

# DNA Results Commentary

The Warburton DNA project is hosted by Family Tree DNA and they provide access to the project's results. This document is both a guide to the results on the Family Tree DNA website, and an additional commentary to those results.

As of April 2016 I have over 40 Warburton DNA Results. The first 23 results were from DNA Heritage, but they ceased operations in April 2011 and the project is now hosted by Family Tree DNA. DNA Heritage results and project members were transferred to Family Tree DNA.

The Family Tree DNA test only includes 37 markers, whereas the DNA Heritage test included 43 markers. Only 32 markers are common to both tests. I believe that in most cases this will be sufficient to determine matches between individuals who took the different tests.

Family Tree DNA sets up a myFTDNA webpage for each DNA participant. You can log in to this webpage at <https://www.familytreedna.com/login.aspx> using your kit number, and a password that is provided by Family Tree DNA when you joined the project. I set up passwords for those transferring from DNA Heritage.

On the myFTDNA webpage you are able to see your results and matches, manage your personal information, order new tests, and join projects. As Project Administrator I can access your myFTDNA webpage but I can only make limited changes. The one thing I do ensure is that the name and location of your easiest known ancestor is recorded so that it appears in the project results.

The personal information section of the webpage lets you specify the level of new matches that will be notified by email to both the participant, and to the Project Administrator. As I cannot influence these settings I would recommend you opt to receive email notification and show contact information for Y-DNA37 matches only (Y-DNA25 matches if you tested at DNA Heritage). This will reduce many meaningless notifications.

You can also indicate whether your DNA results can be public, or only viewed by project members. I would recommend this is set to public, but some are set to 'project members only', and I suspect this may now be the default.

Family Tree DNA also provide a Warburton DNA Project webpage which I maintain. It includes an introduction page, a table of results, a join page, and a link to donate to the General Fund. It can be accessed at <http://www.familytreedna.com/public/warburton/default.aspx> but only the results of members who have marked their results as public will be shown. To see all the results, find the list of your Projects on your myFTDNA webpage, and click on the Warburton project. This will take you to the same Warburton Project webpage but now the results will include all project members.

## Definitions

The following definitions are provided to help understanding of this commentary:

1. Y-chromosome: A part of the human genome that is only present in males. The human genome consists of 23 pairs of chromosomes. One of these pairs consists of two X-chromosomes in females, and one X-chromosome and one Y-chromosome in males. It is passed unchanged from father to son, except for occasional copying errors.
2. Mutation: This is a copying error. There are two types of mutation of interest:
  - 2.1. Short Tandem Repeat (STR): A change in the number of times a small piece of DNA is repeated at a specific location. The location has a name (e.g. DYS390) and is sometimes called a marker. DNA tests can be defined by the number of markers tested (e.g. Y-DNA37 is a 37 marker test).
  - 2.2. Single Nucleotide Polymorphism (SNP). This is change in a single DNA molecule. DNA is a string of (millions of) molecules. There are four types of molecule, designated by a letter (A, C, G, T). A SNP occurs when the type of molecule changes. SNPs are originally identified by their location, but significant ones are given names (e.g. M269, U106, S6881, FGC13477).

## Commentary on Results

3. Haplogroup: The group of people who share a specific mutation, usually a SNP. The mutation can be referred to as a haplotype. The word population has been divided into a small number of basic haplogroups defined by a letter (e.g. R, G, I, J). Originally these haplogroups were subdivided using a string of numbers and letters (e.g. R1b), but more recently subdivisions are referred to by a defining SNP (e.g. R-M343 is equivalent to R1b).
4. Haplotree: This is a type of evolutionary tree known technically a Phylogenetic Tree, It is a tree that shows the evolution of the human Y-chromosome. Its branches are defined by the mutations that created them.
5. TMRC: Time to Most Recent Common Ancestor, calculated in generations (see **Mutations Table** on the Warburton Website) and converted into dates at 35 years per generation before 1945.
6. Non paternal event: This occurs when a son does not take the surname of his natural father, thus introducing a new DNA profile to the Warburton name. This could arise from illegitimacy, infidelity by a wife, adoption, e.g. by a step father, or in honour of an inheritance, as when the Egerton family became Egerton Warburton when they inherited Arley Hall.

## Project Evolution

There have been considerable developments in testing and interpretation of DNA results in the 10 years since the Warburton Project began.

As well as a value for the number of repeats for each marker in an STR test, the results include a predicted haplotype. The definition of this haplotype has changed over time. Now it is represented by a letter which signifies a high level haplotype, and the name of the most recent Single Nucleotide Polymorphism (SNP) to occur. For the majority of Warburton results this is R-M269. Beyond simply identifying matches that signify a recent common ancestor, there is an increasing emphasis on identifying a participant's most recent SNP. This SNP will occupy a specific position in a haplotree that has a developing historical narrative.

Perhaps the most significant development of the last 10 years has been a complete rethink of the historical narrative for haplogroup R, the most common haplogroup in Western Europe (see **Deep History** below). It was originally thought to have moved north from Iberia following the melting of the ice after the last Ice Age. Now it is believed it originated in Western Asia and migrated into Europe much later, within the last 5,000 years. Its rapid rise to become the most common haplotype in Western Europe is attributed to its horse based culture, and lactose tolerance, though much of this is still conjecture. Nevertheless the combination of DNA and archeological study is slowly piecing the story together.

The Warburton project is still based on the 37-marker Short Tandem Repeat (STR) test. A few participants have taken additional tests, including various Single Nucleotide Polymorphism (SNP) tests. There have also been a few 12-marker tests for specific purposes.

My view has evolved to believe a future Y-chromosome testing strategy depends on the desired objective, and there are three possible objectives for any future testing:

1. **To find matches with fellow Warburtons.** It must be recognised that, apart from aristocratic families, the lack of available records means only the fortunate will be able to trace their ancestors back as far as 1600 and many trails will end much later. DNA may be the only way to link families who share a common ancestor who is not present in the records, or who is present in the wrong place. A 37 marker STR test is still sufficient to determine if a match exists with other Warburton groups.
2. **To establish a position on the Haplotree.** There are several projects at Family Tree DNA devoted to particular parts of the haplotree e. g. the R-U106 project. As they extend the haplotree wider and deeper, an objective might be to establish one's position on that tree. It only takes one person in a traditional family tree to find his position in the tree and the answer applies to all the males in his tree who share his surname (assuming no non-paternal event has occurred). It also applies to those in other trees that have been associated by a DNA match. An STR test will produce a predicted haplotype, but this will be at a high level within the tree. However STR mutations are more frequent, and bi-directional, whereas SNPs are usually unique so a SNP test will give a more exact tree structure. So once an STR result has produced a predicted haplogroup it is possible to test a set of SNPs associated with that haplogroup. For example all but 9 of the Warburton tests so far predict a haplogroup of R-

## Commentary on Results

M269, which is a major subclade of R-M343. For \$99 a pack of SNPs within R-M343 can be tested at FamilyTree DNA. This will identify the area of the haplotree to which you belong and this can be further refined with specific SNP tests. This approach will also help anyone subject to a non-paternal event to identify their genetic ancestors. A match on a SNP that occurred in the last few hundred years would give a strong indication that might be verified by further genealogical research.

- To extend the Haplotree to lower levels.** The Haplotrees continue to be extended towards the present day. This involves identifying new SNPs. Tests like BigY look for new SNPs rather than just testing known ones. On average the SNPs uncovered by BigY occur every 130-140 years. Most people who have taken the BigY test have a number of SNPs unique to them. Some, but perhaps not all of these will be shared by their cousins within their own clan or group of matched clans. Haplotrees could eventually be extended to overlap genealogical trees. However, BigY tests are expensive, and the additional information from testing more cousins would diminish. Once a number of recent SNPs have been uncovered, cheaper tests can be developed to test just the unique SNPs to identify the structure of those SNPs within a clan or group.

## Deep History

The following description of the deep history of the human haplotree is taken from documents created by the R-U106 project at Family Tree DNA. The original documents, **U106 Explored**, and **The Pre-History of the House of Wettin** are available on this website. It also uses information from the [www.eupedia.com](http://www.eupedia.com) website, and some of my earlier investigations.

### Introduction

The deep haplotree 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.

### 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 vary widely from 120,000 to 380,000 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, when 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.

Haplogroup G descends from macro-haplogroup F, which is thought to represent the second major migration of *Homo sapiens* out of Africa, at least 60,000 years ago. Its main branch, macro-haplogroup IJK would become the ancestor of 80% of modern Eurasian people. Haplogroup G had a slow start, evolving in apparent isolation for tens of thousands of years, possibly in Southwest Asia, cut off from the wave of colonisation of Eurasia.

A little over 45,000 years ago, the precursor of haplogroup R split from haplogroups G and I. This point is defined by the recently analysed 45,000-year-old remains from western Siberia.

Haplogroup R, arose between 24,000 and 34,000 years ago. This is again limited by the archaeological remains of Mal'ta Boy, who was buried 24,000 years ago in Siberia. By this time haplogroup R and its precursors had probably expanded across much of north-west Asia, where they existed as hunter gatherers.

Within haplogroup R, most people are part of R1. Although he lived in Asia, the majority of western Europe is descended from him. Within R1, there is a bifurcation into two groups: R-M420, and R-M343. R-M343 is thought to have arisen less than 18,500 years ago.

## Commentary on Results

### Expansion into Europe

The original modern human population in Europe would appear to consist of haplogroups G and I. Nowadays haplogroup G is found all the way from Western Europe and Northwest Africa to Central Asia, India and East Africa, although everywhere at low frequencies. Most Europeans belong to the G-P15 subclade,

Haplogroup I is the oldest major haplogroup in Europe and in all probability the only one that originated there. It is thought to have arrived from the Middle East as haplogroup IJ sometime between 40,000 and 30,000 years ago, and developed into haplogroup I approximately 25,000 years ago. In Europe Haplogroup I splits into I-M253, and I-M438 which includes sub-clades M223 and P37.

The date of the expansion of sub-clades of Haplogroup R1 into Europe can probably be tied to the sudden growth in the number of branches below M269, which can be very roughly dated to around 4000 BC. The origin of this migration and its route into Europe are not well determined at present.

However, archaeological remains show that there were extremely few haplogroup R men in Europe before 2600 BC, when remains from both R-M420 and R-M343 are found in Corded Ware and Bell Beaker burials (respectively) in south-eastern Germany. R-M420 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.

In Europe R-M343 is very much dominated by M269. Apart from some minor branches, most M269 men also have the P311 SNP. P311 then splits into a larger P312 branch and the smaller U106 branch. Two large groups accounting for nearly half of all Warburton results, are the Cheshire Group and the Lancashire group. These are both U106. The other Warburton haplogroup R results have yet to be determined below M269.

The P312 branch is generally found more on Europe's Atlantic Coast, while the U106 branch is generally found more in Europe's heartland. This has led to P312 being referred to synonymously with "Celtic" peoples while U106 is "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. 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 4600 years old. See **U106 Explored**, and **The Pre-History of the House of Wettin** on the Warburton Website for more detail on the latest on the development of the U106 haplogroup.

### Warburton Haplotypes

Over 75% of Warburton results are haplogroup R, and they are all M269. M269 alone makes up over half the population in Western Europe. It includes 40-70% of the population of continental Western Europe rising to 81% in the Basque country, 85% in Ireland, and over 90% in parts of Wales.

The Western Atlantic Modal haplotype is a term given to the most common alleles (values) for the R-M269 haplogroup for the 12 markers included in the Family Tree DNA Y-DNA12 STR test (also referred to as Panel 1).

About 25% of R-M269 in Europe are R-U106 which is most common in the Netherlands and Northern Germany. It probably originated in Austria around 2500-3250 BC. Both the Cheshire and Lancashire Groups are R-U106.

R-DF98 is a recently discovered SNP that occurred between 1500 BC and 1900 BC. DF98 is the defining mutation for The King's Cluster, a sub-section of the R-U106 project which includes the Cheshire Group

There are 5 Warburton results from haplogroup I, including three from I-M253 and one each from I-M223 and I-P37.

## Commentary on Results

I-M253 is associated most strongly with Finland and Scandinavia. It probably originated 4-5,000 years ago and initially dispersed from Denmark. Research by Ken Nordtvedt into STR patterns linked the Warburton results to a subgroup that originates in Denmark or North Germany and therefore was probably introduced into Britain by the Anglo-Saxons.

I-M223 has a predominantly British subclade, another predominantly Germanic subclade, plus others scattered across Europe. STR predictors and comparisons suggested an origin for the Warburton result in the Netherlands, northwest Germany, or Denmark. This covers the sources of both the Saxon and Danish Viking invasions.

I-P37s by far the largest branch of I-M438 and the one most strongly linked to Neolithic cultures in south-east, south-west and north-west Europe. STR comparisons for the Warburton result link it to a subclade found mainly in north-western Germany, but there are appreciable numbers in the British Isles.

There is one Warburton from haplogroup G who has tested as G-P303.

There are 3 related Warburtons from haplogroup J, with a predicted haplotype of J-M172. This is the most predominant sub-group of the J haplotype in Europe. It is believed to have originated in the Middle East between 15,000 and 22,000 years ago.

It is associated with the Neolithic expansion into Europe from the Fertile Crescent. This began about 10,000 years ago but reached Britain only about 6,000 years ago. It followed a route along the Mediterranean, around Spain and to the British Isles where it is most common in Southern England and Central Scotland.

## The Warburton Profiles

So far the results have uncovered groups of matching profiles, and several unmatched results. Unmatched results cannot share a common male line ancestor with any of the other current participants though they may be matched in the future. Two previously unmatched results have been matched in recent months.

The groups of clans linked by matching profiles are described below.

### The Cheshire and Lancashire Groups

The Cheshire and Lancashire Groups cover nearly half of the tests conducted so far. Both are covered in detail in separate documents called **The Cheshire Group** and **The Lancashire Group** on the Warburton Website. However both groups fall within the R-U106 haplogroup and share a common ancestry up to around 2660 BC. The main SNPs associated with the Cheshire and Lancashire Groups are shown in the table on the next page. These dates are still subject to change so the latest version can be seen in **Lancashire and Cheshire Groups SNP Ages** on the Warburton Website.

### The Warburtons of Garryhinch

Three results are from The Warburtons of Garryhinch. This clan consists of the descendants of three brothers who were present in Ireland in the second half of the 17th century. The results come from descendants of two of the three brothers, so their common ancestor is 9 generations back. The first two results show 3 mismatches over 43 markers (if a 2-step mutation is assumed in marker DYS464). The chances of 3 mismatches in so few generations is only 12%, but we have the genealogical evidence of the link.

The third, more recent result has 2 mismatches from each of the first two over 32 markers, a result that can be expected 15% of the time in 9 generations, though as two of the participants are descended from the same brother their common ancestor can be no more than 8 generations back (11.8% probability).

This family claims kinship with the Warburtons of Arley, and although there is no contemporary evidence to corroborate this, the claim has at times been accepted by the family at Arley. Therefore it is possible that this profile is that of the Warburtons of Arley. However there is growing evidence for the Cheshire group's profile being that of the Arley family so without a match outside the Garryhinch family it is likely that any link is through an illegitimate or adopted son.

## Commentary on Results

The predicted haplotype of this profile is J-M172. A more detailed understanding the history of the ancestors of the Garryhinch clan would be gleaned by joining the FTDNA J-M172 project and taking the J-M172 SNP Pack test.

SNP	Date	Range start	Range end
<b>Common Root</b>			
U106	2839 BC	3260 BC	2484 BC
Z381	2659 BC	3230 BC	1997 BC
<b>Cheshire Group</b>			
Z156	2476 BC	3200 BC	1717 BC
Z306	1750 BC	2150 BC	1410BC
Z304	1571 BC	1942 BC	1256 BC
DF98	1541 BC	1912 BC	1221 BC
S1911	1307 BC	1745 BC	934 BC
FGC13477	980 AD	473 AD	1529 AD
<b>Lancashire Group</b>			
L48	2485 BC	3200 BC	1740 BC
Z9 (Z28)	1835 BC	2221 BC	1507 BC
Z30	1654 BC	2020 BC	1343 BC
Z7 (Z31)	1492 BC	1843 BC	1195 BC
Z8 (Z351)	441 BC	702 BC	218 BC
Z1	410 BC	672 BC	173 BC
Z346	249 BC	527 BC	13 BC
Z343	219 BC	497 BC	17 AD
FGC11784	25 AD	378 BC	370 AD
S6881	753 AD	445 AD	1184 AD
<b>Lancashire Group - Branch A</b>			
23999089	circa 1000 AD		
<b>Lancashire Group - Branch B</b>			
15227518	1095 AD	624 AD	1521 AD
19162443	1266 AD	701 AD	1734 AD

### Warburtons West Cheshire

A recent result is from a member of the Tilston Clan of South West Cheshire. It matched a previous result from the Liverpool and Oldham clan. The four mismatches on a 37 marker test give a TMRCA of 19 generations, and a date of 1280 AD (635 AD - 1630 AD). The shared surname implies their ancestor lived in the later part of this range, but his date must be quite early. Migration from West Cheshire to Liverpool seem logical.

The haplotype for this group is R-M269, but hasn't been refined further.

## Commentary on Results

### Warburtons of South Cheshire

Another recent result is from a member of the Coppenhall Clan of South Cheshire. It matched a previous result from a participant in Audley, whose tree has been developed into the Audley clan. The results were identical over their common 32 markers giving a TMRCA of 5 generations, and a date of 1770 AD (1280 AD - 1945 AD). No link between the two trees has yet been found.

Peter, the earliest ancestor of the Coppenhall clan appeared in Coppenhall before his first marriage. His age at death implies he was born around 1769, but the location unknown. The parish record of Peter's second marriage named his father John.

William of the Audley clan was born in Marthall, Cheshire in 1760, father John. In all 5 children of John were baptised at Over Peover, but they don't include a Peter. John's wife's name is unknown and no marriage has been found. He may have married elsewhere.

The haplotype for this group is R-M269, but hasn't been refined further.

### Warburtons of Warburton

Three results are from The Warburtons of Warburton. Of these 2 match. Their common ancestor is William Warburton (1733-1822), who is 6 generations back from the participants. One of these participants is related to Norman Warburton, author of **Warburton: The Village and the Family**, in which he also published his own tree back to the 16th century in Warburton village.

The predicted haplotype is I-M253 which is most common in Scandinavia, suggesting a Viking link. However interpretation of the deep history of I-M253 has undergone radical change in recent years. More information could be gleaned by joining the FTDNA I1 project and undertaking further SNP testing.

The third result is a mismatch, and is haplotype R-M269. The identified common ancestor of all three participants is 8 generations back, and is the grandfather of William (1733-1822).

Unless there is an error in the tree, at least one of the haplotypes was introduced by an unrecorded non-paternal event in one of the 10 links from William (1733-1822), up to his grandfather, and down to the third participant.

The earliest ancestor of this clan is a Thomas Warburton who died in 1627 and is buried in Warburton village. It is known that a junior branch of the Warburtons of Arley Hall remained in the old manorial residence at Warburton Park, and the latest references to this Park are from the early 17th century. However it isn't known if Thomas was part of this line. If he were we should expect a match with the Cheshire Group so both DNA profiles might be the result of non-paternal events. The one chance to resolve this is to test someone who isn't descended from William (1733-1822), but is distant as possible from R-M269 participant

### Known Illegitimacies

The following results are known to have come from the descendant of an illegitimate son who took his mother's name. These are:

- a. A descendant of John Charles Warburton of the Wilmslow clan, who was born in 1808 in Wilmslow, Cheshire, the illegitimate son of Alice, the daughter on Peter Warburton and Alice Holt. In due course traditional genealogical research may determine which clan Peter belongs to. The predicted haplotype is R-M269
- b. A descendant of Robert Warburton who was born in 1820 in Stockport. Although Robert named his father as Josiah on one of his marriages, recent research shows he was one of three illegitimate children of Alice Warburton of the Mobberley clan. The family is the subject of an article in issue 12 of The Button Files (see **Newsletters** on the Warburton Website). The predicted haplotype is R-M269.
- c. A descendant of Frederic George Warburton born 1847 in Audley, Staffordshire. This clan is now documented as the Audley clan and is part of the South Cheshire Group. Frederic's mother was Julia Warburton (later Smith). The predicted haplotype is R-M269. Two close STR matches over 25 markers have tested as R-L21 so the participant is currently testing the R-L21 SNP pack.
- d. A descendant of John Warburton of the Coppenhall clan who was born in 1863. Although his parents on his baptism are William and Ann, the 1871 census shows

## Commentary on Results

him living with William who is his grandfather, and William's daughter Ann who is unmarried. The predicted haplotype is R-M269.

- e. A descendant of John Warburton of the Tilston clan who was probably born in 1684. A recent new result from this clan has linked it into the West Cheshire group. Meanwhile the original result has been matched with members of the Stewart family so it almost certainly arises from an unrecognised non-paternal event. The predicted haplotype is R-M269.
- f. A participant whose father was suspected to be illegitimate. The predicted haplotype is I-M253.

## Unmatched Results

There are several unmatched results. These are from:

- a. A descendant of Ralph Warburton of the Sandbach clan who was born circa 1817 in Sandbach, Cheshire to a father named Joseph. The predicted haplotype is R-M269.
- b. A participant in Australia whose earliest known ancestor was born in the Rochdale, Lancashire area circa 1770. This clan has not yet been documented, and I am no longer in contact with the participant. The predicted haplotype is R-M269.
- c. A descendant of Thomas Warburton (1809-1866) of the West Virginia clan who emigrated to the USA from Newark, Nottinghamshire. There is no earlier evidence of the family in Nottinghamshire, and they probably moved there to work in the coal mines. The predicted haplotype is R-M269.
- d. A descendant of Joseph Warburton (circa 1767-1844) of the Poynton clan who first appeared in Marple, Cheshire, and later lived in Torkington. Many of his descendants were colliers who lived in Poynton. All these villages are close to Stockport. The predicted haplotype is R-M269.
- e. A descendant of John Warburton who lived at Pool Bank farm, Bowdoin in the second half of the 16th century. A branch of the family later moved to Timperley. The predicted haplogroup is I-M223.
- f. A descendant of George (1826-1910) whose parents were Thomas and Ann nee Walsh of Sharples. The predicted haplotype is I-P37.
- g. A descendant from a Quaker Family that originates with Jacob Warburton who was born in 1782 in Bury, Lancashire. The predicted haplotype is G and the participant has further tested to be G-P303.

In addition I have a number of other results within the Warburton DNA Project. Some are Warburton relations who have used the project as a flag of convenience, others (Duttons in the Cheshire Group and Graves/Sexton on the Lancashire Group) are close matches and believed distant relations. There is also a Warbinton who tested to see if he was a Warburton, but who so far hasn't matched.

I was sent the profile of the Mongan family of Australia. They are believed to be descended from the brother of Charles Terence Mongan Warburton, the Bishop of Cloyne, who adopted the Warburton name in 1792 (see The Mongan Warburtons in Warburton Clans). The predicted haplotype is R-M269. It is documented in Interesting **Non-Warburton DNA Results** on the Warburton Website along with a Warbritton who is not that different from the Cheshire group, three other close matches to the Cheshire group, and someone who has a legend of Warburton decent but didn't match.

## TMRCA Calculations

When calculating the TMRCA based on STR tests the factors involved include genetic distance, mutation rates, and the length of a generation. The criteria I am using currently to perform these calculations are discussed below. For dates based on SNPs I have used the dates calculated by the R-U106 Project.

## Mutation Rates



## Commentary on Results

Mutation rates seem to vary considerably between markers, and maybe for a single marker between families. I have revisited this question a number of times and I have put a document called **Mutations Table** on the Warburton Website with the details and sources for some of the published rates.

The mutation rates I am currently using are based on those published by Marko Heinila, mainly because they are fairly recent (May 2012), and cover all 111 markers in the Family Tree DNA Y-DNA111 test. For each matchable set of markers I have calculated an average mutation rate from Heinila's individual marker rates as follows:

- FTDNA - 37 Markers - 0.36% - This seems quite high compared with the other rates but the 5 unique FTDNA markers are quite volatile.
- DNAH - 43 Markers - 0.25%
- Common - 32/34 Markers - 0.24%
- FTDNA 25 - 0.25%
- FTDNA 67 - 0.26%
- FTDNA 111 - 0.26%

The **Mutations Table** includes a table showing the the results of calculating the number of generations to the most recent common ancestor for each combination of genetic distance and number of markers compared when using average mutation rates based on Heinila.

### Calculations

I have used Dean McGee's calculator at :

<http://www.mymcgee.com/tools/yutility111.html#Instructions> to perform the calculations, but not for calculating average mutation rates as it doesn't handle each element of multiple markers separately.

The McGee calculator uses the Infinite Allele Mutation model to perform calculations. One drawback is that this method does not handle back mutations, so some people add an allowance (10% per 1000 years) to cover this. I have chosen to ignore this at this stage.

Also you can only choose to handle a difference of 2 or more between markers as either single multi-step mutations, or a series of single sep mutations. As in practice it is possible to distinguish some of these by comparing with the mode I have 'forced' the most likely genetic distance where necessary. I have counted two mutations where both participants differ from the mode, but treating a difference of 2 or more from the mode as a single mutation.

There is an alternative calculation method, Ken Nordtved's variance method, but this does not handle multi-step mutations and so tends to overestimate the TMRCA. Also I have yet to find a web-based calculator that uses this method.

As a cross-check I have also used Ann Turner's calculator (a Windows only downloadable .exe file) to calculate the likely number of mutations from the mode over the estimated 20 generations since the first Warburton was recorded, given the number of markers tested and the average mutation rate. These results are also in the Mutations Table.

### Range

TMRCA calculations produce a range of probabilities. These ranges are quite wide. I have chosen to show a range which encompasses 1 standard deviation from the mean. There is a two thirds probability of any actual TMRCA falling within this range (i.e there is a 16% chance it falls before the earlier date, and an 84% chance it falls before the later date). On the other hand the R-U106 Project dates I have used for SNPs use a 90% probability range.

### Date Calculation

A date can be obtained from the number of generations calculated above using the formula  $SD - (YD * \text{Number of Generations})$ .

SD is a start date based on the time of the last Y-chromosome transmission. 1947 is a commonly used date, but I have chosen to use my own date of birth which is 1945.

YD is the years per generation. Many sources seem to suggest numbers like 25 years per generation. However these tend to consider lines of inheritance and so consider only time to the

## Commentary on Results

first born son. When I look at my own ancestry the average generation over the last 10 generations is 37 years. In one instance my 3x great grandfather was born when his father was 59, and he was only the 4th of 8 children of his father's second marriage. I suspect there is probably quite a variation between different families. Some years ago I attended a wedding where the groom's grandmother, and the bride's great grandmother were present, and the groom's grandmother was the elder of the two.

I have seen 30 years quoted in relation to DNA calculations, and recent studies in Europe (particularly Iceland) are suggesting 33-37 years. I am using 35 years in my current calculations. This means that since the first person (Sir Peter) adopted the Warburton name in the 13th century we have had an average of 20 generations ( $20 * 35 = 700$  years before 1945). Therefore to consider whether 2 modern Warburtons have a common ancestor we need to look at the probability of a common ancestor in the last 20 generations.