The Pre-History of the House of Wettin
Identification through DNA of the “Kings’ Cluster”

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(1) INTRODUCTION

This deep phylogenetic 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 U106. It shows how U106, which now represents many tens of millions of men worldwide, branched off from the rest of the Y-chromosome at different points in prehistory.

(2) OUT OF AFICA

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, it 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... etc. Recent estimates of his age vary widely from 120,000 to 330,000 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 70,000 years ago, while 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 fanned out mankind expanded throughout the world. 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 analyzed 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 archeological remains of Mal’ta Boy, who was buried 24,000 years ago in Siberia. By this time, our ancestors had probably expanded across much of north-west Asia, where they existed as hunter-gatherers.

(3) EXPANSION INTO EUROPE

Within haplogroup R, most people are part of R1, descended from an individual living 24,000 to 34,000 years ago. The majority of western Europe is descended from the R1 founder. Within R1, there is a bifurcation into two groups: R1a, or M420, and R1b, or M343. R1a is strongest in 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 Europe can probably be tied to the sudden growth in the number of men worldwide, branched off from the rest of the human Y-chromosome tree at different points in prehistory.

(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 P312 branch is generally found more on Europe’s Atlantic Coast, while the U106 branch is divided along its male lines. This is a rapidly-evolving field, thus the information is subject to considerable change over time.

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 page at right). The date of this man’s birth is likely to be during the European Bronze Age, and the possible range of dates correspond to a series of archaeological horizons spreading eastwards over Europe at the same time.

Within P311, U106 represents about 1/8th of Europe, or 110 million men worldwide. We estimate its age to be between 2500 and 46000 years old. We trace what is known about the migrations from Asia to Europe on the next page.

Deep ancestry of U106

Acknowledgements

The information in this tree comes from a variety of sources, but I am most grateful to the International Society of Genetic Genealogy (ISOGG) for maintaining the underlying tree structure displayed here. The anthology of haplogroup statistics on repuda.com has also been instrumental in creating these data.

How to read this chart

This chart shows how the male-line genetic (phylogenetic) 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 95.5% confidence intervals, what we call “2-sigma”. We are 95.5% sure that the real dates lie between these two boundaries. By dividing the uncertainty in half, we can recover the 68.3% confidence interval, or “1-sigma” range. Dates are rounded to the nearest 50 years. For example, we are 95.5% sure that the U106 founder lived between 3068 BC and 1952 BC. We are 68.3% sure that he lived between 2774 and 2216 BC.

This date was calculated using SNP-counting methods which are detailed in the accompanying U106 document.

Haplogroup Frequencies in Europe

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.

<table>
<thead>
<tr>
<th>COUNTRY POPLN.</th>
<th>%R1b-M343</th>
<th>%U106</th>
<th>R1b &amp; U106 POPLN.</th>
</tr>
</thead>
<tbody>
<tr>
<td>British Isles</td>
<td>80.0%</td>
<td>6.0%</td>
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<tr>
<td>Scotland</td>
<td>72.5%</td>
<td>12.5%</td>
<td>3682075</td>
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<td>England</td>
<td>57.0%</td>
<td>20.0%</td>
<td>30217099</td>
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<tr>
<td>Wales</td>
<td>81.3%</td>
<td>9.5%</td>
<td>2557985</td>
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<tr>
<td>Total</td>
<td>6783642</td>
<td>62.0%</td>
<td>4780765</td>
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<tr>
<td>Italy</td>
<td>4715880</td>
<td>42.8%</td>
<td>19803336</td>
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<td>5940477</td>
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<td>Denmark</td>
<td>5586854</td>
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<td>54.0%</td>
<td>9041268</td>
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<tr>
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<td>59.9%</td>
<td>6666189</td>
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<td>France</td>
<td>6546000</td>
<td>52.7%</td>
<td>34019200</td>
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<tr>
<td>Germany</td>
<td>8175760</td>
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<td>37.0%</td>
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<td>2271952</td>
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<td>Eastern Europe</td>
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<td>20.0%</td>
<td>1995800</td>
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<td>2871369</td>
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<td>23.5%</td>
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<td>10.9%</td>
<td>2413000</td>
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<tr>
<td>Turkey</td>
<td>7666784</td>
<td>14.0%</td>
<td>10735300</td>
</tr>
<tr>
<td>Total</td>
<td>10414499</td>
<td>15.0%</td>
<td>10735300</td>
</tr>
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</table>

European Colonies (estimated)

| United States    | 230000000  | 46.0% | 105800000       |
| China            | 20000000   | 46.0% | 90000000        |
| Russia           | 10000000   | 46.0% | 10000000        |
| Canada           | 8000000    | 46.0% | 5000000         |
| Total            | 101480000  | 46.0% | 101480000       |

Total 1041 million N/A N/A 385 million 110 million
Archaeological M269 remains in modern Russia.

Piers Ollier

Kings of Judah: 3 Amos — 1 Kings

Central and Western Europe

Portugal: First Bell Beaker culture

Romania: Iron/Carpathian-Tripolye culture

First archaeological M269 remains in western Europe.

**U106 family tree**

*Updated: 10 Mar 2018, Dr. Ian McDonald for the U106/S21 group*

**DESCRIPTION**

This phylogenetic tree of U106 shows the relationships between the 602 U106 and U2 testers with Family Tree DNA Y-DNA High results as of 26 Feb 2016, plus additional data from the U106 project curators of John Broom, along with the SNP names that define these relationships. Each tester is represented by a vertical line. Family groups related after 1520 AD are grouped into one line and labeled. Convergence dates have been read from the horizontal lines 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 lost related. It does not necessarily indicate when that SNP formed.

**Rome**

1. SV320
2. A612
3. Z8
4. Z343
5. Z344
6. Z37885
7. Z37884
8. 5156
9. ZP134
10. S500
11. ZP91
12. Z372
13. S8350
14. S5695
15. S5741/Z375
16. Z8191
17. BY650
18. ZP108
19. ZP136
SNP-based phylogeny of the Y-DNA R-DF98 "Kings’ Cluster"

This SNP tree is used as a basis for the STR tree structure shown on these pages
Tests that cannot yet be grouped are listed on page 9
Most-recent common ancestor for Kings' Cluster
Best estimate around 1350 BC.
95% confidence interval: 2000 - 1150BC

Phylogenic family tree of DF98: overview and minor branches

S1911
Most-recent common ancestor for S1911
Best estimate around 1350 BC.
95% confidence interval: 1750 - 950BC

See page 6

S18823
Most-recent common ancestor for S18823
Best estimate around 1350 BC.
95% confidence interval: 1750 - 900BC

See page 7

S8350
The House of Wettin
See page 8
Minor clades

See page 5

Kings' Cluster

See page 6

S18823

Most-recent common ancestor for S18823
Best estimate around 1450 BC.
95% confidence interval: 1850 - 1000 BC

S22069

House of Wettin (S8350++)

Most-recent common ancestor for S22069
Best estimate around 1250 BC.
95% confidence interval: 1700 - 850 BC.

S8350

The House of Wettin

in historical times

See page 8
R-DF98 members not placeable in the R-DF98 phylogeny

Substructure within DF98 that has been confirmed by SNPs is shown on the previous pages

**Substructure within DF98 that has been confirmed by SNPs**

- Using differences in the Y-chromosome of people matching this group, we have inferred their family tree at the time they last shared a historically shared branch point. The dates given here are very approximate, but include reasonable estimates for all elements of time.
- The clusters that have a long timeline (i.e., over 1000 years) are thought to reference the geographical features at the time of their origin. Also included are the dates of when DNA markers were shared between two branches before the most recent common ancestor (MRCA).
- Differences in the Y-chromosome between two branches is therefore often usual, less than the range of dates before.
- These clusters are presented with "confidence intervals" e.g., the date for the 95% confidence interval, based on the data we have.
- The last name in each circle/driver tree is the most recent branch point that has been shared.
- The acronym "DF98" refers to a group of Y-DNA SNPs that have been shared by multiple families.

**Kings' Cluster**

- **DF98**
- **Y-DNA test**
- **confirmed or very probable DF98**
- **Unconfirmed additional members and groups**
- **tstDF98 or individual SNPs at Ysq, or Chroma2 BigV/FGC**

**confirmed or very probable DF98**

- **but (deeper SNP tests needed: Ysq, Chroma, BigV or FGC**

**Unconfirmed additional members and groups**

- **tstDF98** or individual SNPs at Ysq, or Chroma2 BigV/FGC

**Confirmed or very probable DF98**

- **but (deeper SNP tests needed: Ysq, Chroma, BigV or FGC**

**Substructure within DF98 that has been confirmed by SNPs**

- **is shown on the previous pages**

**Substructure within DF98 that has been confirmed by SNPs**

- **is shown on the previous pages**
TRIBAL ORIGINS

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-Heidelberg area as a tentative origin, but lack sufficient SNP testing of the German lines to confirm this. There is a strong S18823 > S22069 > M6509 presence here. Surprisingly the Wettin family is the Wettin group’s sole representative outside of Britain, raising the unlikely but plausible possibility that this family could have come from a British lineage.

Geographical Distribution

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, which may bifurcate into a northern and southern group. We presume that the Irish members are mostly families 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-Heidelberg area as a tentative origin, but lack sufficient SNP testing of the German lines to confirm this. There is a strong S18823 > S22069 > M6509 presence here. Surprisingly the Wettin family is the Wettin group’s sole representative outside of Britain, raising the unlikely but plausible possibility that this family could have come from a British lineage.

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 1500 BC: the uncertainty in such estimates depends most strongly on the rate of SNP formation, which is roughly once every 120 to 145 years, giving an uncertainty of ~400 years of 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 millennium BC was a time of considerable change in Europe. M269, now generally thought to have arrived in from the Black Sea area, around 3000 BC, possibly via the river Danube. DF98 congregates around the headwaters of the Danube, where it meets the headwaters of the Rhine. It is thought our ancestors spread from here to the Rhine delta, then across to Britain, where they probably first arrived around 1500 BC. Successive waves of migration have brought DF98 to the British Isles since then. Given the prevalence of 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.

This evidence is suggestive of DF98 with being formed and transmitted during the expansion and migration of the Tumulus Culture throughout Western Europe during the later part of the second millennium BC. However, other places of origin are still quite possible. While more-accurate dating (and ultimately archeological DNA) would give us a clearer picture, this currently appears to be a serious contender for our origins.

Underlying image: The London Geographical Institute’s “The People’s Atlas”, 1920
Scan courtesy of hpkiss.org