ 15 \ 18 \ 18 \ 38.5 \ 40 \ 11 \ 12 - 11 \ 9 \ 15 \ 16 \ 8 \ 10 \ 10 \ 8 \ 10 \ 10 \ 12 \ 23 \ 23 \ 23 \ 17 \ 10 \ 12 \ 12 \\
15 \ 8 \ 12 \ 22 \ 20 \ 14 \ 12 \ 11 \ 13 \ 11 \ 11 \ 12 \ 12 \ (L21-L159.2, \text{1775\pm200 \text{ ybp}})
\]
Fig. 6. 67 marker haplotype tree of 56 haplotypes of R1b1a2-L159.2 subclade.

The two base haplotypes differ by only 1.5 mutations, that is by 12 generations, or 300 years between their common ancestors. All 40 haplotypes contain 319 mutations from the above base haplotype which gives 319/40/0.12 = 66 → 71 generations, that is 1775±200 years to a common ancestor. A common ancestor of the both parts of the tree lived approximately (1350+1775+300)/2 = 1710 ybp. This is the older base haplotype within the margin of error.

L21-L193

A haplotype tree of 24 haplotypes of this subclade is shown in Fig. 7.

The whole tree has the following base haplotype (11 deviations from L21 are marked in bold; some of them are larger than 1 mutation):

One can notice that the first 25 markers in L193 do not have any mutation from L21; however, the rest of the 67 marker panel add 10 mutations.

All 24 haplotypes contain 138 mutations from the above base haplotype, which gives $\frac{138}{24}/0.12 = 48 \rightarrow 51$ generations, that is $1275 \pm 170$ years to a common ancestor.

Fig. 7. 67 marker haplotype tree of 24 haplotypes of R1b1a2-L193 subclade

11 mutations between L193 and L21 base haplotype are equivalent to 2550 years between their common ancestors. This places THEIR common ancestor at approximately $(2550 + 3750 + 1275)/2 = 3800$ ybp. This is the L21 base haplotype (3775 ybp) within the margin of error.
L21-L226 ("Irish III" subclade)

This subclade has been studied in (Klyosov, 2010a,b,d,e), and the following base haplotype was identified.

15 8 12 22 20 13 12 11 13 11 11 12 12 (L21-L226, 1500±170 ybp)

A timespan to a common ancestor was determined as 1450±290 years (13 haplotypes), 1325±225 years (22 haplotypes), 1425±225 years (27 haplotypes), 1275±150 years (44 haplotypes), 1175±135 years (146 haplotypes).

Fig. 8 shows a haplotype tree for 50 haplotypes of subclade L226
Fig. 8. 67 marker haplotype tree of 50 haplotypes of R1b1a2-L226 subclade

The tree has exactly the same 67 marker base haplotype as shown above, and has 335 mutations. It gives $335/50/0.12 = 56 \rightarrow 60$ generations, that is $1500 \pm 170$ years from a common ancestor. It practically coincide with the earlier data, shown above, within margin of error. A slightly higher last figure is more correct, since it was calculated with an improved and recalibrated mutation rate constant for 67 marker haplotypes of 0.12 mutation/haplotype/generation compared with thye reconsidered value of 0.145 mutation/haplotype/generation (Klyosovand Rozhanskii, 2010).
L21-P314.2

A haplotype tree of this subclade is shown in Fig. 9.

Fig. 9. 67 marker haplotype tree of 13 haplotypes of R1b1a2-L21-P314.2 subclade

Its base haplotype is as follows, 12 deviations from the L21 base haplotypes are marked in bold:

13 23 14 11 11 14 12 13 13 13 28 – 17 9 10 11 11 26 15 19 29 15 15 16 17 –
All 13 haplotypes contain 126 mutations from the above base haplotype, which gives $126/13/0.12 = 81 \rightarrow 89$ generations, that is $2225\pm300$ years from a common ancestor of those 13 haplotypes. 12 mutations from the parent L21 base haplotype translate to 2775 years between both of their common ancestors, which results in approximately $(2775+2225+3750)/2 = 4375$ years; this is an ancestor of L21 subclade within margin of error.

One can notice that while calculated directly using branches/subclades, an ancestor of the L21 subclade lived $3750\pm380$ ybp, however, when calculated from downstream subclades, the “age” of the common ancestor of L21 is as follows:

- 3940 ybp, calculated with L21 null mutation haplotypes
- 4050 ybp, with L21-L226 subclade
- 4060 ybp, with L21-L159.2 subclade
- 4375 ybp, with L21-L314.2 subclade
- 4400 ybp, with L21-L144 subclade

It might reflect margins of error, however, it might point at an “older” age of the L21 subclade rather then determined directly from L21* haplotypes.

**R1b1a2-P312**

Subclade P312 was studies by us in (Klyosov, 2009b, 2010a,f) and found that its base haplotype as follows

13 24 14 11 11 14 12 12 12 13 13 29 – 17 9 10 11 11 25 15 19 29 15 15 17 17 – 11 11 19 23 15 15 18 17 36 38 12 12 – 11 9 15 16 8 10 10 8 10 10 12 23 23 16 10 12 12 15 8 12 22 20 13 12 11 13 11 11 12 12 \(\text{(R1b1a2-P312, 3950±400 ybp)}\)

in which DYS456 is fluctuating between 15 and 16 depending on a dataset. With 464 P312 haplotypes (Klyosov, 2010a) it was close to 15 in this work, with 37 haplotypes, it is 15.72, that is close to 16. Apparently some local branches which always present in any haplotype dataset cause these (slight) variations.

The P312 haplotype tree is shown in Fig. 10, and its base haplotype for the whole tree is shown below.
Fig. 10. 67 marker haplotype tree of 337 haplotypes of R1b1a2-P312 subclade. Six haplotypes in the dataset are marked as P312, they are scattered around the tree. 329 haplotypes are marked as P312*, and two (807 and 808) as P312**. Three haplotypes have DYS425=0, they do not form a separate branch.

All 337 haplotypes contain 4956 mutations from the above base haplotype, which gives 4956/337/0.12 = 123 \rightarrow 141 \text{ generations, that is 3525±360 years from a}
common ancestor. The first 37 markers contain 3663 mutations, which gives \(3663/337/0.09 = 121 \rightarrow 138\) generations, that is 3450±350 ybp; the first 25 markers contain 1981 mutations, which gives \(1981/337/0.046 = 128 \rightarrow 147\) generations, that is 3675±380 ybp. One can see that those are practically the same figures (3525, 3450, 3675 ybp) within margin of error.

However, various datasets of P312 haplotypes can produce slightly different data, albeit within margins of error. For example, a 273 haplotype P312 dataset (October 2010) having exactly the same base haplotype as shown above for the 337 haplotype dataset, contained 1804 mutations in the first 25 markers, which gave \(1804/273/0.046 = 144 \rightarrow 168\) generations, that is 4200±430 years to a common ancestor. That is why to consider only principal figures in TSCAs and ignoring margins of error might be misleading.

Apparently, the most accurate calculation of a timespan to a common ancestor of the P312 subclade was performed by a colleague of mine, Dr. Igor L. Rozhanskii. Using the logarithmic method, he subdivided P312 haplotypes on the 273 haplotype tree into several branches (they formed some yet unidentified subclades of P312) which showed the same TSCA by the logarithmic and the linear method. All these branches resulted in a common ancestor for P312 who lived 4350±700 ybp. Three “post-Iberian” downstream subclades, L21, U152 and SRY2627 gave 4000±500 ybp for their common ancestors. Finally, a common ancestor of the P312 and U106 subclades gave a common ancestor who lived 4800±700 ybp. This is the same figure which was shown above for a common ancestor of presumably L11 subclade in Europe, which also fits the time for the beginning of the Bell Beakers.

**P-312 null mutation haplotypes**

All 2299 67 marker haplotypes of R1b1a2-P312 and its subclade contained 67 of DYS425=0 haplotypes. Since that null mutation can be traced along a number of subclade branches starting from P312 down to (parallel)

- P312-U152-L2-L20,
- P312-L21-M222,
- P312-L21-M193, and
- P312-L176.2-SRY2627

some information can be obtained on P312 directions of migrations and their timing. Three null mutated P312* haplotypes were from Ireland five of their downstream U152* were from Portugal, Hungary and Germany, who yet more downstream U152-L2-L20 were from Germany. This may provide a hint of a movement of descendant haplotypes from Iberia to North East, to Germany.
Fifteen of P312-L21 null mutated haplotypes were all from Ireland and England, 28 of P312-L21* were from Ireland, England and Scotland, and four P312-L21** were from Spain, Ireland and Sweden. Both branches, L21M222 and L21-L193, were represented with one null mutated haplotype each, both from Ireland. Finally, six null mutated P312L176.2-SRY2627 were all from the Isles, namely from Ireland and England.

Fig. 11 shows the respective haplotype tree. It contains two principal branches, one at the bottom, which is obviously the older one, consisting of 25 haplotypes, and another a younger one, of 37 haplotypes.

Fig. 11. 67 marker haplotype tree of null mutation (DYS425=0) 67 haplotypes (284 and 297 are identical, as well as 345 and 346) of R1b1a2-P312 and its subclades.
The older branch has the following base haplotype:

11 11 19 23 15 15 18 17 36 38 12 12 – 11 9 15 16 8 10 10 8 10 100 23 23 16 10 12 12 15
8 12 22 20 13 12 11 13 11 11 12 12 (P312 null, sub-branch, 3575±400 ybp)

It is exactly the R1b1a2-P312, 3950±400 ybp base haplotype, shown above, only
with DYS425=0. The branch contains 374 mutations in all 25 haplotypes, which
gives 374/25/0.12 = 125 \(\rightarrow\) 143 generations, that is 3575±400 years from a
common ancestor. It means that null mutated P312 haplotype which later became
a common ancestor of this haplotype arose very close in time to its parent P312
ancestral haplotype.

The younger branch (in the upper part of the tree in Fig. 11) has the following
base haplotype:

11 11 19 23 16 15 18 18 36 37 12 12 – 11 9 15 16 8 10 10 8 10 9 0 12 23 16 10 12 12 16
8 12 22 20 13 12 11 13 11 11 12 12

It deviates from the parent R1b1a2-P312, 3950±400 ybp base haplotype, by 8
mutations (marked above), besides the DYS425=0 mutation. All 37 haplotypes
contain 234 mutations from the above base haplotypes, which gives 234/37/0.12
= 53 \(\rightarrow\) 56 generations, that is 1400±170 years to a common ancestor. 8 mutations
separates their common ancestors by 1800 years, which places THEIR common
ancestor at \((1800+1400+3950)/2 = 3575\) ybp, which is exactly the common
ancestor for the older branch. Therefore, the older null mutated haplotypes is the
parent one of the younger null mutated branch.

P312-U152

Suboclade U152 was studies in (Klyosov, 2010a) as a 84 haplotype 67 marker
dataset, and it was found that its base haplotype is as follows:

11 11 19 23 15 15 18 17 36 39 12 12 – 11 9 15 16 8 10 10 8 10 10 10 12 23 23 16 10 12 12
15 8 12 22 20 13 12 11 13 11 11 12 12 (U152, 4125±450 ybp, 84 haplotypes)

and its common ancestor lived 4125±450 ybp. Its base haplotype differs by only
one mutation (marked above) compared to its uncestral P312 base haplotype.
In the same study 302 of 25 marker U152 were considered. They contained 1968 mutations, which gave $1968/302/0.046 = 142 \rightarrow 166$ generations, that is $4150\pm425$ ybp.

Fig. 12. 67 marker haplotype tree of 312 haplotypes of R1b1a2-P312-U152 subclade and downstream subclades. Subclade U152, haplotypes 1-162; subclade U152-L2, haplotypes 163-275; subclade U152-L20, haplotypes 276-308; subclade U152-L4, haplotypes 309-312.

A tree of 312 U152 haplotypes from the 2299 haplotype dataset is shown in Fig 12. Its base haplotype is

13 24 14 11 11 14 12 12 12 13 13 29 - 17 9 10 11 11 25 15 19 29 15 15 17 17 - 11 11 19 23 15 15 18 17 36 **38** 12 12 - 11 9 15 16 8 10 10 8 10 10 12 23 23 16 10 12 12 15 8 12 22 20 13 12 11 13 11 11 12 12  (U152, 3800\pm380 ybp, 312 haplotypes)

that is exactly as that in P312 parent subclade. The CDYb allele, shown above in bold, equals to 38.02 as an average in all 312 alleles.
All 312 haplotypes have 4950 mutations from the above base haplotype, which gives $4950/312/0.12 = 132 \rightarrow 152$ generations, that is 3800±380 years to a common ancestor.

All 312 haplotypes (U152 and downstream subclades) contain 17 base haplotypes in the 12 marker format. It gives $[\ln(312/17)]/0.022 = 132 \rightarrow 152$ generations, that is 3800 years to a common ancestor. The identity of the results of the linear and logarithmic methods points at the one common ancestor for all the 312 haplotypes in the dataset.

162 haplotypes of only U152 subclade contain 9 base 12 marker haplotypes, which gives $[\ln(162/9)]/0.022 = 131 \rightarrow 150$ generations, that is 3750 years to a common ancestor. It means that removal of downstream subclades (L2, L20, and L4) from the 312 haplotype dataset as well as removal of 8 base haplotypes which belong to downstream subclades does not change the calculated timespan to a common ancestor of U152 subclade.

**U152-L2**

113 haplotypes of this subclade have the following base haplotype:

```
11 11 19 23 16 15 18 17 36 38 12 12 – 11 9 15 16 8 10 10 10 10 12 23 23 16 10 12 12
15 8 12 22 20 13 12 11 13 11 11 12 12  (L2, 4025±410 ybp, 113 haplotypes)
```

All haplotypes contain 1867 mutations from the base haplotype, which gives $1867/113/0.12 = 138 \rightarrow 161$ generations, that is 4025±410 years from a common ancestor. The 1.5 mutations, separating the L2 and U152 base haplotypes (shown in bold; they all are fractional mutations) are equivalent to 300 years between their common ancestors, and place THEIR common ancestor approximately $(300+4125+4025)/2 = 4200$ ybp. It is the U152 subclade itself, within margin of error.

In a total tree of 808 haplotypes of R1b1a2P312 subclade, or 312 haplotypes of P312-U152 subclade subclade, L2 haplotypes are scattered around the whole tree. It means that the L2 subclade does not have a distinct branch. It it expected, since haplotypes P312, U152 and L2 subclades are practically identical, and their common ancestors (of the present day haplotypes of these three subclades) lived practically in the same time. Therefore, except the SNP itself, nothing makes those haplotypes different at visual inspection or in their position on a haplotype tree.
The data obtained in this work fits well with a 95 haplotype 25 marker dataset. All haplotypes contained 631 mutations, which gave $631/95/0.046 = 144 \rightarrow 168$ generations, that is $4200\pm450$ years from a common ancestor (Klyosov, 2010a).

**U152-L2-L20**

Haplotypes of this subclade were considered in (Klyosov, 2010b), however, only 15 of 37 marker haplotypes were available that time (end of 2009). They contained 175 mutations, which gave $175/15/0.09 = 130 \rightarrow 149$ generations, that is $3725\pm470$ ybp.

Fig. 13. 67 marker haplotype tree of 32 haplotypes of R1b1a2-P312-U152-L20 subclade.
An updated haplotype tree of 32 haplotypes in the 67 marker format is shown in Fig. 13. It results in the following base haplotype (deviations from that of the parent L2 base haplotype are marked):


(L2-L20, 3650±400 ybp)

All haplotypes contain 489 mutations from the base haplotype, which gives $489/32/0.12 = 127 \rightarrow 146$ generations, that is 3650±400 years from a common ancestor. What it looks like 4 mutations between the L20 and L2 base haplotypes, is in fact 1.74 mutations on average, since all of them are fractional ones. It is equivalent to only 360 years between their common ancestors, and places THEIR common ancestor to approximately $(360+3650+4025)/2 = 4000$ ybp. It is the U152-L2 subclade itself, within margin of error.

**U152-L2-L20-L4**

The whole dataset of 2299 haplotypes includes only four 67 marker haplotypes of this subclade, which form a distinct branch on the tree (Fig. 14)
Fig. 14. A fragment of the 67 marker haplotype tree of 312 haplotypes of R1b1a2-P312-U152 with some subclades. Haplotypes 309-312 belong to subclade U152-L2-L20-L4, and form a separate branch (center). They are flanked by U152 haplotypes.

Most (or all) of these four are Ashkenazi from Latvia, Poland, and Ukraine. They have a base haplotypes as follows (19 mutations from the parent base L20 haplotype are marked; recLOH in DYS385a=14 was counted as one mutation):

13 24 14 11 **14** 14 12 12 12 13 13 29 – 17 9 10 11 **12** 25 15 19 **28** 15 **16** 17 17 – **12** 12 19 23 15 15 18 **20** 36 **36** 13 12 – 11 9 15 16 8 10 10 8 10 11 **11** 12 23 **24** 16 10 12 12 15 8 **13** 22 20 **12** 12 11 13 11 11 **14** 12 (L2-L20-L4, 1275±290 ybp)

These four haplotypes contain 23 mutations from the base haplotype above, which gives 23/4/0.12 = 48 → 51 generations, that is 1275±290 years from a common ancestor.
19 mutations between the L20 and L4 base haplotypes are equivalent to 4675 years between their common ancestors, and place THEIR common ancestor to approximately 4800 ybp. It is much “older” than that of the parent subclade, and can be explained by a poor statistics of the four haplotype dataset.

P312-L176.2

There are only five haplotypes of this subclade among all the 2299 haplotypes of P312 dataset (see Fig. 15, haplotypes number 1 through 5) Among these five two haplotypes are from England, one from Ireland, one from France, and one from Germany. The base haplotype is as follows (10 fractional deviations/mutations compared to the base P312 haplotypes are marked they amount to 6.6 mutations):

13 24 14 11 14 12 12 13 13 30 – 17 9 9 11 11 25 15 19 29 15 15 17 17 –
11 11 19 23 16 14 19 16 37 38 13 12 – 11 9 15 16 8 10 10 10 12 12 23 23 16 10 12 12
15 8 12 22 21 14 12 11 13 11 11 12 12 (R1b1a2-P312-L176.2, 3675±560 ybp)

Said five L176.2 haplotypes contain 77 mutations from the above base haplotype, which gives 77/5/0.12 = 128 → 147 generations, that is 3675±560 to their common ancestor.

6.6 mutations between P312 and L176.2 base haplotypes separate their common ancestors by 1450 years, and place THEIR common ancestor approximately at 4500 ybp. This is P312 itself within margin of error.

P312-L176.2-SRY2627

A tree of 155 haplotypes, which contains 141 haplotypes of SRY2627, five haplotypes of its upstream L176.2, and nine of its downstream L165 haplotype is shown in Fig. 15. All 141 haplotypes contain 1896 mutations from the base haplotype

13 24 14 11 11 14 12 12 13 13 29 – 17 9 10 11 11 25 15 19 29 15 15 17 18 –
11 11 19 23 16 15 18 17 37 38 12 12 – 11 9 15 16 8 10 10 10 12 12 23 23 16 10 12 10
16 8 12 22 20 13 12 11 13 11 11 12 12 (P312-L176.2-SRY2627, 3150±320 ybp)

which gives 1896/141/0.12 = 112 → 126 generations, that is 3150±320 years to a common ancestor.
Fig. 15. 67 marker haplotype tree of 155 haplotypes of R1b1a2-P312-L176.2 (haplotypes 1-5) and its subclades L176.2-L165 (haplotypes 6-14) and L176.2-SRY2627 (haplotypes 15-155). There is a branch of null mutation SRY2627 haplotypes on the upper-right hand side (haplotypes number 104-108), and an isolated null mutation haplotype (number 80) on the lower right-hand side.

Since most of the mutations between L176.2 and SRY2627 are fractional ones, there are not 12 of them, as marked above, but 8.2 mutations, which separate their common ancestors by 1825 years, and place THEIR common ancestor to approximately 4300 years before present. It is too high for that for L176.2, with its common ancestor of 3675±560 ybp, however, it might be within margin of error.

One can notice that the mutational difference between SRY2627 and its presumably parent L176.2 base haplotype is larger (12 “visible” mutations and 8.2 actual ones, equivalent to 1825 years between their common ancestors).
compared the “grandfather” P312 base haplotype (6 “visible” mutations and 4.7 actual, which is equivalent to 1000 years between their common ancestors). On the other hand, the “ladder” of the subclades and their datings seems to be right: P312 (3950 ybp) → L176.2 (3675 ybp) → SRY2627 (3150 ybp). In other words, the L176.2 branch deviates (by their haplotypes) from both P312 and SRY2627, albeit should be between them. Something might be missing in the phylogeny of these subclades. The answer what is missing is given below, after the section on the L165 subclade.

P312-L176.2-SRY2627 null mutation

There are only six haplotypes in this group among the 2299 haplotypes of the P312 dataset (five of them are located in the upper right-hand side in Fig. 15, haplotypes 104-108). Those five haplotypes have the following base haplotype

11 11 19 23 15 15 18 18 38 39 12 12 – 11 9 15 16 8 10 10 8 10 10 22 23 16 10 12 10 19 
8 12 22 21 13 12 11 13 11 11 12 12                  (SRY2627, null, 325±120 ybp)

in which mutations from the SRY2627 base haplotype are marked. Those five haplotypes have only 8 mutations from the above base haplotype, which gives 8/5/0.12 = 13 generations, or 325±120 from their common ancestor. These individuals are likely rather close relatives (from Ireland and England). A comparison with the remotenull mutation haplotype (number 80)

11 11 19 23 16 14 18 17 37 38 12 12 – 11 9 15 16 8 10 10 8 10 10 23 23 16 10 12 10 15 
8 11 23 20 13 12 11 13 11 11 12 12                  (SRY2627, null, singular haplotype #80)

shows 21 mutations between them, which translates to 500 years between their common ancestors, and places THEIR common ancestor to approximately (5300+325)/2 = 2800 ybp. This fits rather well with the “age” of SRY2627 of 3150±320 ybp.

P312-L176.2-L165

This is a subclade, “parallel” to SRY2627 subclade, both with the upstream P312-L176.2 subclade. There were only 9 haplotypes among the 2299 haplotype P312 dataset, and they were spread around the tree (Fig. 15) in three different branches. This is an indication that the subclade is old, maybe almost as old as the parent P312 subclade.
With haplotypes, spread around a tree in such a nonsymmetrical manner (one branch of 7 haplotypes, and two single haplotypes in opposite position around the tree) it would be inaccurate to consider all nine haplotypes as randomly distributed and coming as such from one common ancestor. This common ancestor might be a phantom one, since the largest branch (with 7 haplotypes) would “pool” mutations to itself, resulting in a distorted base haplotype, hence, distorted number of mutations. Instead, the system of 9 haplotypes should be treated as three independent “branches”, two of them are single haplotypes.

The 7-haplotype branch has the following base haplotype

11 11 19 23 16 15 18 17 37 38 12 12 – 11 9 15 16 8 10 8 10 10 10 12 23 16 10 12 12
15 8 12 22 20 14 12 11 13 11 11 12 12

(L165, 7-hapl. branch, 2325±360 ybp)

with 71 mutations from it. It gives 71/7/0.12 = 85 → 93 generations, that is 2325±360 years from its common ancestor. The apparent 8 mutations between L153 and its parent P312 base haplotypes (marked above) is fact amount to 8.72 mutations (two of them are 1.43 and 1.29 on average). It translates to 1925 years between their common ancestors and places THEIR common ancestor to (1925+2325+3950)/2 = 4100 ybp. This is indeed a common ancestor of the P312 subclade within margin of error.

However, this is only one subbranch of L165 on the haplotype tree (Fig. 15). When we add two singular haplotypes (numbers 6 and 7 on the tree, Fig. 15)

11 10 19 23 17 15 19 16 38 38 12 12 – 11 9 15 16 8 10 8 10 10 8 23 24 16 10 12 12
15 8 13 22 20 14 13 11 13 11 12 12

(L165, Scotland, singular haplotype #6)

13 24 14 10 14 14 12 12 13 14 13 30 – 18 9 10 11 11 24 15 19 29 15 15 16 17 –
11 11 19 23 16 15 17 18 38 39 11 12 – 11 9 15 16 8 11 10 8 10 10 12 23 24 16 10 12 12
15 8 12 22 20 13 12 11 14 11 11 12 12

(L165, England, singular haplotype #7)

they three have 29 mutations from their presumed base haplotype. This places THEIR common ancestor to approximately 3000 ybp. His (base) haplotype was apparently (minimized on mutations between all the three base haplotypes)

11 11 19 23 16 15 18 17 38 38 12 12 – 11 9 15 16 8 10 8 10 10 10 12 23 24 16 10 12 12
15 8 12 22 20 14 12 11 13 11 11 12 12

(L165, ~ 3000 ybp)
As it was expected, this figure, 300 ybp, obtained by comparing haplotypes around the tree, is (slightly in this particular case) higher than calculated from all 9 haplotypes. They have 105 mutations, which gives 105/9/0.12 = 97 → 108 generations, that is a (slightly lower) value of 2700±380 years from a common ancestor.

What might be missing in the phylogeny of P312

As it was mentioned above, and not once, calculations in the L176.2 subclade along with its downstream subclades SRY2627 and L165 typically produce TSCA values higher than it is expected. It seems that a root of these subclades is missing, and the P312 subclade, which supposed to be their root, has a lower TSCA (around 4000 ybp) that it should have had. It is not a surprise, though, since it was already calculated above that P312 along with U106 have a common ancestor who lived ~ 4800 ybp. Now let us check if P312 itself could arose that time, and not around 4000 ybp.

When we consider all three base haplotypes which hint that their common ancestor could have lived earlier than 3700-4100 ybp, we find that all of them have 20 mutations (marked below) from a deduced base haplotype.

\[
\begin{align*}
\end{align*}
\]

20 mutations in three base haplotypes translate into 20/3/0.12 = 1500 years plus their average “age”, which is 3275 years, which gives 4775 years from a common ancestor of all the three subclades. It supposed to be either the common ancestor of the P312 subclade himself, or an immediate P312 downstream, unidentified as yet. Again, it is the beginning of Bell Beaker times in Iberia.

Some details to these data can be found by considering the 1000 Genomes Project (http://dna-forums.org/index.php?/topic/14907-two-potentially-large-p312-snps/). Rich Rocca has reported that considering samples from Iberia and former Spanish colonies in Colombia, Mexico and Peru he was able to identify several
new candidates SNPs (all indexed starting with Z) downstream of P312 and upstream of L176.2 (see chart below). All these new candidate SNPs were found to be negative in P310, U152, L21 and U106 (Rich Rocca, ibid.).


In fact, all these new findings are unrelated to TSCA calculations in this paper, and serve – in this context - no more than an illustration of a complexity of phylogeny of R1b1ba2, though, as well as any other haplogroup.

P312-L238

This subclade contains only two haplotypes among all 2299 haplotypes in the dataset, one from England and one from Sweden. They are very similar with each other, and sit next to each other on the haplotype tree on the same small branch (Fig. 4):
Nine mutations between them place their common ancestor to approximately 1000 ybp.

**Geographical distribution of R1b1a2-P312 subclades**

The main challenge in getting anything significant from a regional distribution of P312 and/or U106 subclades and timespans to their common ancestors is in the fact that all of them are often alike, and if not, they might reflect more recent movements, mixing, migrations, etc. The Ga\l\l\ic wars of Julius C\ae\s\ar, for example, has changed the population landscape a great deal two millennia ago. There were other major population-related event such as black plague of the 14th century, almost permanent wars in Europe since those times (and before), world wars, etc. As a result, the geographical spread of P312 and U106 in Europe is far flung and uneven, and hardly reflects their distribution 4000-3000 years before present.

Let us see what can be observed from geography of R1b1a2-P312 distribution, if anything. It would be helpful if we put forward a general hypothesis based on several observations, and see if data on regional distributions of P312 and its subclades are compatible with that hypothesis.

This hypothesis was in fact advanced earlier and briefly described in the beginning of this paper (Klyosov, 2008-2011, see references there). According to it, an upstream subclade of P312 and U106 (likely R1b1a2-L11/L151/P310/P311, along with L51/M412) has arrived to Iberia ~ 4800 years before present, split P312 and U106, which moved up North to continental Europe as Bell Beakers, and spread over Europe between 4500 and 3200 ybp. It seems that both P312 and/or U106 went through a severe population bottleneck in the 3rd millennium BC, which had lasted almost a thousand years. Therefore common ancestor of current bearers of P312 and U106 can be detected only around 3700-4100 ybp. Only superposition of the their respective base haplotypes along with their TSCAs made possible to calculated that their common ancestor (presumably R1b1a2-L11) lived 4800 ybp, at the very beginning of Bell Beaker movements.
This part of the hypothesis is supported by archaeological data, according to which the oldest artifacts related to the Bell Beakers were found in the Pyrenees and dated by 2900-2500 BC (Muller et al, 2001).

The following maps, published by Myres et al (2010), provide additional support to this hypothesis. One can see that all upstream (of P312 and U106) subclades—M269 → L51 → L11 have the highest density in Iberia.

![Map of M269 subclade in Europe](image1)

The current distribution of the M269 subclade in Europe (Myres et al, 2010)

![Map of L51/M412 subclade in Europe](image2)

The current distribution of the L51/M412 subclade in Europe (Myres et al, 2010)

![Map of L11 subclade in Europe](image3)

The current distribution of the L11 subclade in Europe (Myres et al, 2010)

![Map of P312 subclade (with subclades) in Europe](image4)

The current distribution of the P312 subclade (with subclades) in Europe (Myres et al, 2010)

![Map of P312* subclade in Europe](image5)

The current distribution of the P312* subclade in Europe (Myres et al, 2010)
The most significant data here is that the P312* subclade, separated from its downstream subclades, still has the highest presence in the Pyrenees. Subclade M153, which is the immediate subclade of P312, is presented only in Spain among all 2299 haplotypes in the dataset. It has a common ancestor of ~3640 ybp. As many as 37 haplotypes of this M153 subclade were found among 750 R1b haplotypes in the Pyrenees (Adams et al, 2009), and the Basques had it as 15 haplotypes from their 37, the highest amount among all other R1b subclades (Klyosov, 2010c).

The Bell Beakers apparently moved in two principal directions – to the continental Europe, and directly to British Isles, apparently by sea. The last direction is supported by the following two maps.

The current distribution of the **L11** (xU106, P312) subclade in Europe (Myres et al, 2010)

The current distribution of the **L21** (xM222) subclade in Europe (Myres et al, 2010)

One can see that the L11 subclade, the ancient and upstream one with respect to P312, is presented on the Isles, when its downstream subclades are removed. Otherwise it has a weak presence on the continent. In the same manner, L21, an immediate downstream subclade of P312, has the highest presence in Ireland, when its downstream M222 is removed. On the other hand, bearers of L21 subclade could reach the Isles by land from the Pyrenees via South-Western part of Europe (now France) and to the Isles:
Subclades P312, U106, and their immediate subclades U152, L21, and L176.2 (subclades of U106 were not considered in this study) all coalesce to their common ancestors who all lived between 4100 and 3700 ybp (see the chart in the beginning of this article). Besides, common ancestors of the immediate subclades of U152, namely L2 and L20, also lived in the same time span (4025 and 3650 ybp on average, respectively). P312 null mutation subclade (3575 ybp) and U152 null mutation subclade (3525 ybp) also lived at the same time or close to it.

It seems that U106 and U152 either moved out as Bell Beakers from the Pyrenees, or arose in the continental Europe, after the Beakers left the peninsula. They both practically do not show their presence in Iberia nowadays (see the maps below).

It seems that all other regions in Europe, such as nowadays Scandinavia, North-Western Europe, Germany, Poland, Central Europe have been populated by R1b1a2-P312, U106 and their subclades along the Bell Beakers migration route, between 4500 and 3200 ybp. However, since the migrants carried their
haplotypes across Europe without principal population bottlenecks, $\delta$CAs are just about the same across Europe, namely between $\delta$00 and 3200 ybp.

Archaeological data in general supports this pattern of DNA genealogy. According to them (see map below, from www.buildinghistory.org/distantpast/bellbeaker.shtml with a reference to Muller et al, 2001), the oldest Bell Beaker sites were found in the Pyrenees (4900-4500 ybp) and nearby (France - North Italy), and datings of Bell Beaker sites shifts to slightly later times in Central Europe, Germany and Scandinavia.

In principle, archaeology chronological data show that the development of Bell Beakers took place from the west (more specifically from the southwest) toward the east and northeast. The same data follows from DNA genealogy, as it is shown in this article.

The South-Eastern part of Europe, including the Balkans, was a principal destination of yet another migration wave of R1b1a2, but largely of L23 subclade, with a particular feature of DYS393=12. This allele is typical for the Russians, R1b1a2 inhabitants of the Caucasus (Armenians, Dagestanis and others), Anatolia, Middle East, Asia Minor. This is apparently an immediate source of the L23 subclade in Europe. There is almost none of that subclade in Iberia, it apparently did not survive the migration route from Middle East across North Africa into Pyrenees (see above). Indeed, the map above does not show Bell Beaker sites in South-East Europe and Asia Minor, and East of Germany (except
in Northern Poland in later times). Some traces of Bell Beakers on the Balkans are attributed to Bronze Age, significantly later times.

The following map, taken from the World Families Forums (RL277+)

One can see that the highest amount of that subclade is in Asia Minor (up to 3.4%), in South Italy up to 1.1%, on the Balkans in North Italy up to 0.4-0.6%, and close to zero in Central Europe, in the Isles, in Northern Europe.

The next map, from the same source as quoted above, shows some alleged ways how R1b1a2-P312 could have reached the Isles by sea.

The above statement that before arrival to the Iberian peninsula R1b1a2 bearers went across North African shore from Midle East to the Atlantic, is supported by archaeological data that the area with Bell Beakers takes also parts of northern Africa in Algeria and Morocco
(http://www.novelguide.com/a/discover/aneu_01/aneu_01_00103.html)
Now, let us take a look at haplotypes of the R312-L21 subclade across Europe. Much of the data arranged by the regions and considered below were provided by Mark Jost. He expressed a concern that the 67 marker panel includes fast mutated markers as well as markers subjected to reLcOH mutations, and suggested to employ a 49 marker panel, in which 18 markers are removed (see above, the Methodology). Since it is a widespread (and not justified, as it is shown below) concern, this work also shows that it does not matter which haplotype panel to employ. A panel should be properly calibrated, this is the only one thing that matters.

**Ireland, L21**

Let us start with the most representative population in this dataset, Ireland, which contains 153 haplotypes. We will first compare 49 and 67 marker panels (Fig. 16 and 17). In both of them the haplotype tree looks rather symmetrical and “smooth”, with a good likelihood of being derived from one common ancestor. Local small branches always present in any haplotype tree, and they should not cause any concern unless they form a separate distinct branch.

The 49 marker L21 Irish 153 haplotype dataset has the following base haplotype:

```
11 9 8 10 10 8 10 16 10 12 12 15 8 12 22 20 13 12 11 13 11 11 12 12
(Ireland, L21, 49-marker panel, 3650±380 ybp)
```
In fact, it is exactly the same as that of the “overall” L21 1024 haplotype dataset, considered above, except said 18 markers are eliminated.

All 153 haplotypes contained 1550 mutations, which gives 1550/153/0.08 = 127 → 146 generations, that is 3650±380 years to a common ancestor. 0.08 here is the mutation rate constant measured in mutations per haplotype per generation (25 years, see explanations above). The “overall” L21 dataset of 1024 of 67 marker haplotypes has a common ancestor who lived 3750±380 ybp. They are practically the same figures, with a difference of only 2.7% between them, well within the margin of error.

![Diagram of 49 marker haplotype tree of 153 Irish R1b1a2-L21 haplotypes]

Fig. 16. 49 marker haplotype tree of 153 Irish R1b1a2-L21 haplotypes

In the 67 marker format the Irish 153 haplotype L21 dataset reveals the following base haplotype:
(Ireland, L21, 67-marker panel, 3575±365 ybp)

It is exactly as that deduced from 1024 L21 haplotypes, with a common ancestor of 3750±380 ybp (see above).

Fig. 17. 67 marker haplotype tree of 153 Irish R1b1a2-L21 haplotypes

The missing 18 ("fast and palindromic") markers added in the 67 marker panel (compared to those in the 49 marker haplotypes) 746 mutations, making it 2296 mutations. It gives 2296/153/0.12 = 125 → 143 generations, that is 3575±365 years to a common ancestor. It is again practically the same figure as that for 49
marker haplotypes and for the “overall” L21 dataset of 1024 haplotypes. An average between all the three figures results in 3658±88 ybp, that is 2.4% variation. In other words, ancient bearers of the L21 subclade “brought a timespan to their common ancestor” to Ireland without any noticeable change.

It should be noted that the 153-haplotype series contains 8 of 12-marker base haplotypes, which gives \( \frac{\ln(153/8)}{0.022} = 134 \rightarrow 155 \) generations, that is ~ 3875 years to a common ancestor. One can see that the logarithmic method gave results within margin of error with that by the linear method, 3575±365 ybp. It shows that the dataset is “smooth” indeed, and is derived from one common ancestor.

**England, L21**

Another example – England. The L21 dataset contains 74 haplotypes (Fig. 18). In the 49 marker format it has the following base haplotype

\[
13\ 24\ 14\ 11\ 12\ 12\ 12\ 13\ -\ 17\ 11\ 11\ 25\ 15\ 19\ 30\ -\ 11\ 11\ 16\ 15\ 18\ 17\ 12\ 12\ -\ 11\ 9\ 8\ 10\ 10\ 10\ 10\ 16\ 12\ 12\ 15\ 8\ 12\ 22\ 20\ 13\ 12\ 11\ 13\ 11\ 11\ 12\ 12
\]

(England, L21, 49-marker panel, 3950±420 ybp)
Fig. 18. 49 marker haplotype tree of 74 English R1b1a2-L21 haplotypes

The only difference in DYS449 (marked) is actually not a real difference: it is 29.42 in the Irish haplotype, hence, rounded to 29, and it is 29.62 in the English haplotype, therefore, rounded to 30. In fact, the differences 0.2 mutations. In all 1024 L21 haplotypes the average allele there equals to 29.50.

All 74 of 49 marker haplotypes contain 805 mutations from the above haplotype, which gives $\frac{805}{74}/0.08 = 136 \Rightarrow 158$ generations, that is $3950 \pm 420$ years to a common ancestor.

The 67 marker dataset adds 424 mutations, making it $\frac{1229}{74}/0.12 = 138 \Rightarrow 161$ generations, that is $4025 \pm 420$ ybp. The difference between 49 and 67-marker panels is less than 2%.
Scotland, L21

The L21 Scottish dataset contains 78 haplotypes (Fig. 19). In the 49 marker format it has the following base haplotype:


(Scotland, L21, 49-marker panel, 3325±350 ybp)

Fig. 19. 49 marker haplotype tree of 78 ScotlandR1b1a2-L21 haplotypes

Again, the deviations (marked above) are minimal ones between the Irish, English and Scottish base haplotypes. In DYS391 the respective averaged alleles are 10.69, 10.58 and 10.40. In DYS449 they are 29.42, 29.62, and 29.73,
respectively. There might be some trend, however, its analysis is beyond the scope of this article. As it was noticed above, in all 1024 L21 haplotypes the average DYS449 allele is 29.50.

All 78 haplotypes contain 730 mutations from the above base haplotype. It gives $730/78/0.08 = 117 \rightarrow 133$ generations, that is $3325 \pm 350$ years to a common ancestor. The 18 markers in the 67 marker panel add 372 mutations, which gives $1102/78/0.12 = 118 \rightarrow 134$ generations, that is $3350 \pm 350$ years to a common ancestor. The difference between 49 and 67-marker panel is less than 1%.

One can see that on some reason a timespan to a common ancestor of the L21 subclade is consistently lower in Scotland compared to England and Ireland. The difference is rather small and on the verge (or within) of the margin of error, hence, there is no reason to discuss it seriously, particularly in absence of any supportive data, such as archaeological ones.

**Wales, L21**

There are 38 haplotypes available. The base haplotype is identical as that in England, with DYS449=29.74, and DYS391=10.79:

(Wales, L21, 49-marker panel, 3700±410 ybp)

391 mutations in the dataset give $391/38/0.08 = 129 \rightarrow 148$ generations, that is 3700±410 years to a common ancestor. It is essentially the same as those in England (3950±420 ybp) and Ireland (3650±380 ybp).

**France, L21**

The base haplotype of a dataset of 20 haplotypes is identical as that in Ireland, with DYS449=29.30, and DYS391=10.65:

(France, L21, 49-marker panel, 4100±490 ybp)

225 mutations in the dataset give $225/20/0.08 = 141 \rightarrow 164$ generations, that is 4100±490 years to a common ancestor. It is tempting to say that it “older” compared to those in the Isles and points at a route from France to the Isles, however, it is in fact within the margin of error.
Germany, L21

The base haplotype of a dataset of 14 haplotypes is identical as those in Ireland and France, and generally as that of the L21 subclade, except an allele at DYS534 (marked below). While it is on average 15.33 for all 2299 haplotypes (P312), 15.19 in 1024 L21 haplotypes, 15.32 in England, 15.25 in France, 15.13 in Wales, it is 15.64 in Germany.

(Germany, L21, 49-marker panel, 3700±480 ybp)

The noticeable deviation of this marker in Germany from those from Iberia, France, the Isles, might indicate the distant location of the region from South Western Europe, where L21 is apparently arose around 4000 ybp.

145 mutations in the dataset give $145/14/0.08 = 129 \rightarrow 148$ generations, that is 3700±480 years to a common ancestor.

Spain, L21

The base haplotype of a dataset of 11 haplotypes is identical as that in all 1024 L21 haplotypes, described above. DYS449 averaged allele among 11 haplotypes is 29.73, which is close to 29.50 in all 1024 L2 haplotypes, and practically to all regional populations considered in this article.

(Spain, L21, 49-marker panel, 3675±500 ybp)

113 mutations in the dataset give $113/11/0.08 = 128 \rightarrow 147$ generations, that is 3675±500 years to a common ancestor. It is again within margin of error with all other regional populations considered here.

One might say that the Spain L21 population (of 11 haplotypes) is “younger” compared to some other European population. It is not true. First, all of them are within margin of error. Second, statistics is becoming progressively poorer with reducing datasets being analyzed. Third, it was noted above that bearers of P312 haplotypes in the Pyrenees apparently went through a severe population bottleneck, which some of them moved as the Beakers up to the continental
Europe. Therefore, a timespan to common ancestors could be shorter in the Pyrenees compared to their more lucky descendants in the continental Europe.

**Spain + Portugal, P312*, 67 markers**

When P312* subclade is considered in the 67 marker format, it contains 20 haplotypes from Spain and Portugal, with exactly the same base haplotype as that of the total P312 dataset (see above):

11 11 19 23 15 15 18 17 36 38 12 12 – 11 9 15 16 8 10 10 8 10 10 12 23 23 16 10 12 12
15 8 12 22 20 13 12 11 13 11 11 12 12 (Spain + Portugal, P312*, 3950±400 ybp)

The base haplotype of a dataset of 11 haplotypes is identical as that in all 1024 L21 haplotypes, described above. DYS449 averaged allele among these 20 haplotypes is 29.00 (in the L21 series it was 29.50).

307 mutations in the dataset give $307/20/0.12 = 128 \rightarrow 147$ generations, that is $3675\pm500$ years to a common ancestor, exactly as it was with 11 49 marker haplotypes from Spain. However, five Portuguese haplotypes gave $84/5/0.12 = 140 \rightarrow 163$ generations, that is $4075\pm600$ ybp.

Overall, dataset contained 32 of 67-marker haplotypes of the Iberian origin. They contained 209 mutations in the 25 marker format, 401 mutations in the 37 marker format, and 526 mutations in the 67 marker format. It gives:

209/32/0.046 = 142 \rightarrow 166 generation, that is $4150\pm500$ ybp

401/32/0.090 = 139 \rightarrow 162 generations, that is $4050\pm450$ ybp

526/32/0.120 = 137 \rightarrow 159 generations, that is $3975\pm430$ ybp

These are practically the same timespans, within margin of error.

**Other regions, L21 subclade, 49 marker haplotypes**

The rest of regions in Europe with respect to their L21 haplotypes are represented by small number of haplotypes, hence, the data are not accurate and have wide margins of error. We will briefly describe them, however, any strong conclusions cannot be made from the data below.

**Norway**, 9 haplotypes, $82/9/0.08 = 114 \rightarrow 129$ generations, $3225\pm480$ ybp.
**Sweden**, 6 haplotypes, \(55/6/0.08 = 115 \rightarrow 130 \text{ generations}, 3250 \pm 550 \text{ ybp.} \)

**Luxemburg**, 4 haplotypes, \(37/4/0.08 = 116 \rightarrow 132 \text{ generations}, 3300 \pm 630 \text{ ybp.} \)

**Finland**, 4 haplotypes, \(19/4/0.08 = 59 \rightarrow 63 \text{ generations}, 1575 \pm 260 \text{ ybp.} \)

**Poland, P312* subclade, 67 marker haplotypes**

The rest of regions in Europe with respect to their P312* haplotypes are represented by small number of haplotypes, hence, the data are not accurate and have wide margins of error. Here is an example of haplotypes from Poland, with an addition of some haplotypes from Lithuania and Ukraine.

**Poland**, 4 haplotypes in the P312* dataset, \(50/4/0.12 = 104 \rightarrow 116 \text{ generations, that is} 2900 \pm 500 \text{ ybp} \)

**Poland/Lithuania/Ukraine** 7 haplotypes (the above 4 haplotypes plus 3 haplotypes from Lithuania and Ukraine, provided by Larry Mayka) \(116/7/0.12 = 138 \rightarrow 161 \text{ generations,} 4025 \pm 550 \text{ ybp.} \)

***

As a conclusion, consideration of R1b1a2-P312 haplotypes and downstream subclades and calculations of timespans to common ancestors of the respective populations resulted in a ladder of TSCAs associated with the phylogenetic (subclade) tree. The pattern obtained supports the hypothesis according to which an upstream subclade of P312 and U106 (likely R1b1a2-L11/L151/P310/P311, along with L51/M412) has arrived to Iberia ~ 4800 years before present, split P312 and U106, which moved up North to continental Europe as Bell Beakers, and spread over Europe between 4500 and 3200 ybp. It seems that both P312 and U106 went through a severe population bottleneck in the 3rd millennium BC, which had lasted almost a thousand years. Therefore, a common ancestor of current bearers of P312 and U106 can be detected only around 3700-4100 ybp. Only superposition of the their respective base haplotypes along with their TSCAs made possible to calculate that their common ancestor (presumably R1b1a2-L11) lived 4800 ybp, at the very beginning of Bell Beaker movements. This part of the hypothesis is supported by archaeological data, according to which the oldest artifacts related to the Bell Beakers were found in the Pyrenees and the Bell Beaker movement was in the direction from South-West to North and North-East of Europe and the Isles. It is of interest that archaeologists often
claim that the theory of a "Beaker People" has been discarded, since they could not attribute "Beaker People" to any certain population in Europe. According to them, it was "Bell Beaker phenomenon", not "people". Now, with appearance of DNA genealogy, we can state that there were the "Beaker People". There were R1b1a2-P312 people and bearers of P312 downstream subclades.

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MacDonalds and Scottish R1b1a2 Haplotypes
(an updated version)

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Introduction

This article updates an earlier paper [Klyosov, A.A. (2010) MacDonalds and Scottish R1b1b2 haplotypes. Proc. Russian Academy of DNA Genealogy, 3, No.10, 1696-1735], since after the publication the mutation rate constant for 67 marker haplotypes was decreased by 21% after its careful re-calibration [Klyosov, A.A. and Rozhanskii, I. L. (2010) Reconsideration of an average mutation rate constant for 67 marker haplotypes– from 0.145 to 0.120 mutations per haplotype per generation. Proc. Russian Academy of DNA Genealogy, 3, № 12, 2039-2058].

Clan Donald R1b1a2 haplogroups and lineages

The Clan Donald USA Project (http://dna-project.clan-donald-usa.org/tables.htm) after a recent consideration contained 657 R1b haplotypes, 288 of them were in the 67 marker format.

A haplotype tree of those 67 marker haplotypes is shown in Fig. 1. The numbering has been done in according with the listing of R1b haplotypes in the same order as they were presented by the end of August, 2010. The Project organizers employed a color code for designation of different subgroups of R1b on the list. A connection between the numbering and the color code is as follows:

Red
Pink
Brown
Maroon
Green
Dark Blue
Blue Green

1-71
72-82
83-88
89-100
101-183
184-193
194-196
Yellow Gray  197-204
Violet        205-210
Orange        211-215
Magenta       216-242
Pale Violet   243-246
Gray          247-251
Pale Green    252-260
Dark Blue – Green  261-265
Black         266-275
Pale Blue     276-278
Light Brown   279-285
Dark Green    286-288
Yellow Green  289-299
White         300-307
Yellow (unclassified) 308-657

Only 67 and 37 marker haplotypes have been considered and analyzed in this study. In principle, nothing prevents to repeat this work with 25- and 12-marker haplotypes, however, resolution of the haplotype tree would be not so good, since three-quarters and more of alleles in haplotypes will be lost.

The word “Scottish” in the title of this paper is conditional, since many of the listed haplotypes are not necessarily “Scottish”. However, many (and probably most) of them are. After all, names and territories in the field of DNA genealogy are all conditional, taking into account migrations of the past.
Fig. 1. A 67-marker haplotype tree for 288 haplotypes of R1b haplogroup (mainly subclades of R1b1b2) of the Clan Donald USA project [4][4].

http://dna-project.clan-donald-usa.org/tables.htm

The first wide branch of haplotypes in the upper left quadrant belongs mainly to RED subgroup, with its adjacent MAROON and PINK sub-sub-groups. We will consider here whether the last two are independent branches, or downstream ones, descending from the RED branch. Here as the branch looks on the linear tree (a fragment).
Fig. 2. A fragment of the 67-marker linear haplotype tree, depicting the upper left branch of the haplotype tree, shown in Fig. 1. One can see that some “unclassified” haplotypes (numbers above 308) in fact are parts of “color coded” subgroups, such as haplotypes 328, 437, 584 belong to the RED subgroup, haplotypes 347 and 469 remain to be “unclassified” and do not join any subgroup in the tree, and haplotype 14 (RED) is in fact “unclassified”, it does not belong to the RED subgroup, at least according to its haplotype structure.

RED

The Project organizers described the RED branch as follows:

Descendants of the kindred of the Dalriadic royal house in Scotland lie within in this group. However, only a fraction of people in the group are expected to be descendants of the royal house; the group is simply too large and diverse. Fergus, Angus, and Lorne, the sons of Erc, are descended per Irish and Scottish history from Cairbre Riada, king of Irish Dalriada. Cairbre Riada was descended from Conor II High King of Ireland and Sarad, daughter of Conn of the Hundred Battles. Irish history indicates that Cairbre had led his followers from Munster to Antrim. This kindred is traditionally considered to be of Eriann descent. Reverends Archibald and Angus MacDonald appear to have erred in placing Colla Uais in this line of descent. All our participants in this group who have been SNP tested have tested positive for the SNP marker L21/S145, making this group a separate Haplogroup within R1b.

According to the analysis in the preceding work (Klyosov, 2011) and earlier studies (Klyosov, 2010a,b,c) the base (ancestral) L21 haplotype is as follows:

13 24 14 11 14 12 12 12 13 13 29 – 17 9 10 11 11 25 15 19 29 15 15 17 17 –
11 11 19 23 16 15 18 17 36 38 12 12 – 11 9 15 16 8 10 10 8 10 10 10 12 23 23 16 10 12 12
15 8 12 22 20 13 12 11 13 11 11 12 12
(L21, 3750±380 ybp)

A common ancestor of this subclade lived 3750±380 years before present.

Let us see what the RED branch tells us in that regard. 18 haplotypes in the Red1 branch (67 marker haplotype 432, “unclassified”, turned out to be identical with haplotype 12, and was removed from the count) contained collectively 102 mutations from the base haplotype (apparently ancestral)

13 24 14 10 11 14 12 12 12 13 13 30 – 18 9 10 11 11 25 15 19 30 15 15 17 17 –
11 12 19 24 15 15 18 17 36 37 12 12 – 12 9 15 16 8 10 10 8 10 10 12 22 23 16 10 12 12
15 8 11 22 20 13 12 11 13 11 11 12 12
It had 11 mutations (marked in bold) compared to the base L21 haplotype (see above), which corresponds to 2550 years between their common ancestors (actually, to the present time and back to another common ancestor). We will need this figure later.

Such an approach with a haplotype tree building allows us to move two “unclassified” haplogroups, 328 and 437 (see legend to Fig. 2) to the RED branch. They belong there. Bearers of these two haplotypes will probably be delighted.

102 mutations in 18 of 67 marker haplotypes correspond to 102/18/0.12 = 47 generations (25 year generations according to the calibration) without a correction for back mutations (Klyosov, 2009a), or 50 generations with the correction, that is 1250±175 years to a common ancestor for the branch Red1 (Figs. 1 and 2). This is the mid of the 8th century AD plus-minus a century or two.

All mutations in the Red1 base haplotype (above) are rather common, except one, in a pair YCAIIa,b = 1924. Commonly in R1b1a2 haplotypes it is 1923. This “24” is certainly a signature for the RED branch, for all Red1, Red2 and Red3 subbranches, as it will be shown below. It already shows their tight relationships.

Let us move to the Red2 subbranch. 16 haplotypes in the Red2 branch (including “unclassified” haplotype 584, which turned out to be a member of a tight family of four haplotypes, see Fig. 2) contained collectively 115 mutations from the base haplotype

```
13 24 14 10 11 14 12 12 12 13 13 30 – 18 9 10 11 11 25 15 19 30 15 15 17 17 –
11 12 19 24 16 15 18 17 37 38 12 12 – 12 9 15 16 8 10 10 8 10 10 12 22 23 16 10 12 12
14 8 11 22 20 13 12 11 13 11 11 12 12
```

115 mutations in 16 of 67 marker haplotypes correspond to 115/16/0.2 = 60 generations without a correction for back mutations, or 64 generations with the correction, that is 1600±220 years to a common ancestor for the branch Red2 (Figs. 1 and 2). This is the 5th century AD plus-minus a couple of centuries.

The base Red2 haplotype has the same number of 11 mutations compared to the base L21 haplotype, which corresponds to 2550 years between their common ancestors. On the other hand, base haplotypes of Red1 and Red2 branches differ from each other by only 2.85 mutations on average (it looks like four mutations, when rounded up) in the third and the forth panels of the 67-marker haplotypes. This places their common ancestors by only 625 years apart. It means that a common ancestor of the Red1 and Red2 branches lived approximately (625+1250+1600)/2 = 1700 years before present. It seems that a common ancestor of the Red1 branch descended from the Red2 branch. We will examine it later.
The Red3 subbranch contains only 6 haplotypes, which collectively contain 45 mutations from the base haplotype


45 mutations in 6 of 67 marker haplotypes correspond to 45/6/0.12 = 63 generations without a correction for back mutations, or 67 generations with the correction, that is 1,675±300 years to a common ancestor for the branch Red3 (Figs. 1 and 2). This is the 4th century AD plus-minus three centuries. Six haplotypes do not provide with a good statistics, hence, rather large margins of error.

One can see that common ancestors of the Red1, Red2 and Red3 branches lived within a few centuries, 1,250±75, 1,600±220, and 1,675±300 years ago. They are equidistant from a common ancestor of L21 subclade (1 mutations in each of their base haplotypes). Furthermore, their base haplotypes (Red1, Red2 and Red3) differ from each other by only 5 mutations in 201 alleles (marked in bold):


This places THEIR common ancestor at 14 generations (350 years) below their average “age” (1,510±230 years bp), that is he lived 1,860±250 years before present. Their common ancestor, that is the RED branch common ancestor had the following haplotype (base haplotype of the RED branch)

He lived in the 2nd century AD and its haplotype differed by 10 mutations from the base R1b1b2-L21 haplotype, shown below with the mutations marked:


Since the R1b1b2-L21 subclade’ common ancestor lived 3750±380 years before present, those 10 mutations (equivalent to 2275 years between their common ancestors) in the RED base haplotype (with a common ancestor 1860±250 before present) place THEIR common ancestor at approximately (2275+1860+3750)/2 = 3940 years before present. This is the L21 common ancestor himself.

Therefore, a short story is that bearers of R1b1b2 haplogroup (subclades L51 and/or L11) who have arrived to Iberia around 4800 years before present (via the North-African route from the Middle East/Levant which began around 5500 years before present) and moved up to the European continent as the Bell Beakers and with their downstream L21 subclade (with a common ancestor of 3750±380 years bp), eventually got to the Isles and later split off the RED branch, with a common ancestor in the 2nd century AD. He well might have been an ancestor of the kindred of the Dalriadic royal house in Scotland, of Fergus, Angus, and Lorne, the sons of Erc, who descended per Irish and Scottish history from Cairbre Riada, king of Irish Dalriada.

PINK

There are only six 67 marker haplotypes of the PINK subgroup on the tree (Fig. 2). They are clearly part of the RED subgroup, with the PINK base haplotype


with the same characteristic pair of 1924 in YCAII, the same as that is the PINK subgroup. All 6 haplotypes have 19 mutations from the above base haplotype, which gives 19/6/0.12 = 26 \(\Rightarrow\) 27 generations, that is 675±170 years to their common ancestor. The above PINK base haplotype has 8 mutations (marked in bold) from the overall base haplotype of the RED subgroup, which translates to 1800 years between their common ancestors (8/0.12 = 67 \(\Rightarrow\) 72 generations), and places their with the RED subgroup common ancestor at (675+1800+1860)/2 = 2200±300 years before present. Indeed, PINK subgroup is the downstream
branch of the RED subgroup (with a common ancestor of $860\pm250$ years before present, which are the same figures within the margin of error).

**MAROON**

The Project organizers describe this subgroup as follows: *The group is a subset of the red 'Scots' group, consisting mostly of Alexanders"*. Indeed, 11 of 12 group members are Alexanders, and one who is not (and who has only 37-marker haplotype) has the same haplotype structure, and even without any mutations from the base haplotype

\[
13 \ 24 \ 14 \ 10 \ 11 \ 14 \ 12 \ 12 \ 12 \ 13 \ 13 \ 30 - \ 18 \ 9 \ 10 \ 11 \ 11 \ 25 \ 15 \ 19 \ 30 \ 15 \ 16 \ 17 \ 17 - \ 11 \ 12 \ 19 \ 23 \ 16 \ 15 \ 17 \ 17 \ 37 \ 38 \ 12 \ 12 - \ 12 \ 9 \ 15 \ 16 \ 8 \ 10 \ 10 \ 10 \ 10 \ 12 \ 23 \ 23 \ 16 \ 10 \ 12 \ 12 \ 15 \ 8 \ 11 \ 22 \ 20 \ 13 \ 12 \ 11 \ 13 \ 11 \ 11 \ 12 \ 12
\]

It has only four mutations from the base RED haplotype (with a common ancestor of $1860\pm250$ years bp). As one can see, it has a 1923 pair in YCAII, unlike 19-24 in the RED branch. Apparently, we see a result of a back mutation. All 11 of 67 marker haplotypes have 15 mutations from the above base haplotype, which gives $15/11/0.12 = 11.4\pm3.2$ generations from a common ancestor (if to be excessively precise), that is $285\pm80$ years before present.

There is one more way of calculations, taking into account a number of base haplotypes in the dataset (that is identical ones in the dataset). In this case there are four identical haplotypes in the 67 marker set of 11 haplotypes, and seven identical ones in the 37 marker set of 12 haplotypes. At such a small amount of haplotypes in the datasets the method is rather imprecise, and serves just an illustration of the approach. In this case we have $[\ln(11/4)]/0.2 = 8.4$ generations from a common ancestor, and $[\ln(12/7)]/0.09 = 6$ generations. Those are approximate figures, however, they show that the subbranch is indeed rather young. $285\pm80$ years from a common ancestor of the MAROON branch is the most reliable figure here.

The haplotype tree (Fig. 2) suggests that the MAROON branch descended from the Red3 branch (with a common ancestor of $1675\pm300$ years ago). Since there are five mutations between their base haplotypes (marked in bold in the Red3 base haplotype below)

\[
13 \ 24 \ 14 \ 10 \ 11 \ 14 \ 12 \ 12 \ 12 \ 13 \ 13 \ 30 - \ 18 \ 9 \ 10 \ 11 \ 11 \ 25 \ 15 \ 19 \ 30 \ 15 \ 15 \ 16 \ 17 - \ 11 \ 12 \ 19 \ 24 \ 16 \ 15 \ 18 \ 17 \ 37 \ 38 \ 12 \ 12 - \ 12 \ 9 \ 15 \ 16 \ 8 \ 10 \ 10 \ 10 \ 10 \ 12 \ 22 \ 23 \ 16 \ 10 \ 12 \ 12 \ 15 \ 8 \ 11 \ 22 \ 20 \ 13 \ 12 \ 11 \ 13 \ 11 \ 11 \ 12 \ 12
\]
their common ancestors are separated by $5/0.12 = 42 \rightarrow 44$ generations, that is 1100 years, and THEIR (joint) common ancestor lived approximately $(1100+1675+285)/2 = 1530$ years before present. Indeed, this is the Red3 branch common ancestor (1675±300 ybp), within the margin or error.

**BROWN**

The BROWN subgroup haplotypes are available in 37 marker format only. Their base haplotype is

13 24 14 10 11 15 12 12 12 13 13 30 – 20 9 10 11 11 25 15 19 30 15 15 16 17 –
11 12 19 24 15 14 18 16 38 39 12 12

and all six haplotypes in the dataset have 14 mutations from it (marked in bold are 9 mutations from the base RED haplotype). We see again the RED subgroup “signature” 19-24 pair in YCAII markers. The number of mutation gives $14/6/0.09 = 26$ generations, or 27 generations with a correction for back mutations, that is 675±190 years from a common ancestor.

The closest to the BROWN base haplotype is the both the RED one, with 9 mutations between them in the 37 markers, and the PINK one, shown below (mutations between BROWN and PINK base haplotypes are marked in bold), also with 9 mutations between them:

13 24 14 10 11 15 12 12 12 13 13 29 – 18 9 10 11 11 24 15 19 32 15 15 17 17 –
11 12 19 24 15 15 18 17 38 39 12 12

“Closest” in this context means that the both common ancestors (BROWN and RED, or BROWN and PINK) descended from the same common ancestor, who lived earlier than them, or one of them was the common ancestor himself for the both branches. Let us see which case is more justified.

Nine mutations between two 37 marker haplotypes translate to $9/0.09 = 100\rightarrow 111$ generations (with a correction for back mutations), that is 2775 years between them.

-- Since the RED common ancestor lived $860\pm250$ years before present, the RED and BROWN common ancestor lived approximately $(860+2775+675)/2 = 2655$ years ago.

-- Since the PINK common ancestor lived 675±170 years before present, the PINK and BROWN common ancestor lived approximately $(75+2775+675)/2 = 2060$ years ago, at the break between BC and AD.
Clearly, in neither case the BROWN common ancestor has descended from the RED or the PINK one. 9 mutations between two 37 marker haplotypes (111 generations) are too many to be considered “closely related”. So, the conclusion of the Clan Donald site “The brown group is a subset of the red 'Scots' group” is highly doubtful. It is a rather recent branch (675±190 years from their common ancestor), but it likely passed through a population bottleneck before that, and in fact has its roots in much more ancient times (2500-2000 years bp), some time after the L21 formation (3750±380 years bp) and before the RED group formation (1860±250 years bp). That is where the 1924 pair came from.

GREEN

The Clan Donald site describes this subgroup as follows:

The group is centered geographically in northwestern Ireland. It is always referred to as the 'Irish' or 'Niall' group. Clan Donalds with this genetic signature may be descendants of Colla Uais, descendants of the O'Neill, or O'Donnell kindreds with whom we regularly served in Irish military operations, the O'Cahans from the Dowry of fighting men provided to Angus Og upon his marriage to the O'Cahan's daughter or descendants of Colla Menn from whom Gillebride sought assistants to recover his lands from the Norse. All participants in this group who have been SNP tested have tested positive for the marker M222.

According to our data (Klyosov, 2011, 2010a) the base haplotype for RM222 subclade is


with a common ancestor who lived 1450±160 years before present. This subclade embraces about 25% of the Irish R1b1b2 population (Klyosov, 2010a).

Let us see whether the GREEN subgroup matches this base haplogroup and a timespan to the common ancestor. A fragment of the Donald Clan haplotype tree (Fig. 1) encompassing the GREEN branch is shown in Fig. 3. It consists of many “mini-lineages”, as in any real haplotype tree, and we will analyze the branch as a whole.
Fig. 3. A fragment of the 67-marker linear haplotype tree, depicting the right hand side (between 1 and 3 o’clock) wide GREEN branch of the haplotype tree, shown in Fig. 1 (between haplotypes 101 and 183). One can see that “unclassified” haplotype 553 in fact included into this subgroup. The GREEN branch is very clean and does not include other color-coded haplotypes. Only haplotype 182, which was assigned by the GREEN branch by the Clan Donald organizers, landed in the “unclassified” branch in the very upper part of the right-hand side of the tree (Fig. 1).

In fact, relative positions of these minilineages (mini-subgroups, with a few haplotypes in each) do not bear any particular significance. This is illustrated with the same GREEN branch, being a part of a smaller haplotype tree, which includes only haplotypes from 1 through 204 (Fig. 4).

Fig. 4. A 67-marker haplotype tree for first 112 haplotypes in the tree in Fig. 1 (from haplotypes 1 through 204). The GREEN branch is on the right.
One can see that haplotypes on the tree in Fig. 3 and 4 are the same, however, their relative positions vary.

All 40 haplotypes of the GREEN branch contain 331 mutations from the base haplotype of the branch

11 11 19 23 17 16 18 17 38 39 12 12 – 11 9 15 16 8 10 10 8 10 12 12 16 8 12 25 20 13 12 11 13 11 11 12 12

This is exactly the M222 base haplotype, shown three pages up.

This number of mutations give $331/40/0.12 = 69 \rightarrow 74$ generations, that is 1850±210 years from a common ancestor. This is a figure similar with that of 1450±160 years bp for the M222 subclade, obtained earlier with 266 of 67 marker haplotypes (and calculated for the first 25 markers only) (Klyosov, 2010a,b), and with 1575±170 years bp calculated with 172 of 67-marker haplotypes (Klyosov, 2010a).

**YELLOW GREEN**

Below haplotype 22 from the Red1 subgroup in the haplotype tree (Fig. 1) at 9 o’clock, after a short branch of unclassified haplotypes (among which sits a lonely “magenta” haplotype 242, which actually does not belong to the MAGENTA subgroup), there is the YELLOW GREEN branch of 10 haplotypes. Nine of them belong to McConnell family. That is how the Clan Donald site describes the subgroup:

*The group is thought to be from Leinster. It is easily distinguished by the 464X test, whose results turn out 15c-15c-17g-17g. One participant has tested positive for the marker L21.*

In fact, 15-15-17-17 in DYS464a-d is very common among R1b1b2 haplotypes, and is characteristic to the “Atlantic Modal Haplotype”, and also RM269 and its subclades U106, P312, U152, L20, L21, “South Irish”, “North Irish”, “Scottish Borders” and also some unassigned branches (Klyosov, 2010a,b,c).

Since nine out of ten haplotypes in a dataset belong to the same surname, one can expect that their common ancestor lived rather recently. This was exactly what has happened. All ten haplotypes contain only 14 mutations, per 670 alleles, from the base haplotype
in which 10.7 mutations from the L21 base haplotype are marked in bold. Therefore, 14/10/0.12 = 11.7±3.3 generations, that is 29±80 years to a common ancestor. This is the first half of the 18th century, plus-minus about three generations. 10.7 mutations from the base L21 haplotype (350±380 years before present) separate their common ancestors by 2150 years, which is not enough to have L21 as a parent subclade for the YELLOW GREEN subgroup(290±80 ybp). The latter descended from a common ancestor within the L21 subclade. Apparently, it is that “unclassified” branch next to the YELLOW GREEN subgroup with the base haplotype (9.5 mutations from the YELLOW GREEN base haplotypes are marked in bold; they separate the YELLOW GREEN and this unclassified base haplotype by 2150 years)

This unclassified branch is rather close to the L21 base haplotype (see below) and has only 4 mutations from it (marked) in all 67 markers. This separates their common ancestors by 850 years.

All 7 haplotypes in the “unclassified” branch contain 96 mutations from its base haplotype (second to the above), which gives 96/7/0.12 = 114 ± 129 generations, that is 3225±460 years from its common ancestor. This places a common ancestor of the YELLOW GREEN and the unclassified branch to(3225+260+2150)/2 = 2800±500 ybp, which is within the error margin the time when the common ancestor of the unclassified branch had lived(3225±460 ybp). A common ancestor of both L21 (3750±380 ybp) and the unclassified branch (2625±375 ybp) lived 3600±500 years before present, and he was likely (within the margin of error) the founder of L21 himself.

Conclusion: The YELLOW GREEN group descended from an “unclassified branch” (its base haplotype is shown above) which in turn belonged to the L21 subclade and descended from the L21 only 850 years after the L21 was established.
**DARK BLUE**

The subgroup contains 10 haplotypes, with their bearers having the same or similar surnames. Nine of those ten haplotypes are in the 37 marker format, only five of them were determined in the 67 marker format. Their base haplotype is as follows:

```
13 24 14 11 11 14 12 11 14 13 30 – 18 9 10 11 11 25 15 19 29 15 17 17 17
11 11 19 23 15 15 17 17 37 12 12 – 11 9 15 16 8 10 10 8 10 11 12 23 23 15 10 12 12
13 8 12 22 19 13 12 11 13 11 11 12 12
```

- All five of 67 marker haplotypes contain 14 mutations, which gives $14/5/0.12 = 23$ generations, that is $575\pm165$ years to their common ancestor.
- All nine of 37 marker haplotypes contain 12 mutations, and $12/9/0.09 = 15$ generations, that is $375\pm115$ years to their common ancestor.
- In the 25-marker format there were four base haplotype out of ten, hence, $[\ln(10/4)]/0.046 = 20$ generations, that is 500 years to their common ancestor.
- In the 12-marker format there were seven base haplotype out of ten, hence, $[\ln(10/7)]/0.022 = 16$ generations, that is 400 years to their common ancestor.

As one can see, all the variants of calculations by different methods and with different sets of haplotypes give practically the same figures within the margins of error. The average timespan to a common ancestor for the DARK BLUE subgroup is $460\pm90$ years. It is the 16th century AD.

Since it is a rather recent branch, it is difficult to even suggest their subclade comparing their base haplotype with those of different subclades of R1b1a2. For example, it has as many as

- 28 mutations from the base M222 haplotype,
- 21 mutations from the L51 base haplotype,
- 19 mutations from the L226 base haplotype,
- 18 mutations from the “North Irish” base haplotype,
- 16 mutations from the “South Irish” base haplotype,
- 15 mutations from the L23 base haplotype,
- 14 mutations from the U152 base haplotype,
- 13 mutations from the base L21 haplotype.

One can see that it is the closest one to the L21 subclade.
PALE GREEN

The group is described in the Clan Donald as follows:

*This group contains several persons known to descend from the line of the Glencoe chiefs. This line traditionally descends from Somerled. It originated Iain Og, son of Angus Og and brother of John first Lord of the Isles.*

The subgroup contains 9 haplotypes, all McDonald or MacDonald, hence, we can expect to see a rather recent common ancestor of the family Eight of them have their haplotypes determined in the 37 marker format, and only five were determined in the 67 marker format (see Fig. 5). Their base haplotype is as follows:

```
13 23 15 11 14 12 12 13 28 - 19 9 10 11 11 25 15 18 31 15 15 17 17 -
11 11 19 23 17 15 20 19 38 43 12 12 - 11 9 15 16 8 10 10 8 10 10 12 23 23 16 10 12 12
16 8 13 22 20 12 12 10 13 11 11 12 12
```

- All five of 67 marker haplotypes contain 13 mutations, which gives $13/5/0.12 = 22$ generations, that is $550\pm160$ years to their common ancestor.
- All eight of 37 marker haplotypes contain 11 mutations, and $11/8/0.09 = 15$ generations, that is $375\pm120$ years to their common ancestor.
- In the 25-marker format there were five base haplotype out of ten, hence, $[\ln(10/5)]/0.046 = 15$ generations, that is 375 years to their common ancestor.
- In the 12-marker format there were no mutations in ten haplotypes which points out to a recent common ancestor, within a few centuries.

Again, all the variants of calculations by different methods and with different sets of haplotypes give practically the same figures within the margins of error. The average timespan to a common ancestor for the PALE GREEN subgroup is $430\pm100$ years. It is the end of the 16th century AD, plus-minus four generations.

Since it is a rather recent branch, it is difficult to even suggest their subclade comparing their base haplotype with those of different subclades of R1b1a2. For example, it has as many as

- 33 mutations from the L226 base haplotype,
- 32 mutations from the L23 base haplotype,
- 31 mutations from the “South Irish” base haplotype,
- 30 mutations from the base M222 haplotype,
- 30 mutations from the L51 base haplotype,
• 26 mutations from the base L21 haplotype.
• 25 mutations from the “North Irish” base haplotype,
• 25 mutations from the U152 base haplotype.

In the case of the shortest distance— from the U152 base haplotype (4125±450 years bp) it amounts to 6550 years between the PALE GREEN and U152 common ancestors, which places THEIR common ancestor to 5500±800 years before present. In the case of the longest distance— from the L226 base haplotype (1325±225 years bp) it translates to 9400 years between the PALE GREEN and L226, which places THEIR common ancestor to 5600±800 years before present. It is apparently the same common ancestor, which is likely P312 or L11 subclades. Those are times when R1b1b2 were coming to Europe. There are the roots of the PALE GREEN subgroup. Then it is no surprise that its branch on the haplotype tree is surrounded by “unclassified” ancient branches (Fig. 5).

BLACK

The BLACK branch on the haplotype tree is surrounded by “unclassified” haplotypes, from which it was apparently split. There are six haplotypes in the 67 marker format in this group, two more are determined in the 37 marker format, and two more in the 25 marker format. There are only two surnames among the bearers of this subgroup, most of them (seven) are MacDonalds and McDonalds. Again, because of that it could have been expected that a common ancestor of the group lived rather recently. Indeed, there are only 25 mutations in six of 67 marker haplotypes, that is in 402 alleles, from the base haplotype

11 11 19 23 16 15 18 16 37 39 11 12 – 11 9 15 16 8 10 10 8 10 10 12 23 23 16 10 12 12
16 8 13 22 20 13 12 11 13 11 12 12

which results in 25/6/0.12 = 35 → 36 generations, that is 900±200 years to a common ancestor of the BLACK subgroup. Eight of 37 marker haplotypes contain 28 mutations, which gives 28/8/0.09 = 39 → 41 generations, that is 1025±220 years to a common ancestor. These figures are within the margin of error, which are rather large due to a small number of haplotypes. The logarithmic method would not be of help here, since in one of 25-marker haplotypes only one still maintains its base structure, which formally gives [ln(10/1)]/0.046 = 50 → 53 generations, that is 1325 years to a common ancestor. Just one base haplotype more in that series, which statistically can easily happen would have given [ln(10/2)]/0.046 = 35 → 36 generations, that is 900 years to a common ancestor. This simple example shows that with one of two base haplotype in a dataset the logarithmic method would give a margin of error of around 50-70%.
Fig. 5. A fragment of the 67-marker linear haplotype tree, depicting the left hand side (between 7 and 8 o’clock) branches of the haplotype tree, shown in Fig. 1. “Unclassified” haplotypes have numbers above 308.
A haplotype tree for eight of 37 marker haplotypes of the BLACK subgroup (Fig. 6) shows that the dataset might be not a uniform one. It contains three clusters, or lineages, each with its “local” ancestral (base) haplotype. Their superposition gave that “base” haplotype for the BLACK subgroup. It might be a real one or it might be a “phantom” one. It can rather easily be examined and verified, if needed, using the above haplotype tree and comparing the lineages. It helps that the three lineages are of about the same “weight”, so the “overall” base haplotype might be correct.

Fig. 6. A 37-marker haplotype tree for the BLACK subgroup.

A rather unusual DYS393 = 12 (the first allele from the left) is typical for R23 subclade (~ 6200 years to a common ancestor), or it might have appeared due to a simple, random mutation around a thousand years ago in a common ancestor.
of the BLACK subgroup (a relatively rare, but quite possible event). The above BLACK group base haplotype differs by 16.5 mutations from the L23 base haplotype (shown below, mutations are marked):

```
```

Those 16.5 mutations are translated to 4025 years between common ancestors of the BLACK and L23 lineages. This is too little for the L23 subclade which is ~6200 year “old”, which the BLACK is ~ 900 years “old”. Therefore, the DYS393 = 12 was likely just an “ordinary”, random mutation. The group might still belong to L23, but initiated from a more recent ancestor, “halfway” from a common ancestor of L23.

However, there are some additional indications that the BLACK subgroup does not belong to L23, and its parent branch has a more common DYS393 = 13. Fig. 5 shows that the BLACK subbranch is only a halfbranch of a wider one containing 14 haplotypes altogether, which have their common ancestor, upstream from the BLACK sub-lineage and belonging to an “unclassified” series of haplotypes. These 14 haplotypes have the following base haplotype:

```
```

All 14 haplotypes contain 200 mutations from the base haplotype, which gives $200/14/0.12 = 119 \rightarrow 135$ generations from a common ancestor, that is $3375\pm410$ years to a common ancestor. This branch, half of which is “unclassified” is likely an ancestral one (see Fig. 5) to the BLACK subgroup $900\pm200$ years to a common ancestor). Indeed, eight “unclassified” haplotypes surrounding the BLACK subbranch have 109 mutations in their 67 marker haplotypes, which gives $109/8/0.12 = 114 \rightarrow 129$ generations, that is $3225\pm450$ years from their common ancestor. This is the ancestral branch (“unclassified”) for the BLACK subgroup $(900\pm200ybp)$.

**VIOLET, ORANGE, DARK BLUE-GREEN**

These subgroups are all parts of “unclassified” branches of haplotypes, as the haplotype tree shows (Fig. 7). Most of those subgroups contain predominantly 25 and 37 marker haplotypes.
The VIOLET subgroup has four mutations in six 25-marker haplotypes (14.5±7.4 generations), seven mutations in four 37-marker haplotypes (19.4±7.6 generations), four mutations in two 67-marker haplotypes (16.7±8.5 generations), and half of their haplotypes are identical (base) in 25-marker dataset (15.1±8.8 generations), on average 16.4±2.2 generations, that is 410±55 years from their
common ancestor, the beginning of the 17th century AD plus-minus a few generations.

The ORANGE subgroup (including “unclassified” haplotype 436, which in fact is a base haplotype for the ORANGE subgroup) has two mutations in six 25-marker haplotypes (7.2±5.2 generations), five mutations in six 37-marker haplotypes (9.3±4.5 generations), one mutation in three 67-marker haplotypes (28±2.8 generations), and four of their six haplotypes are identical in 25-marker dataset (8.8±4.5 generations), on average 175±80 years from their common ancestor, the middle of the 19th century AD plus-minus three generations.

The base haplotype of the ORANGE branch

13 24 14 10 11 14 12 12 11 13 13 29 - 17 9 10 11 11 27 15 19 30 14 15 17 18 -
10 11 19 22 16 15 18 17 36 39 11 12 - 11 9 15 16 8 11 10 8 10 10 12 23 23 16 10 12 12
15 8 12 23 20 14 12 11 13 11 11 12 12

significantly differs from that for the RED branch (mutations are shown in bold), on as many as 20 mutations in 67 markers (which is equivalent to 5000 years between them). This places a common ancestor of the RED and ORANGE branches at $(5000+1860+175)/2 = 3520$ years before present, that is much earlier than the “age” of the RED branch itself ($860±250$ years, see above).

Understandably, a mutational difference between the ORANGE branch and Red1, Red2 and Red3 subbranches, as “younger” compared with the RED common ancestor, is even larger – 22, 21 and 21 mutations, respectively. In other words, the ORANGE branch is a rather distant cousin to the RED branch.

Compared to the PINK group, the difference between it and the ORANGE group is even larger – 25 mutations (shown below in the base haplotype of the PINK branch), or 6550 years between their common ancestors.

13 24 14 10 11 15 12 12 12 13 13 29 - 18 9 10 11 11 24 15 19 32 15 15 17 17 -
11 12 19 24 15 15 18 17 38 39 12 12 - 12 9 15 16 8 10 10 8 10 10 12 22 23 16 10 12 12
16 8 11 22 20 13 12 11 13 11 11 12 12

This brings a common ancestor of the ORANGE and PINK subgroups to $(6550+175+675)/2 = 3700$ years before present. This is a common time for many R1b1a2 European subclades, such as P312, U106, L21, U152, L2, L20, L176.2.

The DARK BLUE-GREEN subgroup has eight mutations in five 25-marker haplotypes (35→36 generations), 15 mutations in four 37-marker haplotypes (42→44 generations), eight mutations in two 67-marker haplotypes (33→34 generations), and three base haplotypes out of five in the 25-marker dataset (11
generations). Such a discrepancy comes mainly from one haplotype in the dataset, which contributed the most into the mutations, and has the only different surname in the group. After it was removed, the pattern was as follows: two mutations in four 25-marker haplotypes (10.9±7.8 generations), 8 mutations in three 37-marker haplotypes (29.6±10.9 generations), eight mutations in two 67 marker haplotypes (33.3±12.2 generations), and three base haplotypes out of four in the 25-marker dataset (6.3±3.7 generations). Technically, most of the figures are within the same margin of error, and an average timespan to the common ancestor of the DARK BLUE-GREEN groups lived 20±13 generations back, that is 500±325 years ago, around the 16th century AD plus-minus three centuries.

GRAY

The branch of the GRAY subgroup has nine mutations in five 25-marker haplotypes (39→41 generations), 24 mutations in five 37-marker haplotypes (53→56 generations), six mutations in two 67-marker haplotypes (25→26 generations), and only one base haplotype in five 25-marker haplotype dataset (35→36 generations), on average 40±13 generations, that is 1000±325 years from their common ancestor. It is the 11th century AD, plus-minus a few centuries.

WHITE

In this group all eight haplotypes were determined in the 67 marker format. They have a rather recent common ancestor with the MAGENTA group (see Fig. 8).

All the eight haplotypes have only 13 mutations from their base haplotype

\[
13 \ 25 \ 14 \ 11 \ 11 \ 14 \ 12 \ 12 \ 12 \ 13 \ 13 \ 29 \ → \ 17 \ 9 \ 10 \ 11 \ 11 \ 26 \ 15 \ 19 \ 28 \ 14 \ 15 \ 15 \ 17 \ → \\
11 \ 10 \ 19 \ 23 \ 16 \ 15 \ 18 \ 16 \ 37 \ 37 \ 12 \ 12 \ → \ 11 \ 9 \ 15 \ 16 \ 8 \ 10 \ 10 \ 8 \ 10 \ 10 \ 12 \ 23 \ 23 \ 16 \ 10 \ 12 \ 12 \ 15 \ 8 \ 12 \ 22 \ 20 \ 13 \ 12 \ 11 \ 13 \ 11 \ 11 \ 12 \ 12
\]

which gives 13/8/0.12 = 14 generations, that is 350±100 years from a common ancestor of the WHITE group.

Eleven mutations marked here in bold are shown in comparison with the L20 subclade base haplotype in the first 25 markers. However, the same number of mutations the WHITE base haplotype also shows in comparison with the L21 base haplotype in the first 25 markers (the same number of mutations was in all the 67 markers):

\[
13 \ 24 \ 14 \ 11 \ 11 \ 14 \ 12 \ 12 \ 12 \ 13 \ 13 \ 29 \ → \ 17 \ 9 \ 10 \ 11 \ 11 \ 25 \ 15 \ 19 \ 29 \ 15 \ 15 \ 17 \ → \\
11 \ 11 \ 19 \ 23 \ 15 \ 15 \ 18 \ 17 \ 36 \ 38 \ 12 \ 12 \ → \ 11 \ 9 \ 15 \ 16 \ 8 \ 10 \ 10 \ 8 \ 10 \ 10 \ 12 \ 23 \ 23 \ 16 \ 10 \ 12 \ 12 \ 15 \ 8 \ 12 \ 22 \ 20 \ 13 \ 12 \ 11 \ 13 \ 11 \ 11 \ 12 \ 12
\]
Fig. 8. A fragment of the 67-marker linear haplotype tree, depicting haplotypes at the lower right-hand side of Fig. 1. “Unclassified” haplotypes are numbered above 308.

Therefore, a simple comparison of base haplotype cannot definitely resolve the assigning of the branch in this particular case (as in many other cases). However, in this particular case the WHITE group has descended from RL21 subclade, as it will be shown in the next section.

MAGENTA

This subgroup was described in the Clan Donald as follows:

Signatures parallel to this group can be found among the McMahons of Fermanagh (one of the territories of ancient Oriel founded by the Collas who allegedly conquered Ulster around 330 AD). This group was one of the tribes from which Gillebride, Somerled’s father, sought assistance against the Norse.

It is not clear from the above what “signatures parallel to this group” is, and how McMahons of Fermanagh could be related to the MAGENTA subgroup. Fig. 8 shows that the MAGENTA group is made up of at least four lineages. Since all of them are of about the same “weight”, a timespan to their common ancestor can be calculated using all 20 haplotypes of the group. More accurate calculation could have been done by considering each subbranch separately, using the same approach as described in this study, and then considering all four base haplotypes for the separate lineages.

All 20 haplotypes of the MAGENTA branch contain 119 mutations from the base haplotype

\[
13 \ 24 \ 15 \ 11 \ 11 \ 15 \ 12 \ 12 \ 13 \ 13 \ 29 - 17 \ 9 \ 10 \ 11 \ 11 \ 25 \ 15 \ 19 \ 28 \ 15 \ 15 \ 17 \ 17 -
11 \ 11 \ 19 \ 23 \ 16 \ 15 \ 18 \ 19 \ 36 \ 37 \ 12 \ 12 - 11 \ 9 \ 15 \ 16 \ 8 \ 10 \ 10 \ 8 \ 10 \ 9 \ 0 \ 22 \ 23 \ 16 \ 10 \ 12 \ 12 \ 16
8 \ 12 \ 22 \ 20 \ 13 \ 12 \ 11 \ 13 \ 11 \ 12 \ 12
\]

which gives \(119/20/0.12 = 50 \rightarrow 53\) generations, that is 1325±180 years from a common ancestor of MAGENTA group. Hence, the MAGENTA group common ancestor lived in the 7th century AD, plus-minus a couple of centuries.

In the above haplotype 17 mutations from the adjacent WHITE subbranch are marked. 19 out of 20 haplotypes in the MAGENTA branch have null mutation in DYS425. It is remarkably close to a R-L21 null mutation (DYS425) branch.
described in the preceding paper (Klyosov, 2011) with a common ancestor of the base haplotype with a common ancestor of 1500±325 ybp and the base haplotype (four deviations from the MAGENTA base haplotype are marked):

\[
13 24 \textbf{14} 11 11 15 12 12 \textbf{12} 13 13 29 – 17 9 10 11 11 25 15 19 28 15 15 17 17 – 11 11 19 23 \textbf{15} 15 18 19 36 38 12 12 – 11 9 15 16 8 10 10 8 10 \textbf{9} 0 22 23 16 10 12 12 16 8 12 22 20 13 12 11 11 11 12 12 \textbf{12} \quad (L21 \text{ null DYS425, sub-branch, 1500±325 ybp})
\]

Therefore, we have two subbranches, WHITE (550±100 ybp) and MAGENTA (1325±180 years bp), with 17 mutations (equivalent to 4150 years) between their common ancestors. This brings THEIR common ancestor to approximately (350+1325+4150)/2 = 2900 years before present. It is very likely the RL21 null mutation common ancestor himself (3025±460 years before present) [Klyosov, 2011].

**YELLOW GRAY**

Fig. 9 suggests that the YELLOW GRAY group descended from the adjacent “unclassified” branch (six haplotypes 472476). Seven haplotypes of the YELLOW GRAY group contain 34 mutations from the base haplotype

\[
\]

which gives 34/7/0.12 = 40 → 42 generations, that is 1050±210 years from a common ancestor of the group.

Shown above is quite an unusual base haplotype compared with, say, the L21 base haplotype, typical for the Isle haplotypes

\[
13 24 14 11 11 14 12 12 12 13 13 29 – 17 9 10 \textbf{11} 11 25 15 19 \textbf{29} 15 \textbf{15} 17 17 – 11 11 19 23 \textbf{15} 15 \textbf{18} 17 \textbf{36} \textbf{38} \textbf{12} 12 – 11 9 \textbf{15} \textbf{16} 8 10 10 8 10 10 12 23 23 16 10 12 12 \textbf{15} 8 \textbf{12} \textbf{22} \textbf{20} 13 12 11 13 \textbf{11} \textbf{11} 12 12
\]

from which the YELLOW GRAY has as many as 23 mutations (marked), which translates to 5950 years difference between their common ancestors. This means that THEIR common ancestor lived approximately (5950+1050+3750)/2 = 5375 ybp. It might be that the YELLOW GRAY lineage arose before their ancestors had arrived to Europe. It could have been Asia Minor or the Middle East, e.g., Sumers.
Fig. 9. A fragment of the 67-marker linear haplotype tree, depicting haplotypes at the right-hand side (at 3 o’clock) of Fig. 1. “Unclassified” haplotypes are numbered above 308.

The adjacent “unclassified” branch of six haplotypes has the base haplotype


(7 mutations from the YELLOW GRAY base haplotype are marked, they are equivalent to 1550 years between the two common ancestors; some of those mutations them are fractional ones) with 78 mutations in 67 markers, which gives 78/6/0.12 = 108 → 121 generations, that is 3025±460 years from a common ancestor. Therefore, a common ancestor of the YELLOW GRAY branch and the “unclassified” branch lived around \((1550+3025+1050)/2 = 2800±400\) years before present, which is likely the common ancestor of the “unclassified” branch itself.

1223
PALE VIOLET, PALE BLUE and LIGHTBROWN

These three subgroups are small in the Clan Donald records and contain mainly 25- and 37-marker haplotypes.

Regarding the PALE VIOLET group, the Clan Donald site has suggested:

*This group is probably a subset of the Magenta group, but we are not including them together since these people have not tested for DYS425. This group appears to all be descendants of Lt Brian McDonald, chief line of Leinster and Ulster in Ireland who emigrated to Brandywine Creek Delaware in the late 1600s.*

Indeed, the base PALE VIOLET haplotype (shown below) is very close to that of MAGENTA, having from it only three mutations (marked)

13 24 15 11 11 15 12 12 13 13 13 29 – 18 9 10 11 11 25 14 19 28 15 15 17 17 –
11 11 19 23 16 15 18 19 36 37 12 12 – 11 9 15 16 8 10 10 8 10 9 0 22 23 16 10 12 12
16 8 12 22 20 14 12 11 13 11 11 12 12

It is also close to L21 null mutations sub-branches with common ancestors of 1300±170 and 1100±250 ybp (Klyosov, 2011), with deviations of only 5 mutations from each one

13 24 14 11 11 15 12 12 13 13 13 29 – 17 9 10 11 11 25 15 19 28 15 15 17 17 –
11 11 19 23 16 15 18 18 36 37 12 12 – 11 9 15 16 8 10 10 8 10 9 0 22 23 16 10 12 12
16 8 12 22 20 13 12 11 13 11 11 12 12

(L21 null DYS425, 1300±170 ybp)

11 11 19 23 16 15 18 19 36 38 12 12 – 11 9 15 16 8 10 10 8 10 9 0 22 23 16 10 12 12
16 8 12 22 20 13 12 11 13 11 11 12 12

(L21 null DYS425, 1100±250 ybp)

One can see that they are generally the same mutations. Practically the same mutations can be noticed also with yet another young sub-branch of null mutated L21 lineages:

11 11 19 23 16 15 18 18 36 37 12 12 – 11 9 15 16 8 10 10 8 10 9 0 22 23 16 10 12 12
16 8 12 22 20 13 12 11 13 11 11 12 12

(L21 null DYS425, 1050±220 ybp)

The PALE VIOLET group contains only four haplotypes in the 25 marker format, three of them are extended to the 37 marker ones, however, two of the latter are
identical, and only one haplotype in the 67 marker format. Furthermore, the 25 marker haplotypes appear to belong to two different “local” sublineages. All of this makes an estimation of a timespan to their common ancestor very problematic, and can give only a general idea. Eight mutations in four 25 markers haplotypes suggest $8/4/0.046 = 43 \to 45$ generations, that is around $1125\pm410$ years to a common ancestor. Since three of those four haplotypes are mutated, it gives $[\ln(4/1)]/0.046 = 30 \to 31$ generations, that is approximately 775 years to a common ancestor. Since the MAGENTA group has a common ancestor who lived $1325\pm180$ years ago, he (or one of his descendants) might indeed have been the common ancestor of the PALE VIOLET group.

In the PALE BLUE group there two mutations in two 25 marker haplotypes, both mutations in the same haplotype. It technically gives $2/2/0.046 = 22$ generations, that is $550\pm390$ years from a common ancestor, and $[\ln(2/1)]/0.046 = 15$ generations, that is $375\pm375$ years from a common ancestor. On average, it gives $460\pm390$ years before present.

Regarding the LIGHT BROWN group, the Clan Donald site has noted:

*The group is sometimes referred to as "Frisian". It lies within a larger group, not distinguishable from our haplotypes, that has a positive result for the SNP S21/U106.*

Let us verify it. The first 25 marker base haplotype of U106 subclade ($4175\pm430$ year “old”) is

13 23 14 11 14 12 12 12 13 13 29 - 17 9 10 11 11 25 15 19 29 15 15 17 17

There are seven LIGHT BROWN haplotypes available, most of them in 25 marker format only (three of them are available in the 37 marker format, and only one in the 67 marker format). Their base haplotype has only three mutations from that of the U106 base haplotype above (marked in bold):

13 23 14 11 11 14 12 12 12 13 13 29 - 17 9 10 11 11 24 15 19 29 15 16 17 18

All seven haplotypes have 23 mutations from the above base haplotype, which gives $23/7/0.046 = 71 \to 77$ generations, that is $1925\pm445$ years from a common ancestor. Three mutations between the LIGHT BROWN and the U106 base haplotypes translate to 1725 years between them, which places THEIR common ancestor to $3900\pm500$ years before present. It is likely the U106 subclade common ancestor himself.
BLUE GREEN and DARK GREEN

The BLUE GREEN dataset consists of three 37 marker haplotypes containing six mutations from their base haplotype. It gives $6/3/0.09 = 22$ generations, that is $550\pm230$ years to their common ancestor.

Three of 37 marker haplotypes of the DARK GREEN group contain four mutations, which translates to $4/3/0.09 = 15$ generations, that is $350\pm180$ years to their common ancestor. Three mutations in their two of 67 marker haplotypes give $3/2/0.12 = 13$ generations, that is $325\pm190$ years to a common ancestor. An average timespan is $17\pm5$ generations, that is $425\pm125$ years.

Two “unclassified” branches, likely of RL2 and R-U106 subclades

These two branches are clearly visible in Fig. 1 in the most upper right-hand side of the haplotype tree. The first one of 14 haplotypes has the following 37 marker base haplotype

23 16 15 19 17 36 38 12 12

in which 4.14 mutation from the L2 base haplotype are marked. This corresponds to 1200 years between their common ancestors. All 14 haplotypes contain 122 mutations from the above base haplotype, which gives $122/14/0.09 = 97\to 108$ generations, that is $2700\pm360$ years from their common ancestor. Since the L2 common ancestor lived $4025\pm410$ years before present (Klyosov, 2011), a common ancestor of L2 and the “unclassified” branch lived $(4025+1200+2700)/2 = 3960\pm500$ years before present. This was very likely the common ancestor of L2 himself.

The adjacent branch of 17 haplotypes (the next branch, clock-wise in Fig. 1) has 218 mutations from the following 37 marker haplotype

23 16 14 18 18 37 39 12 12

It is identical with the U106 base 25-marker haplotype (see description of the LIGHT BROWN group above), and has exactly the same timespan from the common ancestor. For the U106 subclade it is $4175\pm430$ years, for the “unclassified” branch it is $218/17/0.09 = 143\to 167$ generations, that is $4175\pm500$ years to the common ancestor.
CONCLUSIONS

A short version of the R1b-R1b1a2 haplotype tree (the full version is given in http://www.isogg.org/tree/ISOGG_HapgrpR.htm) is shown below, with the chronology indicated according to (Klyosov, 2011):

```
<table>
<thead>
<tr>
<th>Haplotype</th>
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<th>Date (ybp)</th>
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<tr>
<td>R1b</td>
<td>M343</td>
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<tr>
<td>R1b1</td>
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<tr>
<td>R1b1a</td>
<td>L320</td>
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<td>~ 6200 (a different dataset)</td>
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<td>P312/S116</td>
<td>4100±415 ybp</td>
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<td>R1b1a2a1a1b19</td>
<td>L238/S182</td>
<td>~ 1000 ybp</td>
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</tbody>
</table>
```

1 In Asia
2 4575±580 ybp (a different dataset)
3 3800±380 (a different dataset)

History of R1b and its subclades migration is outlined in (Klyosov, 2011). While the R1b1a1-M73 subclade mainly left in Asia, the R1b1a2-M269 subclade had moved to the Russian Plain (the Eastern European Plain) around 128 thousand years ago, and descendants of its L23 subclade still remains in Russia (with a
common ancestor of 6775±830 years bp [Klyosov, 2009b] though the analysis has
bot necessarily discriminated the L23 subclade and some upstream sunclades
and in the Caucasus, with their common ancestors who lived there at least 6000
years before present. The M269 and L23 bearers split, some of them went
through the Caucasus to Asia Minor/Anatolia (a common ancestor there of
6000±820 years bp), to the Middle East (a common ancestor in Lebanon of
5200±670 years bp) and then via the North African route arrived to Iberia around
4800 years bp. From there, it moved up North to the continental Europe, and it
was considered in (Klyosov, 2011).

As a result, a pattern of the Clan Donald R1b1b2 lineages is rather complicated.
Here is a partial list of the Donald subgroups for which some lineages were
traced to specific subclades:

Red L21 1860±250 ybp
Pink L21  675±170
Brown L21  675±190
Maroon L21  285±80
Green L21→M222 1850±210
Dark Blue L21 (?)  575±165
Blue Green  550±230
Yellow Gray  1050±210
Violet  410±55
Orange  175±80
Magenta L21  1325±180
Pale Violet L21  1125±410
Gray  1000±325
Pale Green U152 (?)  550±160
Dark Blue – Green  500±325
Black  900±200
Pale Blue  460±390
Light Brown U106  1925±445
Dark Green  425±125
Yellow Green L21  290±80
White L21  350±100
“Unclassified” L2  2700±360
“Unclassified” U106  4175±500

**MATERIALS and METHODS**

This section is described in detail in the preceding article (Klyosov, 2011).
References


Klyosov, A.A. (2011) Haplotypes of R1b1a2-P312 and related subclades: origin and “ages” of most recent common ancestors Proc. Russian Academy of DNA Genealogy (ISSN 1942-7484), 4, № 6, 1127-1192
Between us, I like to consider myself as a descendant of Boyar Children. This is a deeply Russian thing. It carries a flavor of ancient stories, legends, folk songs.

However, if you were to randomly ask folks out there on the street who Boyar Children were, nine out of ten would have only a vague idea except they would say that it sounds awfully ancient. Maybe even 99 out of 100 would say no more than that. And I am talking not of Boston where I live now. I am talking about present day Russian cities or villages. The reason is a simple one. The 20th century in Russia was so violent and turbulent that memories of our roots and our past were wiped out rather effectively.

Dvoryane and Boyar Children

Boyar Children were a part of the top society in ancient Russia. The top society in its entirety was consisted of Boyars, Counts Men, Courtiers and Boyar Children. After a while, the first two groups had merged with the last two, and the last two groups had in turn merged and became Dvoryane (in Russian), or Courtiers. This merging occurred during 17-18 centuries.

The word Courtiers literally means “people of the Court”; first the Count’s court, then the Royal, Tsar Court. Initially, the Dvoryane were assembled into the Count Squadron. The Squadron was the best part of the local military forces. Every city had a squadron, or a platoon, or a division of Boyar Children. Ordinary folks had taken arms only in extraordinary situations, and peasants never did. However, the peasants had to provide horses and food for Dvoryane and Boyar Children.

Dvoryane and Boyar Children always were military folks. Using present day language, they were military officers. More than that, they were dynasties of military officers. They had formed a rather closed society of dynasties of combat
servicemen. As Russian historians of the past have written, Court Squadrons were formed from people who not only had clearly shown bravery and valor on a battlefield, but were also of a distinct “breed”. It does not sound too politically correct nowadays, but those who enrolled them into the Squadrons probably knew better. Or at least they had their own opinion.

Boyars were the top strata in ancient Russia, or Rus as it was called back then. Initially, they were children and close relatives of the Count, the closest blood, combat buddies, the backbone of his squadron. Over time, they became the closest advisors to the Count. Their children were called literally, Boyar Children. Since that collective name had carried an important message of nobility, their children and grandchildren continued to be called Boyar Children. They gradually became a rather large group within the military elite, and formed a middle- and junior-level contingent military. This, of course, was not related to the lower and lowest levels of troops since those were not dynasty servicemen. Using present-day language again, Boyar Children commonly filled positions from plain horsemen in noble dynasty cavalries, to majors, depending on experience and duration of service. Colonel and General ranks were held by Counts, Voevodas and, preferably, other Royal blood people.

The word Dvoryane was recorded the first time in a historical document called the Letopis (a series of ancient formal diaries all “signed and numbered”) of 1175. The use of the term “Boyar Children” as a top society can be found in the Letopis of 1281 which described the capture of a traitor Count named Mikhailo Glinski when he was leaving to join Polish troops who were enemies that time. The Letopis says “Mikhailo Glinski is riding alone a mile ahead of his Dvoryane, and Count Mikhailo Golitsa captured him, and the Boyar Children captured all of Glinski’s Dvoryane”.

Initially, Boyars and Boyar Children were of a higher status compared to the Dvoryane since they were strictly military people while many Dvoryane had just maintained the Court though holding responsible positions. In the Court Squadron, they were at the same level and practically indistinguishable from Boyar Children, although as late as in the first half of the 16th century, Boyar Children were of a higher class compared with the Dvoryane. But then with an elevation of prestige of the Tsar and his court, a status of Courtiers/Dvoryane began to exceed the military status of the Boyar Children. In the 16th and 17th centuries, both terms have practically merged, or rather stayed together and are practically always referred to as “Dvoryane and Boyar Children”, in contrast to other people, draft soldiers, peasants, villagers. Both Dvoryane and Boyar Children have served “from their land”, as it was called those times, meaning that they were receiving land for their military service and had to justify the possession by continuing their service and service of their sons and grandsons.
Until the 18th century, the term “Dvoryane and Boyar Children” was the equivalent to the term “warriors”. An expression “to send ahead Dvoryane and Boyar Children” meant to direct the best and brightest cavalry. But this was not all it meant. In the Kursk area, the very South of Russian those days, with Tatars from the South and South-West, Poles from the West, Lithuanians from the North-West, the Kursk area that will be our focus later on, with Kursk as its ancient capital, was completely destroyed by Tatars in the 13th century. It was rebuilt in the 16th and 17th centuries by Dvoryane and Boyar Children who were also military engineers and builders. There were no peasants in the Kursk area at that time to be drafted to build fortresses. In fact, all cities that time in the Kursk area were military garrisons. It was too dangerous for peasants to move there voluntarily. And peasants were free to move at that time anywhere in Russia.

As described by historians of those times, Dvoryane and Boyar Children were the most educated people. They were carriers of culture, they were the most decent strata of Russian society, and role models in all aspects of life.

In the 18th century, the term Boyar Children was disappearing and being completely replaced by the term Dvoryane. For those who retired from military service to their private land, particularly for those who have not served in military forces during the First government revision (1710-1720s), both terms were gradually replaced by the terms “single-courtiers”. Furthermore, those retirees settled on their land which they had earned for their military service and were becoming free farmers. This was typically the end of their nobility. Some of their descendants were able to return to nobility if they successfully claimed former Dvoryane status. This status and title could be given back to them only after special consideration and was additionally confirmed by returning to military service.

In 1566, Ivan the Terrible (Ioann IV, son of Vassily) had determined three tiers for dynasty servicemen. The top, first tier were Moscow Dvoryane and provincial Dvoryane with Moscow Dvoryane serving and owning land in the Moscow area. Provincial or City Dvoryane had served and owned land in other areas, in and around other cities and towns in Russia. The second tier was Boyar Children. They had the same rights as did Dvoryane, however, they typically kept lower military positions and ranks. They could move to the first tier for military achievements. The third tier was for shooters (“strelzy”), cannonmen, and other servicemen. They could be from Dvoryane, but not from peasants and other “plain people”. They formed regiments which were headed by Dvoryane and Boyar Children. The first two tiers had served “by heritage”, from their land, and
children often continued to carry military ranks of their fathers. The third tier had served “by draft”.

In 1642, Tsar Mikhail Romanov (the first Tsar Romanov) had issued a verdict (“ukaz”) which banned by-heritage-servicemen to become peasants and plain soldiers. A verdict issued in 1675 prohibited tier three draftsoldiers to become Boyar Children for whatever achievements. These verdicts had expedited forming of a closed Dvoryane society in Russia.

When Feodor, son of Ivan the Terrible, was Tsar of Russia (1584-1598), the Russian Army included 80 thousand horsemen in the Dvoryane Cavalry. This cavalry was formed exclusively from Dvoryane and Boyar Children. “High Dvoryane”, that is Boyars, had received a salary of 70100 rubles a year, “Middle Dvoryane” 40-60 rubles, and Boyar Children 20-30 rubles a year.

There were few cases in Russia when the status of Boyar Children was granted to lower class people and even to peasants, however these cases, according to historians, were typically unsuccessful. Boris Godunov, son of Feodor, had exercised several such cases, but they happened to be “infirm” and were retracted by subsequent Tsars.

Boyar Children were an absolutely inherent part of the Russian military. On the Southern frontiers of Russia, in the Kursk area, they served as reconnaissance officers, entered into combats, leading their “tens” and “hundreds” of troops, set defense of their cities and towns, storm enemy fortresses, and carried all uneasy military duties. For their service they were paid in the form of land besides monetary compensation. This was called “outlanding”.

Kursk was the largest city in the SouthWest and South-East of Russia. To the South-West of the Kursk area there was a huge territory called the Wild Plain.

### Outlanding of Dvoryane and Boyar Children

There were two principal mechanisms of outlanding One mechanism was a scheduled draft, it was announced in a formal document and indicated who and how much land and money was granted. Another mechanism was an “application for land” to the local or central authorities, including the Tsar himself, when a serviceman or his sons asked for a grant of land for their father.

And here I will mention my forefather, Ivan Klyosov (born 1580), who was the earliest Klyosov found in the archives, and who was granted 300 acres of land in...
the Kursk area in 1639. The Granted Land Book describes it as follows (the Russian National Archives of Ancient Acts [RNAAA], 1209188-15684, p. 159)

Year 7147 (1639) April 12 day according to the manuscript by Tsar and Grand Count Mikhail son of Feodor of all Rus, a Boyar Son Ivan Klyosov, of Reitar Service, following an application by Kursk citizens, Boyar Children Kirey Klyosov, Frol Evsyukov, and Denis Pyzhev and Mina Vozhov and Ostakh Shipilov and by directives by Stolnik and Voevoda Ivan son Vassiliy Butourlin, in Kursk stan of Kursk region, fields and forests were signed off from the mouth of Khmelevsk River upstream and downstream along the right-hand bank of Prut River and after the field investigation the land was measured and recorded as hundred acres into the field and twice as much according to Tsar and Grant Count Mikhail son of Feodor of all Rus the manuscript and the investigation.

After 56 years, the Records of Boyar Children in the City of Kursk and Kursk region of 1695 (Archives of the Kursk Region, 15551-168, p. 678) mentioned for the first time the Klyosov village. In 15 more years, according to the Census of 1710 the Klyosov village was recorded in a Section of “Reitars and Single Courters”, that it had 12 courts and 35 inhabitants, of which seven were adult men and nine were adult women. The rest were children, and everyone there had Klyosov as their last name.

It is worth mentioning here that until the 15th century, last names in Russia were not in use even among Boyars. By the end of the 15th century, last names were more and more frequent among Dvoryane. In the 18th century, practically all Dvoryane and Boyar Children had last names, unlike lower class citizens, whose last names had begun to appear only in the 19th century.

The fact that those people in 1639 who were listed in the Tsars manuscript had last names places them among rather distinguished people.

The Ulaz (verdict) of Tsar Alexey Mikhailovich of 1648 lists norms of land compensations for Boyar Children in the Kursk-Belgorod region:

-- Upper size grants (1st and 2nd tier): 400 and 300 acres
-- Middle size grants (3rd, 4th and 5th tiers): 250, 200 and 150 acres
-- Lower size grants (7th and 8th tiers): 100 and 70 acres

Land was granted only to dynasty service men. An “Order” of 1649 by Alexey Mikhailovich banned people not of Dvoryane and Boyar Children heritage to own land. As a rare exception, plain soldiers were granted 25 acres at best. When a landowner’s sons, and only dynasty service men were landowners, reached 15-18 years of age, they were signed up to the Tsar’s service and thereby acquired rights to have land themselves. After that they were obliged to respond
immediately to each military call and depart to military expeditions with weapons and supplies, bringing other horsemen and foot soldiers depending on the size of their private land. Typically the requirement was one armed horseman per each 100 acres of private land (an Ukas by Ivan the Terrible of September 20, 1556). Landowners could not sell their land, the land had to stay with the dynasty service men while they served. The rule was that “the service should not diminish and the land should not leave the service”.

Sons of wealthy Dvoryane and Boyar Children were registered “from the father’s land” and often were not granted extra land. Sons of not-so-wealthy and have-not Dvoryane were registered “in addition to the father’s land”, that is extra land was granted.

An “Ukaz of outlanding” of 1555 specified: “Father’s land should not be taken away from sons if they are fit to serve”. The same rule was confirmed by the “Order” of 1649. The main principle was that “those who serve must have land”. This was the underlying principle for the system of outlanding. The following principle was that “those who have land must serve”. Only church lands presented an exception.

Present-day readers may have the impression that Dvoryane and Boyar Children were wealthy people and had land with many peasants on them. This was not always true. In 1670s, for example, out of 168 Dvoryane and Boyar Children of the Kursk area registered for service, 99 have not had or were not granted land, the rest were outlanded but as scheduled, “Some got it in a half-force, some even less, and some got just a little”. Military service was a tough service. Monetary compensations were minimal, and mainly they were received at war, as a rule, as a prize for capturing or killing enemies, for being wounded, for escaping as a POW. During peaceful times the compensation was one ruble per man per four-year period.

Last but not least, not all land granted as a compensation was actually obtained. Actual land was often substantially less compared to that granted. Actual land should have been found, and its measurement and legal recording should have been arranged. That was not too easy. Available land often was of a poor quality (marches, ravines, etc.), or too far away, or too close to the enemy. That is why among provincial Dvoryane, there were many “small land-owners”, with much less than 100 acres of land, which was not even enough to present even one horseman to the duty. They often received only 80 or 40 acres or 30 or even 10 acres of land. This was close in size to land which was owned by peasants.

There were 731 Boyar Children in Kursk in 1642. They represented a core of Dvoryane local society. Outlanding compensation for them was between 70 and
500 acres per serviceman, however, most of them did not have peasants on their land. At that time, there were almost no peasants in the Kursk area. Therefore the landowners had lived by their courts which were single courts and later called “single-courtiers”. Furthermore, in the 18th century they had formed a strata in the Russian society that was formally named “SingleCourters”. I will come back to this later with a reference to my ancestors.

In general, in dynasty service families all children had served either directly or indirectly, regardless of their gender. Sons after 15-18 years of age would get on their horses to defend fatherland, and daughters would get married to supply new defenders for the fatherland. There were, of course, some cases when sons of a wounded retired father were not called into service, but left with him “on tillage”, and they would loose all privileges of a dynasty servicemen.

Returning to Ivan Klyosov, a Reitar, for what service and achievements a 59-year old Boyar Son, was land granted by the Tsar’s Ukaz? The archives do not provide an answer to this specific question, however, let’s take a look at the history of the Russian State from the beginning of the 17th century to 1639 when Ivan received his land.

“Fuzzy times” and the beginning of the House of Romanovs

In 1604, when Boyar Son Ivan Klyosov was 24 years of age, Russia entered into “Fuzzy Times” that lasted nine years until 1613. Boris Godunov was ending his seven-year Tsarist rule. He died unexpectedly in April of 1605. The end of his government was, by all means, a catastrophic one. The Southern lands were devastated by Tatars, there was plague and four years of drought in a row. To add insult to injury, some rumors had appeared and spread that a little son of Tsar Ivan the Terrible had not died in 1591 at the age of nine but had miraculously survived. This had initiated turbulences in the masses who cited God’s punishment, because the rule of Boris was unlawful, was achieved through deceit and would not do any good.

In October of 1604, “Dimitry the Impostor” (as he was known later) had entered Moscow State and went to the Kursk region. Initially, he was met with a “fire fight” (an expression of that time, meaning cannon shots) but as a result of a political disagreement between the defenders of the city, Kursk surrendered. After the death of Boris Godunov, the Russian military took Dimitry’s side. In June of 1605, the successor of Tsar Boris, little Feodor was killed. The following month, the widow of Ivan the Terrible and mother of little Dimitry recognized the newly appeared Dimitry as her son. That same month July, Dimitry was approved for the throne. However, his Tsarship did not last long, and he was
assassinated less than a year afterwards, in May of 1606, after mother of little Dmitry had admitted that her recognition of Dmitry the Impostor was false.

Vasily Shuisky became the next Tsar for four years period. However, provincial Dvoryane did not attend the ceremony. Fuzzy Times continued.

Meanwhile, the Tatars were taking an advantage of a political and military mess in the center of the Moscow State and increased the intensity of their invasions into the Kursk-Belgorod region. Besides Tatars, Kossaks and other “thieve groups” invaded as well. That kept Dvoryane and Boyar Children on a permanent lookout and in fights. In August of 1610 a Tsar manuscript arrived to Kursk and other cities of Russia that said “disturbances and disagreements between the Russians are making the country weaker, and Poles and Lithuanians are moving on to Russian soil and shedding blood and devastating Orthodox Christian churches and monasteries. The Polish King is staying at Smolensk, and the Polish Getman at Mozhaisk, and the Impostor in Kolomensk. Seeing all of this, Tsar Vassily Shuisky decided to resign and become a plain citizen, and wished that all our people unite and protect our Russian Orthodox beliefs and our wives and children”.

Four months after it the Dmitry Impostor the Second was killed in October 1612, Moscow was liberated from Polish and Lithuanian troops.

During these nine years of Fuzzy Times, and the changing Tsars, Kursk Dvoryane and Boyar Children continued to carry out their duties during all the instability and disorganization. Ukaz of the Boyar Duma had directed that all Dvoryane without exception must enlist their service by May 29, 1611, and those who declined would lose their land. The Ukaz, however, stated: “Land should not be taken away from wives and children of fallen and wounded Dvoryane”.

In 1613, Mikhail Feodorovich Romanov became the Tsar before he completed 17 years of age. Kursk had sent a whole delegation of Dvoryane and Boyar Children to the Sobor which approved the new Tsar. All of them signed the Approval Manuscript on behalf of Kursk Dvoryane.

Tsar Mikhail was the Russia ruler from 1613 through 1645. This time period was saturated with military fighting for Kursk by Dvoryane and Boyar Children. These were times of placing life in Russia back in order, times of flourishing and elevating Russia. At the same time it was a period of heavy fighting on the Southern and South-Western borders of Russia, deadly dangerous times for Dvoryane and Boyar Children. What role has Boyar Son and Reitar, Ivan Klyosov, participating in during those times?
In 1612, a year before Mikhail had become Tsar, and when Ivan Klyosov was 32 year of age, Polish Getman Zholkevsky with his 70,000-strong army besieged Kursk. The Polish troops could not take the city and left after several bloody battles in which the Poles had suffered great losses.

In February and March of 1613 there were battles in the Kursk region with Polish and Lithuanian troops that ended with their defeat. Reports to the Tsar described the valor of Dvoryane and Boyar Children. These reports were the first ones received by the newly established Tsar and brought a renewed spirit to the Russian troops.

Meanwhile, there were practically non-stop military expeditions on the Western and Southern frontiers of Russia against Poles, Lithuanians, Tatar and Cherkas (Kossaks). In 1616, the Dvoryane and Boyar Children cavalry in Kursk alone was 753-members strong.

In 1616, Lithuanian troops had invaded the Kursk region, and a 340-man cavalry of Dvoryane and Boyar Children were sent to fight them. In 1617, Lithuanians had invaded the Kursk region again, and the Kursk forwarded 380 mounted Dvoryane and Boyar Children along with foot soldiers with the “fire fight”. In 1618, Lithuanians had invaded the Kursk region again. In 1620, the Tsar sent an Ukaz to Kursk in which he ordered Dvoryane and Boyar Children to have “two horses each” in case the Tatars came. Meanwhile, Polish and Lithuanian kings had sent envoys to the Tsar to sign “a truce for 14 years, from the present 127 (1619) to 7141 (1633)”.

During this relatively peaceful time period, a number of Dvoryane and Boyar Children had reached significant numbers – 885 in 1625, 864 in 1629, 997 in 1631, 1130 in 1642. However, peaceful times were relatively short, since the Tatars did not sign a truce and did not have any intention for peace. In 1616, they came near Kursk and were completely defeated within 15 miles of the city. Men, women and children who had been taken prisoner were freed. In 1622 a large troop of Tatars was crushed after they entered the Kursk area. In 1623 another large troop returned, and a 300-strong cavalry of Dvoryane and Boyar Children was sent to meet them along with mounted Kossaks and 100 foot soldiers with the “fire fight”. There was a heavy battle that devastated the Tatars. In 1628, a regiment of Dvoryane and Boyar Children met the Tatars who had captured many Russians, and freed them. The Tatars went towards Kursk, and within 10 miles from the city, they were defeated and their commanders captured.

In 1632, Lithuanians and Tatars had attacked Belgorod, South of Kursk, and took many prisoners and approached Kursk. United troops from several cities in the area led by Dvoryane and Boyar Children defeated the Tatars in a battle. In 1633,
Polish troops burnt Belgorod and the suburbs around it. Being encouraged by that, another Polish army went by Kursk and besieged it. After a long period of time, during which they devastated the suburbs, they lost many troops and left the city. The Poles invaded the area in 1634, and besieged Kursk with a 12,000 strong army. They had stayed at Kursk from the 4th to the 16th of April, and threw fireballs into the city but could not take the city and left.

In response, troops from the Kursk region stormed and took the Polish cities of Borzna and Poltava. This went down in history as the war between Russia and Poland of 1633-1634. A truce was signed on May 17, 1634.

Service in action by Dvoryane and Boyar Children was practically uninterrupted during formal peace and real wars. As a result, Dvoryane and Boyar Children were granted land by verdict of the Tsar Ukaz. Among those who obtained land by this Ukaz in 1639 was Boyar Son, Ivan Klyosov.

Boyar Children and Reitars

_The Book of Kursk Registry, 1652, Section “City Boyar Children” (RNAAA 21010-191)_ indicates that Kirey, son of Ivan Klyosov, checked in for duty “being on a horse and with a pishal (a rifle – AK) and was granted a compensation of 300 acres and ten rubles”. Ten rubles was pretty good money at that time. An acre of land in the first half of the 17th century cost about two rubles or a bit less, and this price was practically the same from the North of Moscow to the South, as well as the Kursk region.

Kirey was a seasoned man when called to duty at at 47. Indeed, by that time, Dvoryane and Boyar Children served all their lives – literally, until death or disability. Not many of them lived long enough to resign.

Who were City Boyar Children, anyway? Unlike Moscow Boyar Children, they lived and served in other cities and towns. This name appeared when the Moscow State was formed, and courts of the former Counts did not merge with the central, Moscow Court, but remained in other cities and towns. Hence, City Boyar Children were local landowners and “served from their land”. They were obliged to serve, and represented the principal military force. They represented Dvoryane dynasty servicemen.

Reitars were a separate contingent of Dvoryane and Boyar Children. They were a heavy cavalry. Unlike Dragoons, a light cavalry who would come down from their horse in order to shoot from a rifle and then mount again, the Reitars shot
from on top of their horse. Their armor was so heavy that they often would not have been able to mount again in the field after coming down from the horse. Reitar’s rules of engagement were basically copied from German and Dutch ones. A Reitar is a close copy of the German Reiter or a rider. Russian Reitars had served in Divisions of Foreign Lines along with Western instructors. The very word Reitars had gone along with the times of Peter the Great, as “Reitar Order” (1651-1680) and then the following “Foreign Order” (until 1701) and “Order of Military Matters” which became the Military Collegium in 1717.

Various troops with foreign names, including Reitars, were introduced since the beginning of the 17th century under Tsar Boris Godunov, and particularly under Tsar Mikhail Romanov, when the Russian military system had become poor organization. Reitar regiments were composed of City Dvoryane, Boyar Children and other free citizens primarily with their own horses. To be enrolled as a Reitar, one should come “on horse and armed”. Reitars were trained by foreigners and by Russian Stol’niks and Dvoryane, who were already trained.

“Free citizens” were enrolled along with Dvoryane and Boyar Children although it somewhat “tainted the purity” of dynasty servicemen. However, there were not too many nobles left after heavy and long wars during the Tsarship of Alexey Mikhailovich, son of Mikhail Feodorovich Romanov Ruler in 1613-1645). The following numbers speak for themselves. If in 1631 there were 997 Dvoryane and Boyar Children in Kursk, and in 1642 there were 1130, then in 1672, four years before the end of the rule of Tsar Alexey, they were only 614 Boyar Children in Kursk.

**Military and combat service of Dvoryane and Boyar Children**

The registry “Tales of Kurskers on Service, 1675” (RNAAA, 219732-40) tells us that Sergey, the son of Kirey Klyosov (born ~1630), Ivan’s grandson, reported to Duma Dvoryanin Semyon Ivanovich Zaboryansky that he served his duty to the Tsar in a city regimen, and had a compensation of 250 acres and a salary of 11 rubles. His actual land was 35 acres, and he did not have peasants in his possession. In the past year (1673-74) and the current one (1674-75), he was in a military expedition in the regiment of Count Gregory Romodanovsky.

The fact that Boyar Son Sergey Klyosov did not have peasants in his possession is not surprising since there were very few peasants during the 17th century in the Kursk region. Practically the entire population consisted of military men. Cities and towns were military garrisons. Peasants, who were free to move before 1591, did not have any desire to settle in the dangerous Kursk region. Only in the 18th century did peasants start to move into those areas.
Another registry, “A Sorting Out Book of Boyar Children in the City of Kursk and the Kursk Region, 1695” (The State Archive of Kursk Region [SAKR], 1555-168-419) says that Kondrat, son of Sergey Klyosov (born ~ 1655), “is serving regiment Reitar service from Boyar Children instead of my deceased brother Maxim Klyosov” and that he had just returned this 203 (1695) year for a vacation from the Kazikermen expedition where he had served in a regiment of Stol’nik and Voevoda Ilya Mikhailovich Dmitriev-Mamonov. Kondrat’s land was 30 acres. The Book also indicates that according to Kondrat’s report “he will continue to be on horseback serving our Great Tsars, the rifle of his statecarobin and a couple of pistols ready for an expedition and to shooting in its entirety”. Kondrat was then 40 years of age. He had obtained a grant of 200 acres and 7 rubles of money.

Kondrat’s brother, Vassily, son of Sergey Klyosov, had reported in the same Book (SAKR 1555-1-168-678) that he had served in the City service in Kursk since 1679, with a compensation of 150 acres and 6 rubles of money, and his land of 17 acres is situated in the Klyosov village of the Kursk stan of the Kursk region.

Here we see two different kinds of service, that is “the regiment service” and “the city service”. The city service was a garrison service while the regiment service was service in a military expedition. The regiment service was understandably more honorable.

From time to time, particularly when the intensity of combat service was significantly elevated, there was no available Dvoryane and Boyar Children to call into service. In those cases old resigned dynastymen were called to battle. In the second half of 17th century, the Voevoda of Kursk was allowed by Tsar Ukaz to draft and to direct frontier postsof retired Dvoryane and Boyar Children, who retired because they were old or were sick. These were not isolated cases. Indeed, service in the Kursk region was called “service by blood and death”. Documents from the end of the 16th century describe forces of “Turks and Crimea’s and Nogay’s Tatars, and the Lithuanian King, who fiercely united with Pôk and Ugrs [Finns], Germans and other Sweds”. They commonly hit on the Southwestern part of Russia, namely Kursk, Rylskand Putivl regions. Tatars had constantly penetrated the area often dragging captured civilians by the hundreds. Cities and suburbs were often devastated. This kept Dvoryane and Boyar Children on a constant lookout by means of reconnaissance and skirmishes. Distances that should have been covered by riding dynasty servicemen are mind-boggling. Observation towers were spread over huge territories. There were, for example, seven observation towers to the South of Kursk out in the Wild Field, the nearest one in four days of horseback riding or about 300 milesthrough marshes, forests, prairies. The last one was in 420450 miles away. The towers were reached in a
half-day, a day and sometimes two or three days of horseback riding between them. And all of them could be reached by Tatar troops. To deliver notes, Boyar Children would ride over huge distances often through an enemy territory. That is why their reconnaissance service was considered truly dangerous. Those areas were saturated with servicemen blood.

This was the service of Dvoryane and Boyar Children of the Kursk region. Among them were Boyar Children Ivan Klyosov and his son Kirey, and Kirey’s son Sergey, and Sergey’s son Kondrat, and Kondrat’s brothers Vassily and Maxim, mentioned earlier, and Kondrat’s son Afanasy Klyosov. And Kirey’s brothers Savva and Luka Klyosovs, Savva’s son Ostakhei (Boyar Son, service calls in 1626, 1636, 1639, and 1645), Ostakhei’s son Ivan (Reitar, service call in 1675), Ivan’s son Mikhail (Reitar, call in 1697), Luka’s son Anton (Boyar Son, calls in 1639 and 1645), Kirey’s son Prokofiy (Reitar, calls in 1675 and 1682), Prokofiy’s son Ivan (Reitar, call in 1697), Ivan’s brother Antip (Reitar city service, call in 1697). And also Iov Klyosov and his son Samoyla (Reitar, call in 1697), Dementiy Klyosov and his son Afanasiy (Boyar Son, call in 1630), Afanasiy’s son Pavel (Reitar, call in 1675), Pavel’s son Potap (Reitar, call in 1697), Karp Klyosov and his son Leon (Reitar, call in 1697), Leon’s brother Mikhail (Reitar city service, call in 1697), one more Leon Klyosov and his son Stepan (Reitar, same call in, 1697), Timofey Klyosov and his son Savva (Boyar Son, call in 1645), Kiril Klyosov and his son Trofim (Reitar city service, call in 1697) and Zakhar Klyosov, a cannonman (call in 1645).

All thirty-two Klyosovs were Kursk servicemen.

As it has been repeatedly stated, those times in the Kursk area were quite dangerous. As mentioned earlier, Ivan Klyosov was granted land in 1639. Seven years after that, in 1646, Tatars undertook a large invasion of the Kursk region. Thirty four settlements on granted land were completely destroyed and their inhabitants were kidnapped, mainly young Dvoryane, women and children, whole families, whose men were serving at that time or were killed. Being encouraged by their success, Tatars moved to another area to the neighboring Rylsk. They managed to devastate several settlements there, however, a regiment of Rylsk Boyar Children had attacked them and in a bloody battle freed the women and children, a total 439 people. As a historian wrote, “This explains why every Dvoryane and Boyar Son had armaments hanging on a wall next to his bed.

One of the largest pogroms (destruction of households) by Tatars had happened in 1680 in the Kursk-Belgorod region. They killed and kidnapped 471 men and 368 women. Most of those killed and captured were Dvoryane and Boyar Children with their wives and children. According to historical sources, Tatars
beat to death defenseless children from infants to 15-year olds. Two hundred and ninety four children died including twenty eight boys of 4-years old or less, and forty two girls were burnt alive. In 1680 alone, Tatars killed and led into captivity 3,258 men, women and children, and took away 24,193 cows and horses, 4,828 beehives and burnt to the ground four churches, 688 courts, four windmills and eight settlements. Captured people were sold into slavery in Crimea, Constantinople, Asia Minor, and other countries and regions.

When Tatars appeared in the neighborhood, inhabitants yelled and cried “Tatars are coming, our death is coming”. This was a yell of desperation. Military horseback riders and Dvoryane and Boyar Children should have battle day and night. This was the lifestyle in the Kursk region for Dvoryane and Boyar Children in the 16th and 17th centuries. This was directly related to the military expeditions in which Sergey, grandson of Ivan Klyosov, and his great-grandson, Kondrat, participated.

Chigirin, Azov, and Kazikermen Expeditions

What were the expeditions in the division of Gregory Romodanovsky in 1674-1675, and what was the Kazikermen expedition in the regiment of Mamonov in 1694-1695?

These expeditions were part of the military operations undertaken by Tsar Alexei Mikhailovich before the end of his rule, to secure the right-hand side of the river Dniepr, which was a part of Russia. The lefthand side of the Dniepr, also the Russia side, was united with Russia twenty years back, in 1654. The opposite side was still under the heavy influence of the Turks. Getman (the title – AK) Samoylovich was the highest leader in Ukraine in 1674. He ruled on the both sides of the Dniepr, and was recognized by Russia. Doroshenko, the former Getman in the Western Ukraine, with a residence in Chigirin on the other side of the river, did not recognize Samoylovich and was maneuvering between the Kossacks and Moscow. At the same time, he was playing a game with the Turk Sultan, and, as it was reported that time while negotiating with Russia, sent a request for military help from Crimea by the Turks. Samoylovich alarmed, called for help from Moscow.

Count Gregory G. Romodanovsky with his troops had moved to Chigirin and siezed the city. Doroshenko, understanding the hopelessness of the situation and having no news from the Turks, surrendered Chigirin and forfeited his getmanship. This was the first but far from the last joint military expedition of the Russian troops and Ukrainian kossacks to Chigirin. In fact, this was the beginning of a series of Russian-Turkish wars, that is, wars of the Osman Empire.
and alignment to the Crimean Khanship. Sergey Klyosov participated in this, the first Russian-Turkish war.

Sergey's participation in the war was taken over by his son, Kondrat. The Kazikermen military expedition which he had mentioned in "A Sorting Out Book of Boyar Children in the City of Kursk and the Kursk Region, 1695" (The State Archive of Kursk Region, 15551-168-419), was a part of the advancement to Azov by Tsar Peter, who later became Peter the Great. This was called The First Azov Expedition of 1695. A Cannon Regiment was headed by Bombardir Piter, as he called himself. The entire summer of 1695 Tsar Peter with his 35,000-strong troop had tried to capture the Turkish fortress Azov by throwing into it thousands of bombs but was unsuccessful and had to pull away by fall. In other words, his rule had started with an unsuccessful military operation.

However, it was not completely unsuccessful. At the end of July 1695 a regiment of Boyar Children of Kursk, among which was Reitar Kondrat'son of Sergey Klyosov, and headed by Kursk Voevoda (a military commander - AK), Ilya Dmitriev-Mamonov, had stormed and took over the Turkish fortress Kazikermen at the mouth of the Dniepr river. The storming the fortress involved Kossack troops headed by Getman Ivan Mazepa and Moscow troopson horseback and on foot headed by Boyar B.P. Sheremeteve. The siege and bombarding of the fortress had lasted five days and nights by use of cannons and small firearms. A Kossack historian of that time, Samyila Velichka, wrote: “One night Kazikermen was hit by dozens of bombs and small grenades with fire coming from all carriages. All around the dark night was illuminated as if from lightning”. Finally the fortress wall was destroyed and the troops stormed in. Hand-to-hand combat lasted five hours, and Kazikermen capitulated. Garrisons of the two neighboring Turkish fortresses, Aslam-kermen and Mouberek-kermen, fled to Crimea, abandoning large cannons. This was probably the only good news in the whole Azov campaign. Kondrat Klyosov was probably proud when he reported back home about the expedition.

**Single-courtiers**

By the beginning of 18th century, frontiers of Russia went from South to further West, and life of the military elite in the Kursk region became less tense. Dvoryane and Boyar Children were allowed to retire and permanently settle on their own land. If earlier their land was given to them in a temporary ownership only during the military service, then later, step by step, the restrictions were removed, and ownership rights began to move towards their direct descendants, then to wives and children, then to widows, and finally to side relatives. When sons in the dynasty military family were “ripe to serve”, they either “let in” to the
father’s land and would not receive any extra land, or were granted their own land “to be derived” from their father.

Eventually, when life of the dynasty militarypeople in the Kursk region had became more stable, it turned out that many Dvoryane and Boyar Children did not want to carry their saber on their hip all their life and be called to the troops until they are disabled or dead, and they began to move to their land to become farmers. This was the beginning of the forming of a separate strata of the Russian society of civil land-owners and their children, so-called single-courters. According to records of those times, in the 18th century, many Dvoryane who did not want to continue their military servicemoved to single-courts. In the 19th century, they received a right to become Dvoryane again after they were able to prove their noble roots and enrolled back into military service. As an historian wrote: “Some very old Dvoryane lines, reduced to own relatively little land, became single-courters. During the times of Peter the Great some Dvoryane who owned as many as 100 and 200 peasant courts, did not want to serve and legally registered as single-courters”.

In many cases, however, that transition was a forced one. Reforms by Peter the Great, who had changed Russian society, led to a significant reduction of the number of military dynasties, primarily City Dvoryane and Boyar Children. They faced few options: either to struggle to stay in the military service, or move to administrative work, that is, to become a kind of bureaucrat in the new society, or to settle as farmers on their own land. Many preferred the latter choice.

After some time a number of the Tsar’s verdicts created a new strata of society. Single-courters had taken a new level between Dvoryane and peasants and became middle-class farmers. Many documents of that time called them free farmers, later state farmers, unlike possessed farmers, monastery farmers, or church farmers. State farmers in the Kursk region were not so much field workers; typically, they kept themselves busy with gardening, fishing, beehive-keeping, poultry-keeping, sheep-breeding and horse breeding.

Most Boyar Children did not have their own peasants or “possessed farmers.” After they became single-courters, they labored themselves sometimes hiring workers. However, when they had served in the military, their land was tax-exempt, because they paid for the land with their service. Now their land became state taxed.

The legal unit for taxation was the single-court. Single-courts were further divided into smaller single-courts in which children and other close relatives lived. Single-court families often were quite large, with grandfather and
grandmother, their children with wives and children, sometimes children of the third generation. Everyone in the court was called a single-courter. Only the court was taxed as a unit. Census documents, so-called Revision Tales, which were collected once in a while, have recorded single-courters by courts. There were ten Revision Tales between 1720 and 1858, the number does not include earlier revisions, so-called landrat censuses.

An example of such a large court was the first court in the Klyosov village, according to the First Revision of the Kursk district of 1710 (GAKO 1841-12-177), which was registered as “Single-courters, Reitars”. That court would nowadays be called a cluster. The Revision lists Afanasyi son of Kondrat Klyosov (grandson of Boyar Son Sergey), 35 years of age; his wife, a 7-year old son and 1-year old daughter, two nephews of 16 and 18 years of age; a wife of the older cousin and their 6 months old daughter. Eight single-courters in one court. The second court was assigned to the second grandson of Sergey Klyosov, 50-year-old Eremei, son of Vassiliy Klyosov with his family; the third court was registered to Eremei’s brother, a 40-year old Ivan with his family; the fourth court was their brother 30-year old Gregory, with his family; the fifth court was the widow of their brother, Matvei with his family, and so on. There were 12 courts total with 35 “single-court souls”.

The Second Revision in 1744 has shown that there were 70 people who lived in the Klyosov village that time 69 single-courters and one hired worker. At the beginning of the 20th century, an incomplete family tree of Klyosovs included 176 individuals, and now, including us – my wife and two grandchildren makes 16 generations. A total number of descendants of Ivan Klyosov from the 16th century until now would be hard to count. There should be many hundreds of them. However, World War I, the Russian revolution of 1917, and the following Civil War of 1918-1922, as well as the World War II, have greatly reduced their numbers both directly and indirectly.

The Klyosov courts were not situated too close to each other. The land was not crowded. Three hundred acres is a pretty wide territory, which is the equivalent of 290 football fields. Courts were situated on two river banks on different sides of the land. It was a matter of convenience of Klyosovs. Those who had only 20 acres, almost 20 football fields, had enough land for their family. With time, of course, relatives multiplied and courts divided. Children commonly divide the father’s land fairly, in equal parts, unless children died or moved elsewhere. Single-court villages were closed to outsiders, who were seldomly allowed to get the land. Rarely son-in-laws were such outsiders. They were rare because daughters commonly left to go to their husband’s village, also typically a single court bearing the husband’s name, or – much later - a court in the same village. Sons-in-law rarely came to their bridé’s court, because a sister of brothers would
not get land. She was supposed to go to her husband. Exceptions were when the daughter was the only heir. And indeed, “our land was inherited, a deserved inheritance, earned by tough military service, granted and registered by our ancestor. A son-in-law did not belong there”.

The Klyosov family records are filled with examples of departures of daughters to single-court villages:

From the 1763 Revision Tale:

-- Paramon, son of Afanasiy (yb 1713), wife Ekaterina, brought from Kursk district, village Anakhin, daughter of a singlecourter Anakhin.

-- Matvei, son of Paramon (yb 1740), wife Akilina, brought from village Yakshino, daughter of a singlecourter Yakshin.

From the 1782 Revision Tale:

-- Gregory, son of Paramon (yb 1748), wife Ustinia, brought from Fatezh district, village Shuklina, daughter of a singlecourter Anisim Shuklin.

-- Vassilisa, Daughter of Paramon Afanasievich (yb 1761), given out to marriage to Akim Perkov, a singlecourter from village Perkovo of Kuresk district.

-- Avdei, son of Yakov (yb 1740), wife Mavra, brought from L’gov district, village Polyachkovo, daughter of a singlecourter Ivan Polyachkov.

-- Evpat, son of Lukyan (yb 1734), wife Ekaterina, brought from Kursk district, village Umrikhin, daughter of a singlecourter Stepan Umrikhin.

And so forth.


Klyosov from village Klyosov; witnesses from the bride’s side - Stefan Klyosov from village Klyosov and Stefan Pykhtin from village Pykhtin.

There were quite a few cases like these. However, it was already the 19th century and relatives spread along different and distant family lines.

Land granted to the ownership by the outlanding of dynasty military people, was called quarterland, from the Russian word translated as “quarter” (chetvert’), a land measuring unit equal to an acre. Hence, a right to own this land was called a quarter-right. A son-in-law, who had married an heir, and hence, entered a quarter-community, would not acquire a quarter-right legally, and it was not recorded in the land registry. There was no “possessed” peasants among them, of course, because a free singlecourter female would not marry a slave. That is why grooms and brides were only singlecourtiers from the same circle of the society. Historians, who had lived during those times described that singlecourtiers were known for their vanity with their heritage and stiff upper lips to lower classes. And then “many of them were Dvoryane of a former high society”, but became farmers for their unwillingness to serve in the Army.

And now we come to taxation “from a soul”, or soul-taxation, and to the fate of the single-courter strata in Russia. This fate had resulted from a number of particular historical processes in Russia, namely disappearance of a noticeable part of the Dvoryane by moving it to agriculture, the displacement of an old, conservative lifestyle in rural Russia by a more mobile, aggressive soulless lifestyle. The driving force of it was the role of a merciless state “assembly line” in grinding the conservative Russian lifestyle, which had eventually led to the fall of the Russian State.

This process can also be described in other terms. All of this evolutionary change had reflected an actual process of industrialization of Russia, the development of its modern agricultural system, which was initiated by Peter the Great. As a result, old Russia’s backbone had collapsed in 1917.

The process had begun to accelerate from the time of Peter the Great’s reorganization of the Russian Army. Former military check-ins “on horse and armed”, care for “purity of the military structure” and “purity” of the military elite above all along with care of the dynasty military men themselves by their granting of land, was replaced with unified troops and maintaining unification. A kind of military “assembly line” structure had started to form, in which everything was paid, not by the military officer as before but from the state coffers. The state paid for horses, armaments, uniforms, food, and everything else. The country was divided by those who served and those who supported the army through taxes. Russia, with its conservative lifestyle was not ready for it,
and this led to a remarkable stress for the Russians. For such a sharp turn towards the new political and military system, as well as the whole way of life, Tsar Peter had pushed with his reforms.

Among the slogans of Tsar Peter was “nobody owns land in Russia for free”. This clearly meant taxation of privately owned land. Therefore, single-courtiers, as a strata of the Russian society, was an invention of Peter the Great. Indeed, single-courtiers were initially mainly Dvoryane and Boyar Children, who served according to their heritage and from their land, and who then left the service and settled on their private, granted land. However, as a result of the “industrialization” of Russia for the following 100-150 years, that strata was mercilessly homogenized and stripped its former rights. For starters, this strata was mixed with representatives of a lower-class of the society who were drafted for military service, and who received much smaller pieces of land, typically no more than 10-25 acres. Then with a series of Ukazs, or Tsar verdicts, that strata was transferred from the quarter-right to a “soul-right” in which taxation was from “souls”, not from the land. Finally, single-courtiers were officially named not private farmers, as they used to be, but as “state farmers”.

Of course, nobody in the Russian Government had such a far-fetched plan. It was just happening by itself and pushed forward with each new Ukaz as a part of a general process of pushing Russia forward to an industrialized society.

Flipping through Revision Tales of single-courtiers from the first one in 1710 (it was a preliminary one, and finally set up in 1724), to the tenth, in 1858, one can follow milestones in destroying of the former conservative, patriarchal lifestyle of Boyar Children settled onto their land granted for military service.

In the first Revision, Klyosovs in all 12 courts were described as “Single-courtiers, Reitars” or “Single-courtiers, City” (GAKO 1844-12-177-179). “City” meant that they retired from Kursk military service. In 1711, an Ukaz by Tsar Peter assigned single-courtiers to a separate strata of the society which had legal right to discuss matters between themselves through representatives. The next Ukaz by Tsar Peter enacted on May 14, 1723, assigned to single-courtiers all former military people who have land, including City Dvoryane. At the same time taxation from single-courtiers was significantly increased.

In 1724 the next Ukaz enacted by Peter stated that all single-courtiers were “fixed” on their land which they could not sell or leave. Furthermore, a new obligation was introduced, a rather severe one, that was called “a collective responsibility”. In other words, if a single-courtier left his land and the community, all other villagers had to pay the taxes for those who had left. State coffers needed money.
Needless to say, such measures did not encourage single-courters. They saw a clear curbing of their rights. Overall, Tsar Peter’s reforms treated landowners quite heavy-handedly. In 1724, all single-courters who were not returned to the state service, military or otherwise, were officially named “state farmers” which in the Russian language also meant “state peasants”. “Farmers” was never a respected term in Russia then and now. It was a proverb in Russia during those times that “State peasants live as God says, possessed peasants live their master says”, however, it did not help much. This was a way of converting retired Dvoryane and Boyar Children to farmers and that transfer was significant.

After Peter the Great, the Russian Tsars were Elizaveta, Ekaterina, and in 1796, after Ekaterina’s death, her son Pavel became the next Tsar of Russia. He had initiated a change from the quarter-tax to the soul-tax. In other words, taxation from a court as an administrative unit was removed and replaced with head-taxation, a taxation from every individual inhabitant of courts and villages in general. This was a painful process, mainly for those who had had large land inherited from their ancestors 100-200 years earlier. The reason was that the soul-taxation was introduced along with redistribution of land between the haves and have-nots, and to allocate to every farmer 10 acres of land per soul, or 40 acres to every court. It was accomplished mainly by taking land from large landowners. It turned out that there was not so much land available. Then it was decided to still give 10 acres per soul, and where there was not that much land available, to give 5 acres per “revision soul”. This was very beneficial to small landowners but not to large landowners.

That decision had largely didided society and stressed it. Pavel was Tsar for only five years, however, his “soul-taxation” reform had been implemented for about 100 years and led to many fights, including physical ones between the have and have-not farmers and peasants.

According the last 10th Revision in 1858, village Klyosov had 14 courts, 71 male single-courters and 73 female single-courters (GAKO 184-2-1112-626/639). It seemed that nothing had changed in village Klyosov for the last 150 years except the number of courts and their inhabitants which created a kind of a still picture. Such a stillness was very typical for large land single-courters. This stillness was their happiness and was at the core of a patriarchal lifestyle. There was one more feature in their life clearly distinguishing large land single-courters from other peasants. Single-courters knew their ancestors and predecessors. They knew their relatives, past and present, even quite distant ones and how they were related to each other. An old historian wrote: These memories with their exact precision are carried by only Boyar Children who never forget their nobility and past service of their great-grandfathers; there are no tales in modern villages
composed with recent visitors”. This was considered as “vanity” of single courters by “recent visitors” not having such memories.

Eventually, the Russian Government took over all singlecourt villages move to a soul-taxation. The patriarchal lifestyle had gone, and the villages had started to collapse. My direct predecessors had moved as an extended family to Siberia in 1898, and built their life back again. And then came the 1917 Revolution “of workers and peasants”. My great-grandfather, Ermolay Klyosov, a priest, was shot by a firing squad following a verdict by a “revolutionary tribunal”. During those times, many Klyosovs were accused and sentenced for being rather “haves” than “have nots”. This was their principal guilt, and this was a fact of life then. Here is a far from complete list of Klyosovs sentenced and exiled by the Soviet Government and its representatives:

-- Klyosov Fedor, 1872 y.b., born Tomsk, Siberia, Russia. Was arrested: September 28, 1937. Sentenced December 9, 1939 by “troika” (meaning – his case was considered by three representatives, they were the court, jury, and judge at the same time and place) of NKVD (the predecessor of KGB). The case was described as “an anti-soviet activity”. Shot on January 22, 1938. The case was reversed and nullified in May, 1989.

-- Klyosov Ivan, 1905 y.b., born Kursk Region, Russia. Was arrested: March 3, 1937. Sentence: imprisonment for 3 years. The case was reversed and nullified in September, 1989.


-- Klyosov Prokop, 1875 y.b., born Omsk, Siberia, Russia. Was sentenced on August 8, 1931. Sentenced August 8, 1931 for exile in the Siberian North, died there in 1933.


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My father, Alexey Klyosov, was born in 1923 in Siberia and graduated from Air Force school in 1941. He was drafted right away to the front to fight with Nazi Germany. The war was ended for him in April 1945 with the defeat of Konigsberg in East Prussia, Germany, in which he was taking an active part and was awarded for valor. He had served with the military transportation troops in Insterburg (now Chernyakhovsk) in East Prussia which was later annexed by the Soviet Union and became the Kaliningrad Region, USSR, and now Russia. Then he served and our family lived in Riga, Latvia, and we all moved in 1955 to the largest Soviet missile military base, which then became a space complex Kapustin Yar. Being mortally ill there he was directed to serve at a famous Russian resort called Sochi in a semi-tropical area of Russia on Black Sea as an attempt to save his life. It gave him indeed a few more years of life. His son and my brother, Eugene, had continued family traditions and served for more than 20 years in Siberia with the military transportation troops, and then in Sochi. I live in Boston with my wife Gail for the last 20+ years. Our daughter, Svetlana, with her family and our two grandsons, live in France, in a village between Nice and Cannes. They are all naturalized French nationals.

This is kind of normal biography and a mirror of Russian history with a transition to modern times.


All of us Klyosovs must have about the same haplotype, with only few mutations, as well as most of inhabitants of Russian cities, towns and villages having the same haplogroup R1a1. It is a typical Slavic haplotype and is derived from our ancestors who had lived about five thousand years ago. But that is a different story.

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