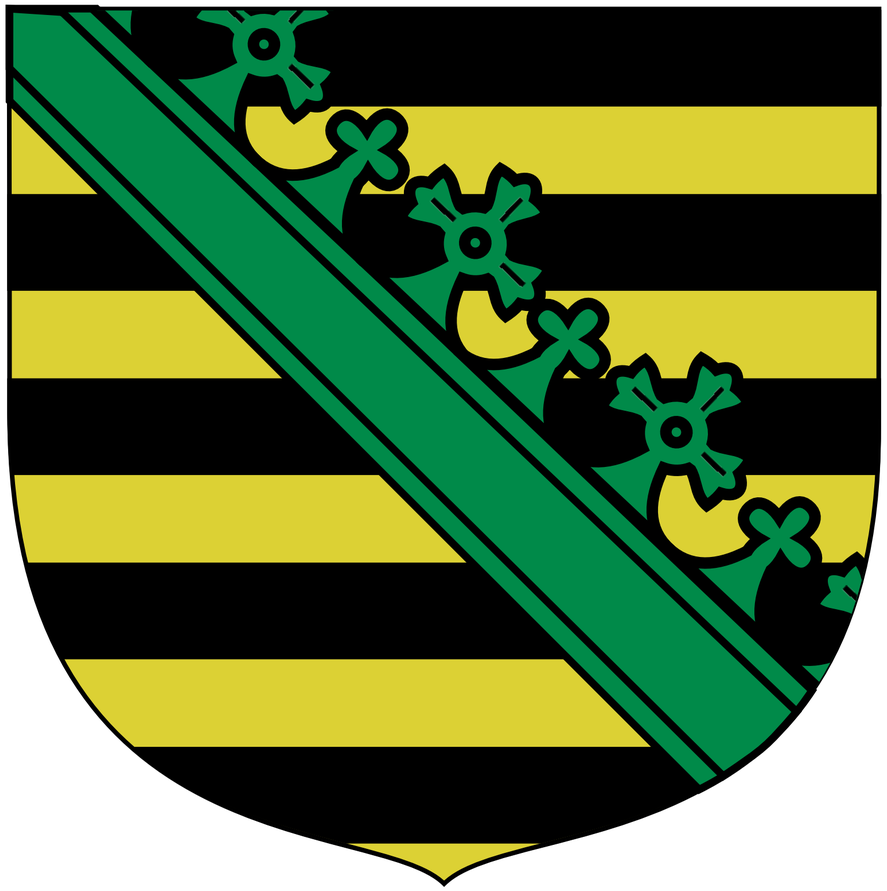
The Pre-History of the House of Wettin

Identification through DNA of the “Kings’ Cluster”



Contents

The history of R-U106

(1) INTRODUCTION

This deep phylogenic tree of the human population represents our current understanding of the way the human family tree has divided along its male lines. This is a rapidly-evolving field, thus the information is subject to considerable change over time.

This tree summarises the extensive tree that lies above R-U106. This shows how R-U106, which now represents many tens of millions of men worldwide, branched off from the rest of the human Y-chromosome tree at different points in prehistory.

(2) OUT OF AFRICA

Ultimately, we all descend from the first life-forms, which lived approximately three billion years ago. Through a long and convoluted process, they evolved into *homo sapiens*. While *H. sapiens* has only been around for about half a million years, this is still older than the common ancestor of the male lines of every person alive today. We call this person Y-chromosomal Adam, because we all descend from him via our father's father's father's father's… etc. Recent estimates of his age place his birth at around 200,000 to 250,000 years ago.

The vast majority of people descend through Haplogroup A. In fact, it's only recently that researchers discovered our most-distant relations hiding among remote Africa tribes. Haplogroup BT arose in Africa about 88,000 years ago, when the most of the human population consisted of a small number of tribes living in the Horn of Africa.

The human genetic tree continued to diversify and flourish as mankind expanded throughout Africa. Around 50,000 to 60,000 years ago, a small group of migrants is thought to have crossed the Red Sea into Arabia, starting the most important in a series of Out of Africa migrations.

Some time not too long after this point, a little over 45,000 years ago, we split from haplogroups G and I, which appear to form the original modern human population in Europe. This point is defined by the recently analysed 45,000-year-old remains from western Siberia, from a man who was haplogroup K (but not haplogroup LT, so near the K2 level).

Our base haplogroup, R, arose from this migration between 24,000 and 34,000 years ago. This is again limited by the archeaological remains of Mal'ta Boy, who was buried 24,000 years ago in Siberia. By this time, our ancestors had probably expanded to across much of north-west Asia, where they existed as hunter gatherers.

(3) EXPANSION INTO EUROPE

Within haplogroup R, most people are descended via the R1 clade. Within R1, there is a bifurcation into two groups: R1a (R-M420), and R1b (R-M343). R1a is strongest in eastern populations, where it can exceed 60% of individuals in Poland and the south-west Russian states. Its British content is thought to be strongly Viking in origin.

R1b (R-M343) is thought to have arisen around 20,000 years ago. In Europe, it is very much dominated by R1b1a2, or M269. This group alone makes up over half the population in Western Europe, and makes up over 90% of some populations. Despite this, its origins are still thought to have been in western Asian populations, and it came to dominate Europe as it expanded throughout the continent.

The date of this expansion into easternmost Europe (Russia and the Ukraine) can probably be tied to the sudden growth in the number of branches below M269, around 4000 BC.

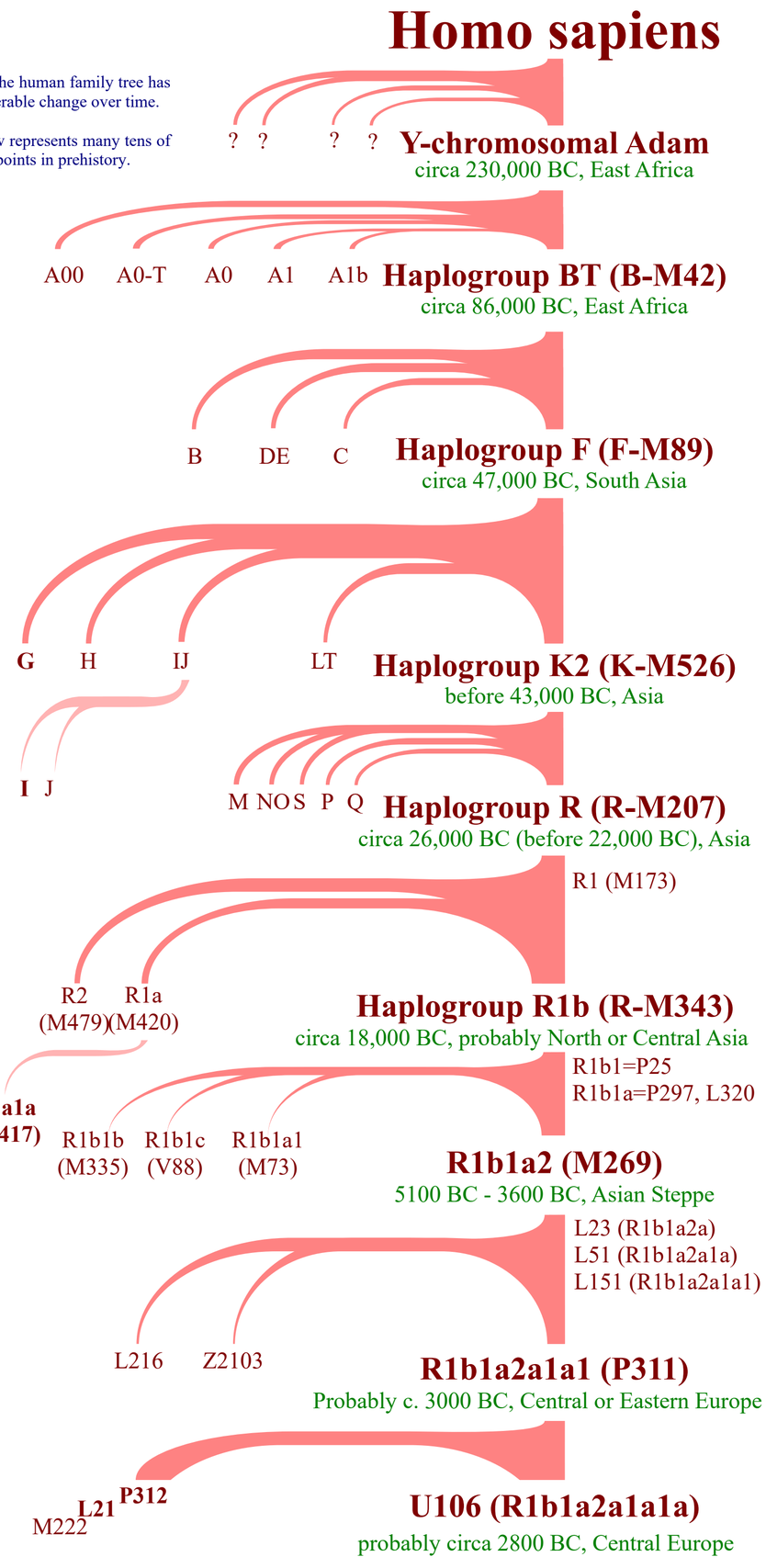
(4) FOUNDING A NEW EUROPEAN POPULATION

Most of the branches above U106 are minor, however there is one important branch at the level immediately above U106, signified by the mutation P311. A split exists at this point in our family tree between the larger P312 branch and the smaller U106 branch. The R-P311 level probably corresponds to our ancestors' arrival into central Europe, somewhere in the region of modern Germany, around 3000 BC or shortly thereafter. Archaeological remains indicate that this is likely coincident with the arrival of the Corded Ware culture.

The P312 branch is generally found more on Europe's Atlantic Coast, being spread by the Bell Beaker culture. Meanwhile, the U106 branch is generally found more in Europe's heartland. This has erroneously led to P312 being synonymised with "Celtic" peoples and U106 with "Germanic". While there is clearly some overlap between membership of these SNPs and populations, both SNPs originate several thousand years before these terms are relevant.

Nevertheless, it is the last common ancestor of these two branches, "Mr. P311" whose clan is now represented by around half of western European men, with a third of a billion diaspora worldwide (see panel at right).

R-U106 represents about 1/8th of Europe, or 110 million men worldwide. We estimate its origin to be between 3700 and 2500 BC, which ties in with the archeaological expectation of circa 2800 BC.



Deep ancestry of U106

Acknowledgements

The information in this tree comes from a variety of sources, primarily the International Society of Genetic Genealogy (ISOGG) and YFull. The haplogroup statistics on eupedia.com have also been instrumental in creating these data.

Created by: Dr. Iain McDonald; updated: 14 Aug 2017

How to read this chart

This chart shows how the male-line genetic (phylogenic) tree splits from its foundation down to the U106 branch. Different ages and geographical origins distances are shown on the chart, which should be interpreted carefully.

Where quoted, ages are given as 95% (~"2-sigma") confidence intervals. We are 95% sure that the real dates lie between these two boundaries. By dividing the uncertainty in half, we can recover the 68% confidence interval, or "1-sigma" range. Dates are rounded to the nearest 100 years.

This date was calculated using SNP-counting methods which are detailed at:
www.jb.man.ac.uk/~mcdonald/genetics.html

Haplogroup Frequencies in Europe

NB: Data have not been updated since 2014.

The following data give the number and percentage of various levels between R1b-M343 and U106 in different parts of Europe, as found by Myers et al. (2007) and selected other studies. These can be used to approximate correction factors to debias our statistics according to how many people of different ancestries have tested. These numbers are only very approximate in many cases and only represent first-order estimates of the underlying population.

COUNTRY	POPLN.	%M269	%U106	M269 & U106 POPLN.		#TESTERS	WEIGHT
British Isles							
Ireland	6429508	80%	6%	5143606	385770	99	4
Scotland	5327000	72.5%	12%	3862075	639240	132	5
England	53012456	57%	20%	30217099	10602491	317	33
Wales	3063456	83.5%	5%	2557985	153172	13	12
Total	*67836420*	*62%*	*19%*	*41780765*	*11780673*	*658*	*18*
Iberia							
Spain	47150800	42%	8%	19803336	3772064	6	629
Portugal	10607995	56%	1.5%	5940477	159119	3	53
Central Europe							
Denmark	5568854	34%	17%	1893410	946705	9	105
Netherlands	16696700	54%	35%	9016218	5843845	32	183
Belgium	11198638	59.5%	25%	6663189	2799659	10	280
France	65460000	52%	7%	34039200	4582200	21	218
Germany	81757600	43%	19%	35155768	15533944	103	151
Switzerland	7785000	58%	13%	4515300	1012050	13	78
Italy	60418711	37%	4%	22354923	2416748	14	173
Austria	8414638	27%	23%	2271952	1935366	2	968
Eastern Europe							
Hungary	9979000	20%	4%	1995800	399160	6	67
Czech Rep.	10261320	28%	14%	2873169	1436584	5	287
Slovakia	5443386	25%	3%	2721693	326603	1	327
Poland	38192000	23%	8%	8784160	3055360	19	161
Lat./Lit./Est.	6032500	10%	4%	603250	241300	12	20
Belarus	9503807	5%	0.5%	475190	47519	1	48
Ukraine	45939820	25%	9%	11484955	4134583	4	1034
Romania	20121641	15%	2%	3018246	402432	1	402
Bulgaria	7621337	10%	2%	762133	152426	0	-
Former Yugo.	20449929	5%	1%	1022496	204499	1	204
Slovenia	2012917	17%	4%	342195	80516	3	27
Greece	11645343	10%	1%	1164534	116453	0	-
Russia	110000000	21%	5.4%	23100000	5940000	7	849
Turkey	76667864	14%	0.4%	10733500	306671	0	-
European Colonies (estimated)							
United States	230000000	46%	15%	105800000	34500000	-	-
Australia	20000000	46%	15%	9200000	3000000	-	-
NZ	4000000	46%	15%	1840000	600000	-	-
Canada	30000000	46%	15%	13800000	4500000	-	-
Total	**1041 million**	**N/A**	**N/A**	**383 million**	**110 million**		

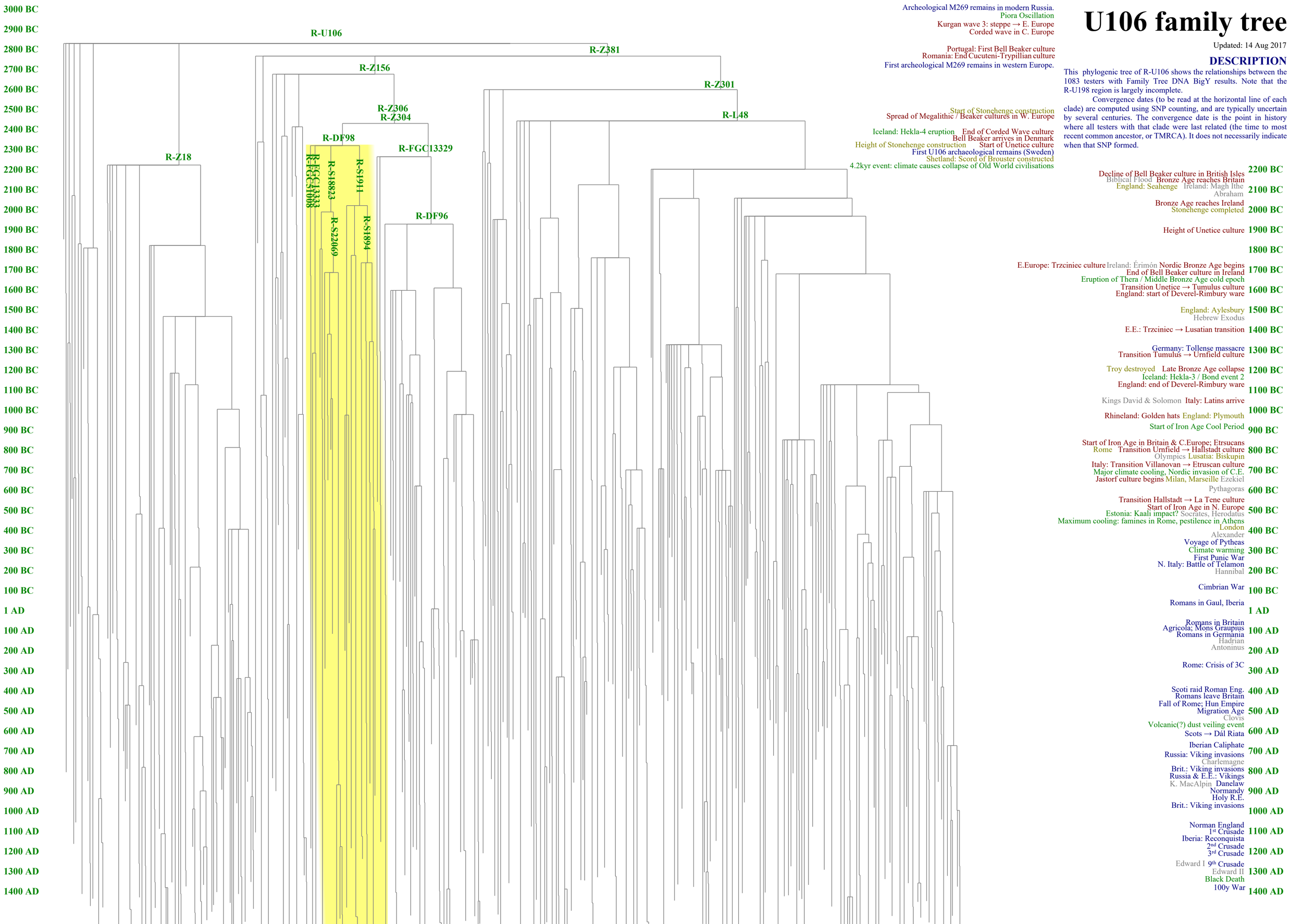
U106 family tree

Updated: 14 Aug 2017

DESCRIPTION

This phylogenic tree of R-U106 shows the relationships between the 1083 testers with Family Tree DNA BigY results. Note that the R-U198 region is largely incomplete.

Convergence dates (to be read at the horizontal line of each clade) are computed using SNP counting, and are typically uncertain by several centuries. The convergence date is the point in history where all testers with that clade were last related (the time to most recent common ancestor, or TMRCA). It does not necessarily indicate when that SNP formed.



Major branching structures within R-DF98

2500 BC
2400 BC
2300 BC
2200 BC
2100 BC
2000 BC
1900 BC
1800 BC
1700 BC
1600 BC
1500 BC
1400 BC
1300 BC
1200 BC
1100 BC
1000 BC
900 BC
800 BC
700 BC
600 BC
500 BC
400 BC
300 BC
200 BC
100 BC
1 AD
100 AD
200 AD
300 AD
400 AD
500 AD
600 AD
700 AD
800 AD
900 AD
1000 AD
1100 AD
1200 AD
1300 AD
1400 AD
1500 AD
1600 AD
1700 AD
1800 AD
1900 AD
2000 AD

DF98
16010726 (C→T)
[AMM486; FGC29253]
Appears equivalent to DF98

FGC51008
FGC13333
S18823
FGC20588
S22069
M6509
S11739
S8350
S1911
S10621
FGC13445
S1894
FGC14758
BY650
S4004

Minor Clades

FGC13333
Page 5

FGC51008
Page 5

CTS7550
Page 5

S18823
Page 6

S22069
Page 6

S8350
Page 7

S1911
S10621
Page 8

S1911
FGC13445
Page 9

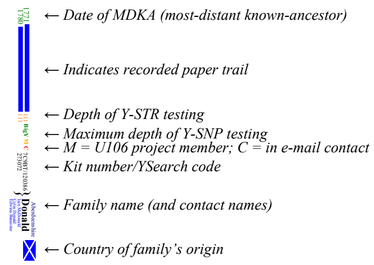
S1911
S1894
Page 10

Key to following pages:

- *Y-STR match, no/private STR data*
- *Predicted structure from STRs*
- *U106+*
- *Tested DF98+ (including DF98* panel tests)*
- *Positive SNP/panel test within DF98*
- *Terminal branch from BigY or FGC Y-Elite*
- *Surname/geographical* and Y-STR link*
- *Surname, Y-STR and autosomal link*
- *Paper trail connection suspected*
- *Paper trail connection known*

**Includes not-shared surname matches with a close geographical link (within ~10 miles).*

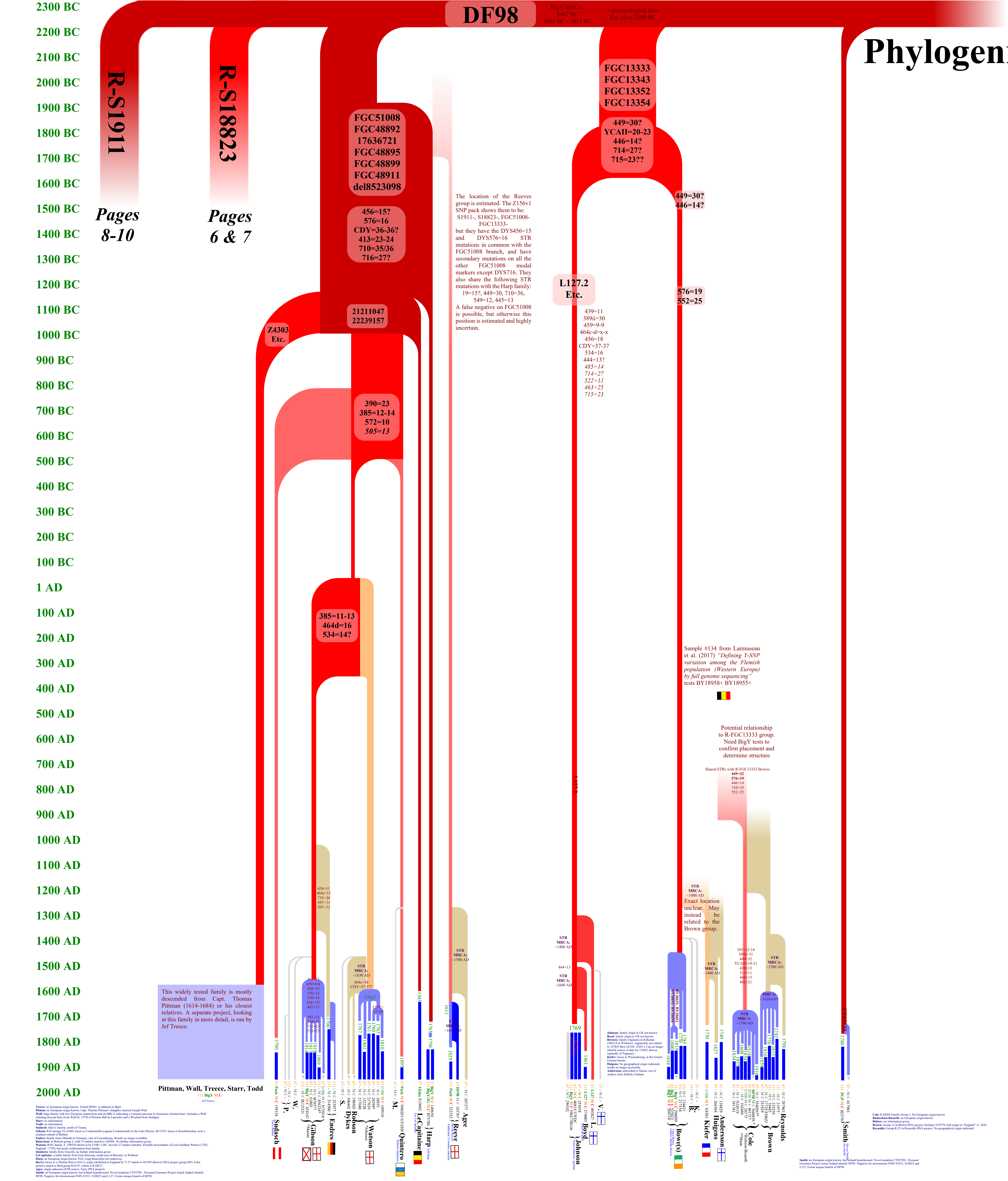
Individuals electing to show their information on public project pages are identified by family (MDKA) name. Individuals identified through private information are Identified by their initials.



Ungrouped tests
Page 11

Known STR imposters
Page 12

Phylogenic family tree of R-DF98's minor branches



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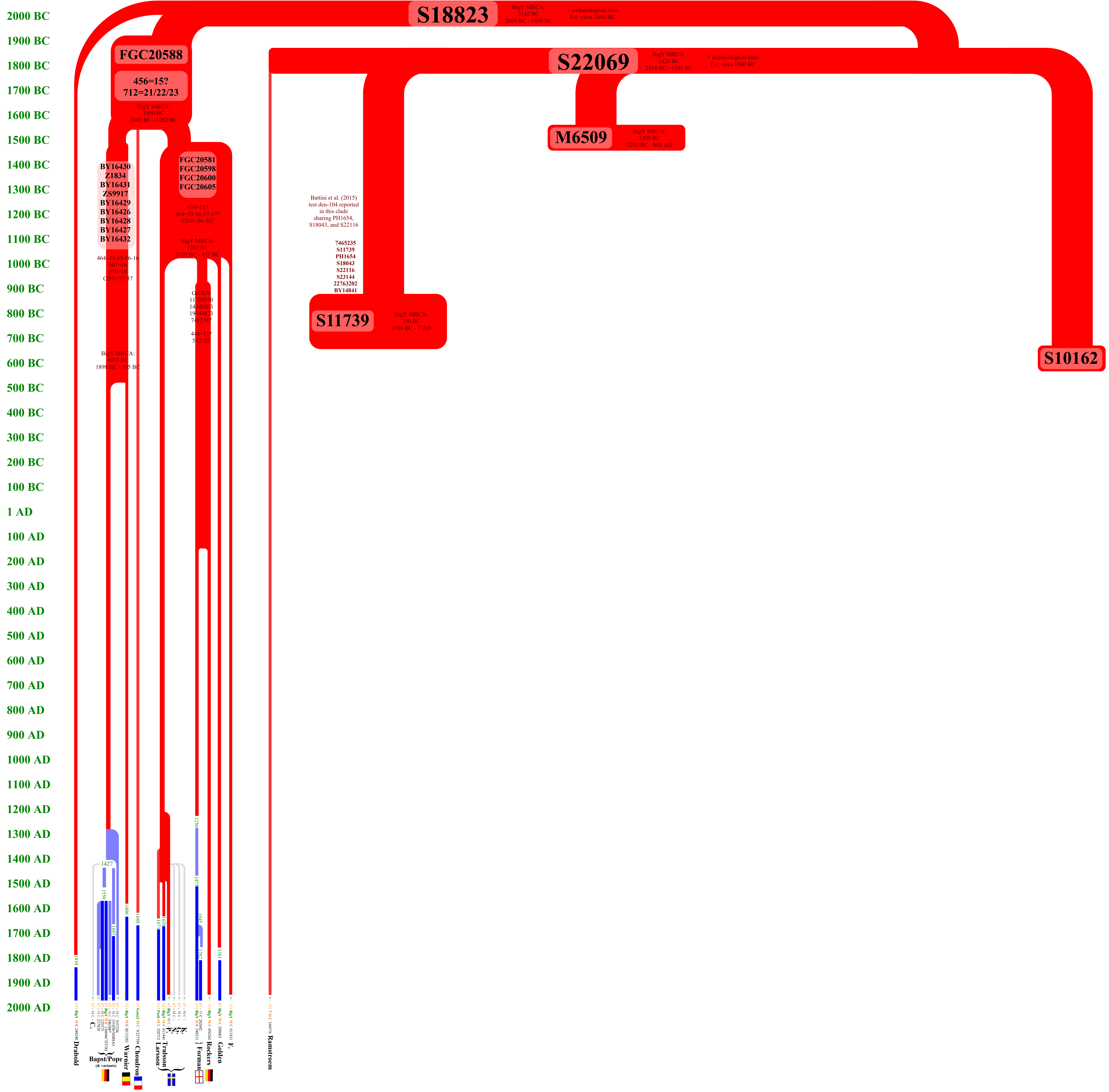
2000 BC
1900 BC
1800 BC
1700 BC
1600 BC
1500 BC
1400 BC
1300 BC
1200 BC
1100 BC
1000 BC
900 BC
800 BC
700 BC
600 BC
500 BC
400 BC
300 BC
200 BC
100 BC
1 AD
100 AD
200 AD
300 AD
400 AD
500 AD
600 AD
700 AD
800 AD
900 AD
1000 AD
1100 AD
1200 AD
1300 AD
1400 AD
1500 AD
1600 AD
1700 AD
1800 AD
1900 AD
2000 AD
S18823
FGC20588
456=15?
712=21/22/23
S22069
M6509
S11739
S10162
BY16430
Z1834
BY16431
ZS9917
BY16429
BY16426
BY16428
BY16427
BY16432
FGC20581
FGC20598
FGC20600
FGC20605
Battini et al. (2015) test den-104 reported in this clade sharing PH1654, S18043, and S22116
7465235
S11739
PH1654
S18043
S22116
S23144
22763202
BY14841
Drabold
Bapst/Pope
Warnier
Choudron
Larsson
Trulsson
Forman
Rockers
Golden
F.
Ramstroem

Phylogeny of R-DF98>S18823

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- *Paper trail connection known*

Phylogeny of R-DF98>S18823>S8350

S18823

BigY MRCA:
2467 BC
3065 BC - 1913 BC

+ archaeological data:
Est: circa 2300 BC

2000 BC
1900 BC
1800 BC
1700 BC
1600 BC
1500 BC
1400 BC
1300 BC
1200 BC
1100 BC
1000 BC
900 BC
800 BC
700 BC
600 BC
500 BC
400 BC
300 BC
200 BC
100 BC
1 AD
100 AD
200 AD
300 AD
400 AD
500 AD
600 AD
700 AD
800 AD
900 AD
1000 AD
1100 AD
1200 AD
1300 AD
1400 AD
1500 AD
1600 AD
1700 AD
1800 AD
1900 AD
2000 AD

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Predicted structure from STRs
U106+
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SNP/panel test within DF98
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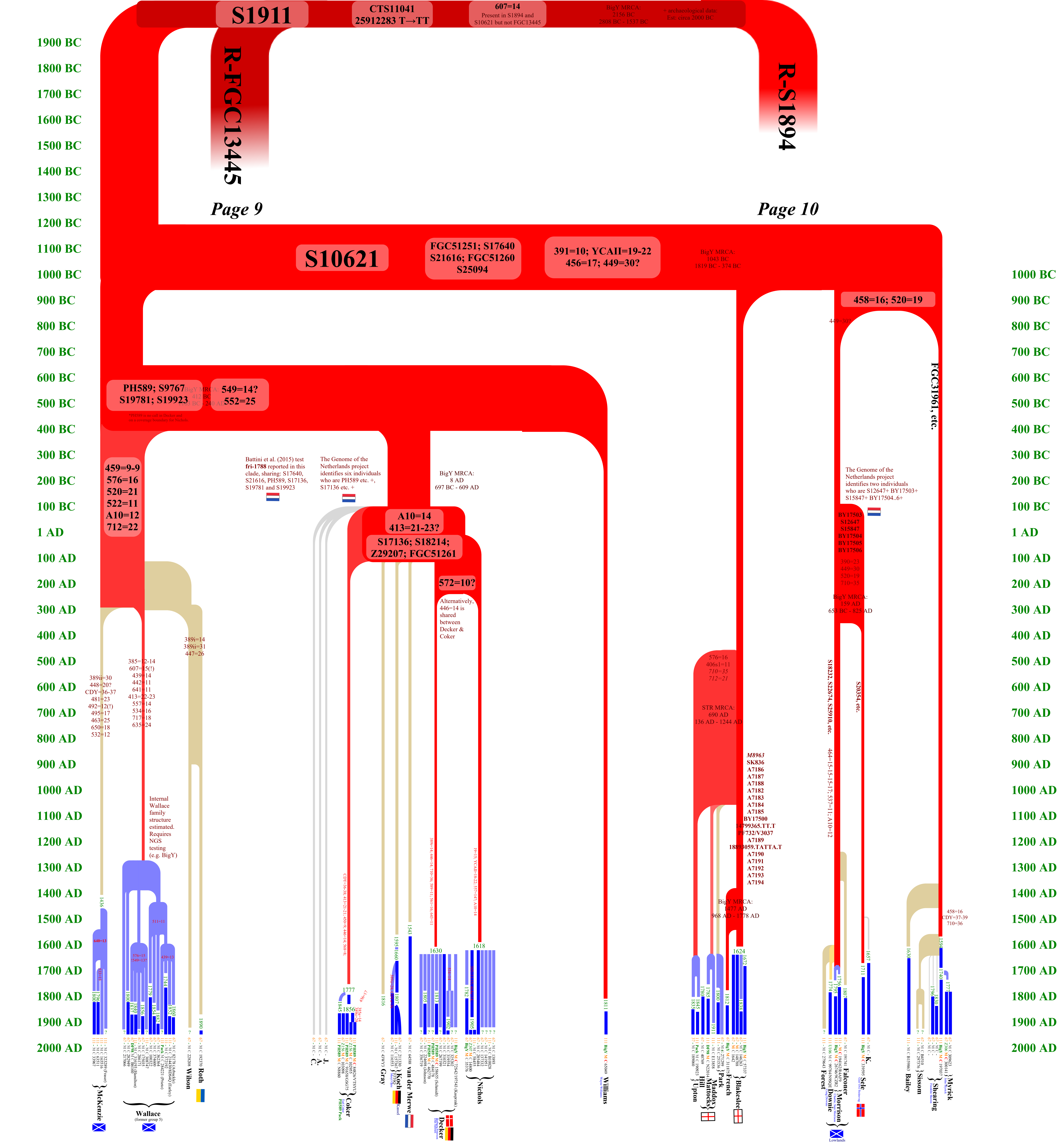
Surname/geographical and Y-STR link*
Surname, Y-STR and autosomal link
Paper trail connection suspected
Paper trail connection known

Treece: no European origin known. Tested DF98+ in addition to BigY.
Pitman: no European origin known. Capt. Thomas Pittman's daughter married Joseph Wall.
Wall: large family with few European connections and an MRCA indicating a common ancestor in American colonial times. Includes a Wall claiming descent from Evan Wall (b. 1379) of Preston Hall in Lancaster and a Weyland from Stuttgart.
Starr: no information.
Todd: no information.
Smith: no European origin known, but Ireland hypothesised. Novel mutation CTS7550+. Personal Genomes Project tested, helped identify DF98. Negative for downstream SNPs S1911, S18823 and L127. Forms unique branch of DF98.
Sudasch: link to Austria, north of Vienna.
Robertson: in Robson group 2, with 37-marker match to 169566. No further information given.
Watson: R1b1 family A. 109510 shown to be U106+ L48-. Several 37-marker matches. Possible descendants of Lord Jonathan Watson (1702, England - 1759), but needs confirmation from family.
Endres: family from Ollmuth in Germany, east of Luxembourg. Results no longer available.
Quintero: family from Tenerife, no further information given.
LeCapitaine: a noble family from Grez-Doiceau, south-east of Brussels, in Walloon.
Harp: no European origin known. FGC Long-Read pilot test underway.
Reeve: traces to a Thomas Reeve (1611), origin identified as England by Y-37 match to #41599 (Reeves DNA project group #05). False positive match to Bird group R1b IV, which is R-DF27.
Agee: origin unknown (STR source: Terry DNA project).

Phylogeny of R-DF98>S1911>S10621



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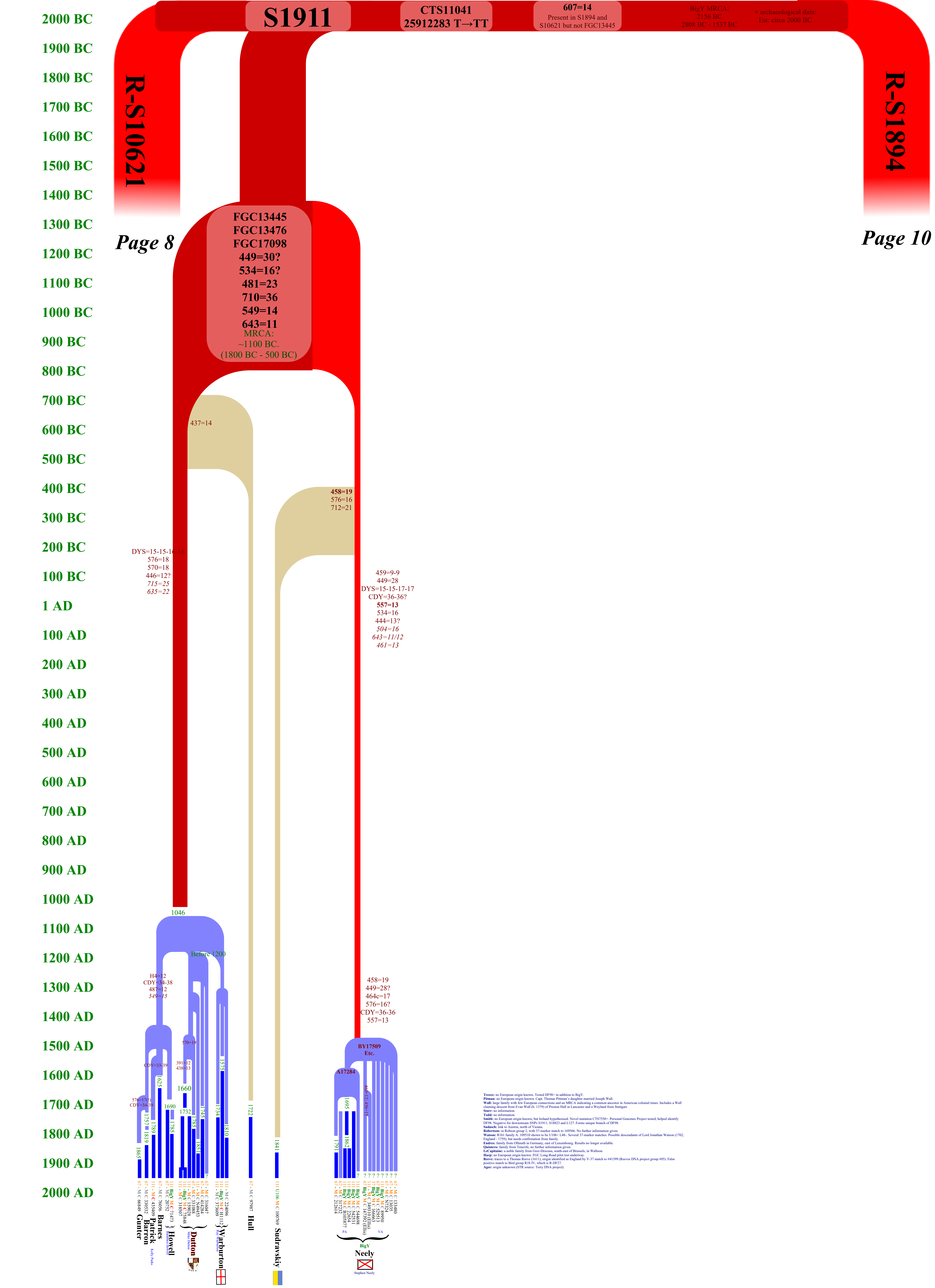
Phylogeny of R-DF98>S1911>FGC13445



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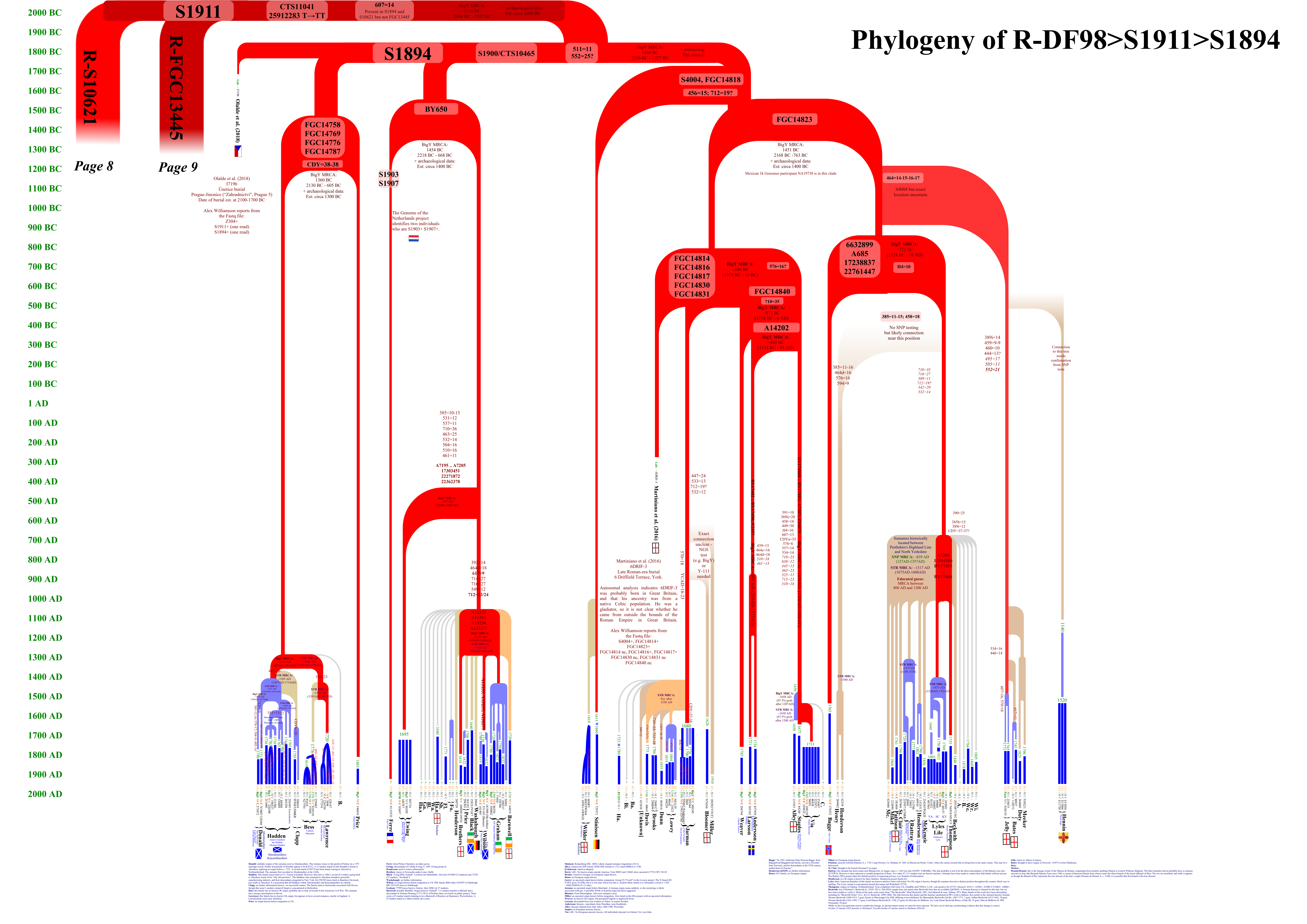
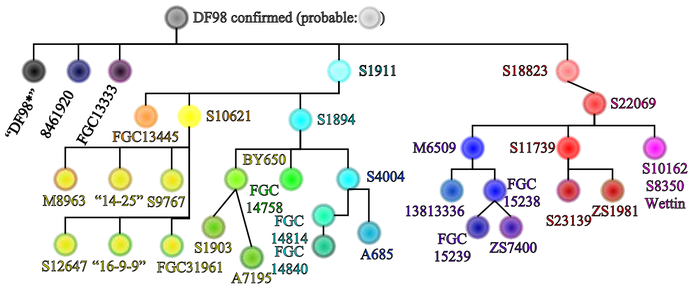
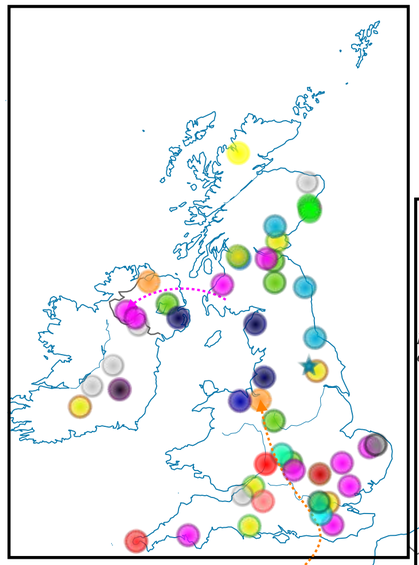
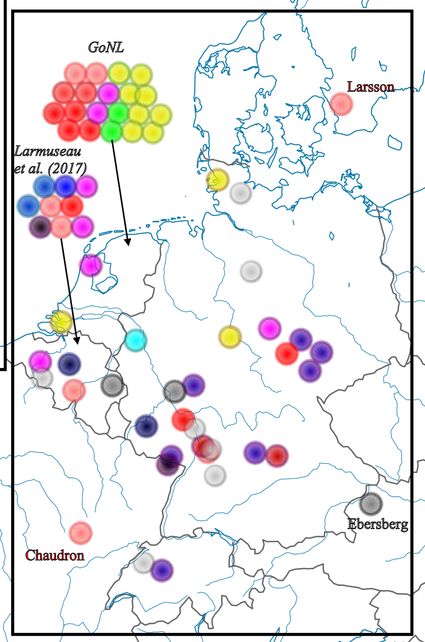


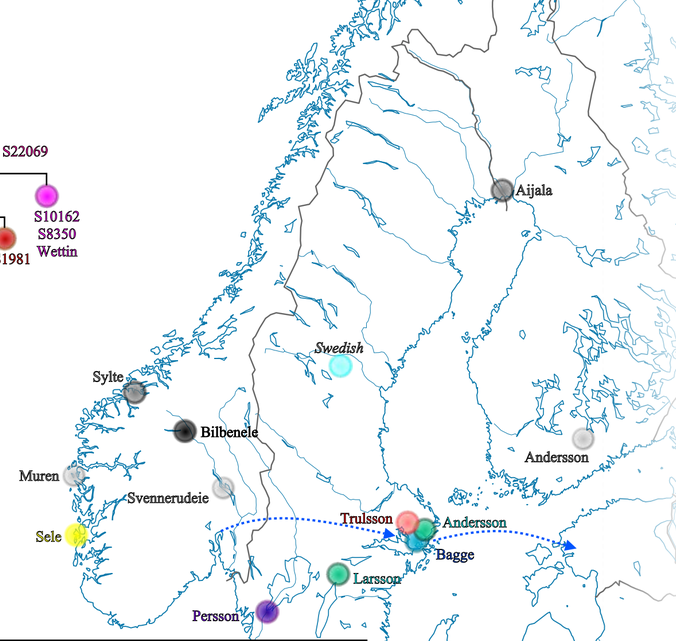
Phylogeny of R-DF98>S1911>S1894
2000 BC
1900 BC
1800 BC
1700 BC
1600 BC
1500 BC
1400 BC
1300 BC
1200 BC
1100 BC
1000 BC
900 BC
800 BC
700 BC
600 BC
500 BC
400 BC
300 BC
200 BC
100 BC
1 AD
100 AD
200 AD
300 AD
400 AD
500 AD
600 AD
700 AD
800 AD
900 AD
1000 AD
1100 AD
1200 AD
1300 AD
1400 AD
1500 AD
1600 AD
1700 AD
1800 AD
1900 AD
2000 AD
S1911
CTS11041
25912283 T→TT
607=14
Present in S1894 and S10621 but not FGC13445
R-S10621
R-FGC13445
Page 8
Page 9
S1894
S1900/CTS10465
511=11
552=25?
S4004, FGC14818
456=15; 712=19?
Olalde et al. (2018)
Olalde et al. (2018)
I7196
Únetice burial
Prague-Jinonice ("Zahradnictví", Prague 5)
Date of burial est. at 2100-1700 BC
Alex Williamson reports from the Fastq file:
Z304+
S1911+ (one read)
S1894+ (one read)
FGC14758
FGC14769
FGC14776
FGC14787
CDY=38-38
BigY MRCA:
1360 BC
2130 BC - 605 BC
+ archaeological data:
Est: circa 1300 BC
BY650
BigY MRCA:
1454 BC
2218 BC - 668 BC
+ archaeological data:
Est: circa 1400 BC
S1903
S1907
The Genome of the Netherlands project identifies two individuals who are S1903+ S1907+.
FGC14823
BigY MRCA:
1451 BC
2168 BC -763 BC
+ archaeological data:
Est: circa 1400 BC
Mexican 1k Genomes participant NA19738 is in this clade
464=14-15-16-17
S4004 but exact location uncertain
FGC14814
FGC14816
FGC14817
FGC14830
FGC14831
FGC14840
710=35
A14202
6632899
A685
17238837
22761447
H4=10
385=11-15; 458=18
No SNP testing but likely connection near this position
Connection to this tree needs confirmation from SNP tests
Martiniano et al. (2016)
Martiniano et al. (2016)
6DRIF-3
Late Roman-era burial
6 Driffield Terrace, York.
Autosomal analysis indicates 6DRIF-3 was probably born in Great Britain, and that his ancestry was from a native Celtic population. He was a gladiator, so it is not clear whether he came from outside the bounds of the Roman Empire in Great Britain.
Alex Williamson reports from the Fastq file:
S4004+, FGC14814+
FGC14823+
FGC14814 nc, FGC14816+, FGC14817+
FGC14830 nc, FGC14831 nc
FGC14840 nc
Exact connection unclear - NGS test (e.g. BigY) or Y-111 needed
Surnames historically located between Perthshire's Highland Line and North Yorkshire
Educated guess: MRCA between 800 AD and 1300 AD
Donald
Hadden
Clapp
Bess
Lawrence
Price
Ferre
Ewing
Henderson
Price
Graham
Barnwell
Wilder
Stinissen
Davis
Brooks
Dunn
Lowry
Jarman
Miller
Bloomer
Weaver
Andersson
Larsson
Staples
Alley
Bagge
Henry
Henderson
Rattray
McKenzie
Lyles
Lile
Beckwith
Thompson
Jelly
Bates
Meeker
Hennin

Geographical Distribution









DESCRIPTION

Displayed on this map are the testers with known European origins. In some cases, these are not known at a country or regional level, where they are shown bracketted without bold font. Where more-detailed information is known, or can be surmised from testers with (near-)identical DNA tests, these are marked with symbols. The colour of the surname and symbol corresponds to the SNP-tested levels on the phylogenic tree.

BIASES

The distribution of cluster members is strongly affected by testing biases. A much larger fraction of the ancestral British population have tested than elsewhere in Europe, due to large uptake in former British colonies like the USA. Similarly, relatively few people from France and from Eastern Europe have tested compared to the size of their populations. We must bear these biases in mind when inferring anything from these distributions.

DISTRIBUTION

Despite these biases, two main population groups are visible in the data. The first is a British group, where S1894 dominates. Many Irish families were planted there during the early 17th century. Indeed, several families have documentary evidence of this plantation.

The second major group is German in origin, and includes the House of Wettin itself. This group is concentrated on the Rhine valley between Frankfurt and the Swiss border, but extends north into central Germany. We identify the Worms-Mainz-Heidelburg area as a tentative origin, but lack sufficient SNP testing of the German lines to confirm this. There is a strong S18823 presence here, particularly S18823 > S22069 > M6509 presence here.

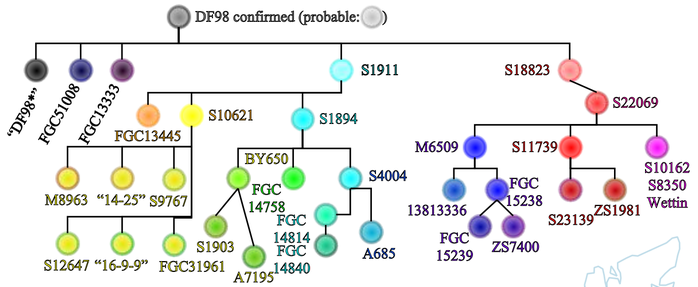
A mixture of unusual lineages also appears in Scandinavia, which may represent ancient migrations (e.g. FGC13333) or recent movements (e.g S4004).

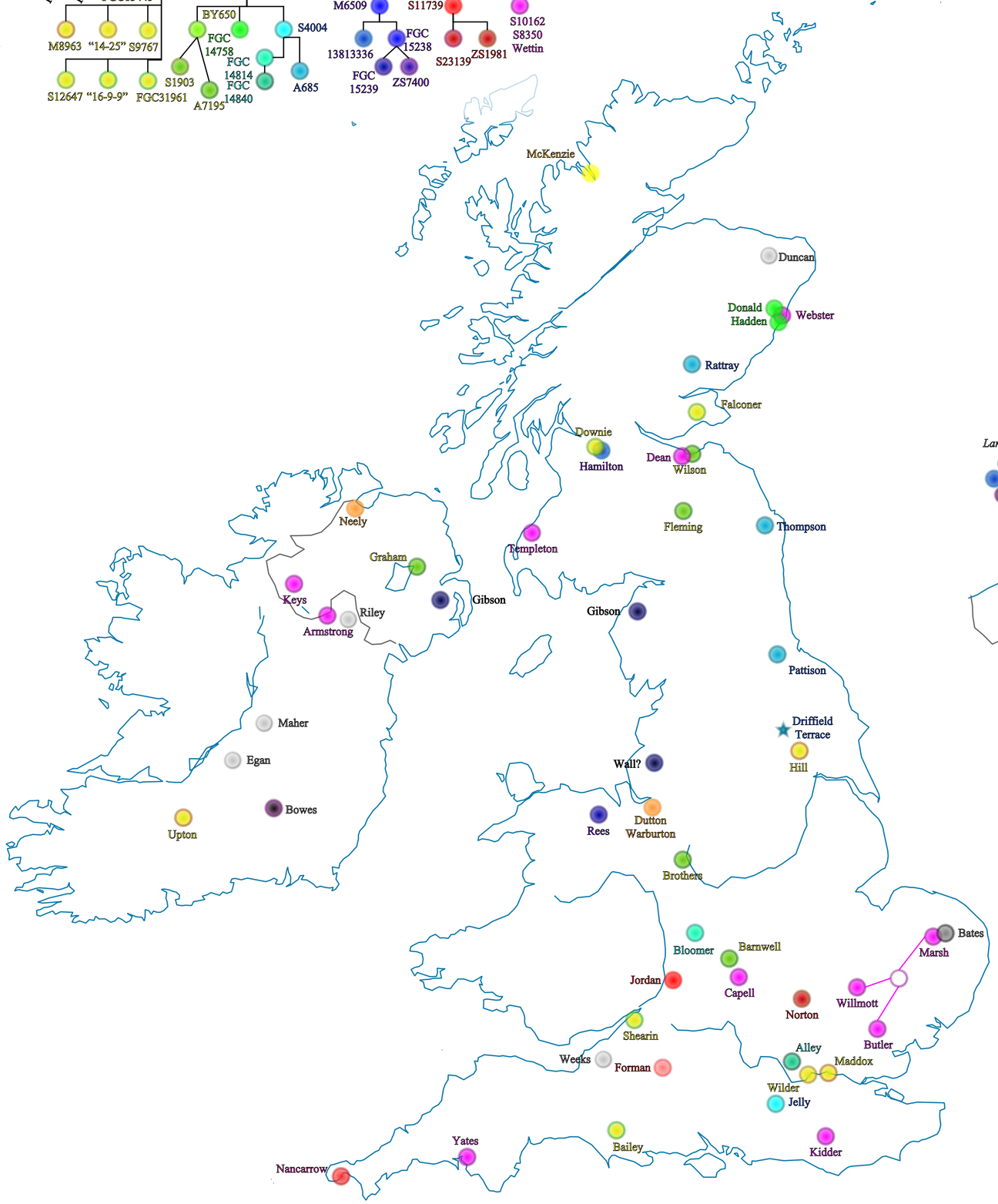
TRIBAL ORIGINS

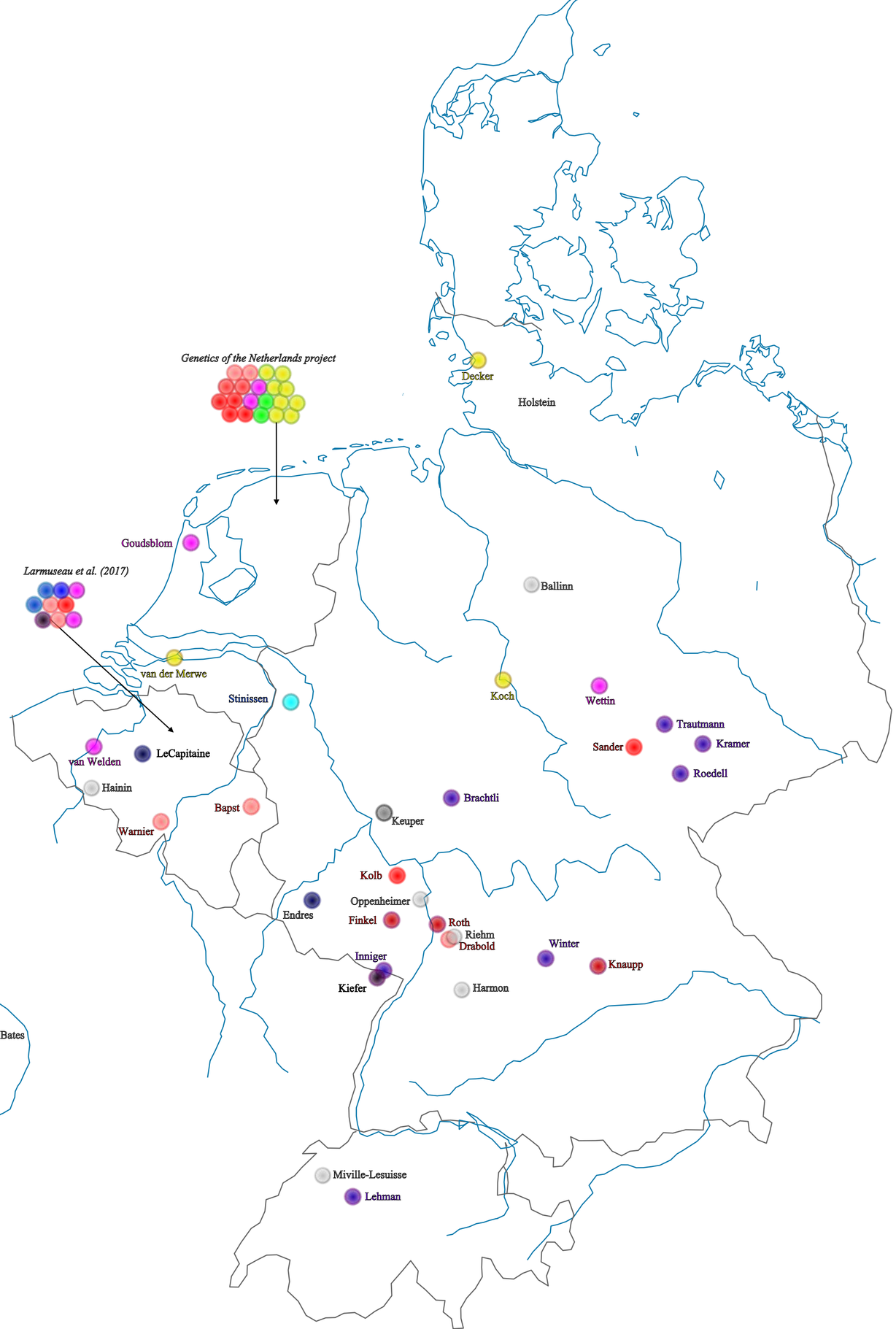
Determining an origin for a population such as this requires accurate knowledge of the foundation of that population, which we do not have. Our best estimate for the foundation of our cluster lies around 2300 BC: the uncertainty in such estimates depends most strongly on the small number of SNPs which we count to derive this age, giving an uncertainty of +/- about 400 years to the age of DF98. The SNP chain we investigate runs as follows: M269 > L51 > L23 > L11 > P311 > U106 > Z381 > Z156 > Z306 > Z304 > DF98.

The third millenium BC was a time of considerable change in Europe. P311 is now generally thought to have arrived in from the western former Soviet Union (possibly the Ukraine or western Russia), around 3000 BC. Ancient DNA evidence shows no substantial U106 populations in western Europe around 2300 BC, suggesting its origin in north-central Europe. DF98 is contemporary with the Unetice culture, although we cannot authoritatively state that it arose within it. Other places of origin are still quite possible, and further results (particularly archaeological DNA) should be able to provide us with further answers in the future.

Arrival of DF98 to western Europe and the British Isles was probably significantly later, perhaps with the Tumulus culture of the late second millennium BC. Given the prevalence of British clusters of tests with convergence ages around 1000 years ago, there seems to be a significant Norman contingent to the DF98 tests of the British Isles.


DF98 confirmed (probable:)
"DF98*"
FGC51008
FGC13333
S1911
S18823
S10621
S1894
S22069
FGC13445
BY650
M6509
S11739
S10162
S8350
Wettin
M8963
"14-25"
S9767
FGC 14758
S4004
FGC 15238
13813336
S23139
ZS1981
FGC 14814
S1903
FGC 14840
A685
FGC 15239
ZS7400
S12647
"16-9-9"
FGC31961
A7195


McKenzie
Duncan
Donald
Hadden
Webster
Rattray
Falconer
Downie
Hamilton
Dean
Wilson
Fleming
Thompson
Templeton
Neely
Graham
Keys
Armstrong
Riley
Gibson
Gibson
Pattison
Driffield
Terrace
Hill
Maher
Egan
Bowes
Upton
Wall?
Rees
Dutton
Warburton
Brothers
Bloomer
Barnwell
Capell
Jordan
Bates
Marsh
Willmott
Norton
Butler
Shearin
Alley
Maddox
Weeks
Forman
Wilder
Jelly
Bailey
Kidder
Yates
Nancarrow


Genetics of the Netherlands project
Decker
Holstein
Goudsblom
Larmuseau et al. (2017)
Ballinn
van der Merwe
Koch
Wettin
Trautmann
Sander
Kramer
Roedell
Stinissen
van Welden
LeCapitaine
Hainin
Brachtli
Bapst
Keuper
Warnier
Kolb
Oppenheimer
Endres
Finkel
Roth
Riehm
Drabold
Winter
Knaupp
Inniger
Kiefer
Harmon
Miville-Lesuisse
Lehman