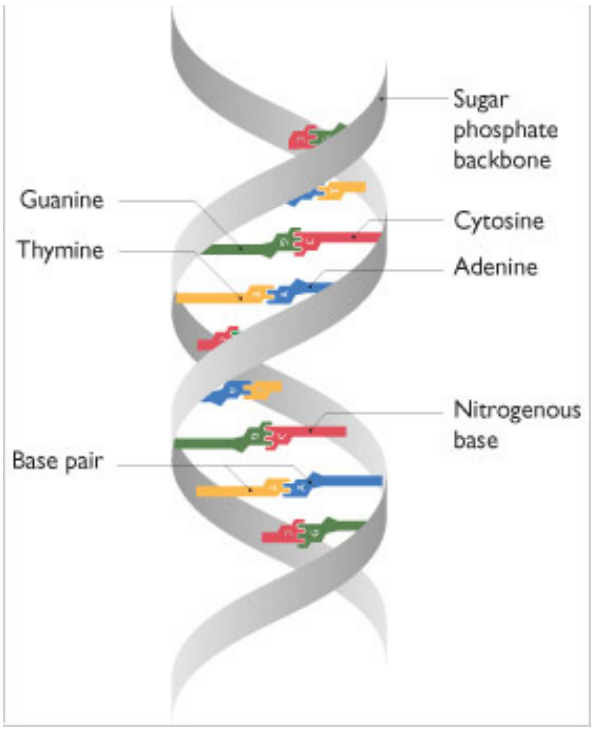
DNA and its Uses in Genealogy

This paper aims to provide a simple explanation of DNA and how it can be used in genealogy. It is meant as an introduction. It uses examples from the **Warburton DNA Project**. and **Warburton One-name Study** to aid understanding. At the end there is a reading list of books I have read that will provide a more professional and detailed explanation.

What is DNA?

The following description and diagram of DNA are taken from the Genetics Home Reference website at *http://ghr.nlm.nih.gov/handbook/basics/dna*:

> DNA, or deoxyribonucleic acid, is the hereditary material in humans and almost all other organisms. Nearly every cell in a person's body has the same DNA. Most DNA is located in the cell nucleus (where it is called nuclear DNA), but a small amount of DNA can also be found in the body of the cell (where it is called mitochondrial DNA or mtDNA).
>
> The information in DNA is stored as a code made up of four chemical bases: adenine (A), guanine (G), cytosine (C), and thymine (T). Human DNA consists of about 3 billion bases, and more than 99 percent of those bases are the same in all people. The order, or sequence, of these bases determines the information available for building and maintaining an organism, similar to the way in which letters of the alphabet appear in a certain order to form words and sentences.



> DNA bases pair up with each other, A with T and C with G, to form units called base pairs. Each base is also attached to a sugar molecule and a phosphate molecule. Together, a base, sugar, and phosphate are called a nucleotide. Nucleotides are arranged in two long strands that form a spiral called a double helix. The structure of the double helix is somewhat like a ladder, with the base

pairs forming the ladder's rungs and the sugar and phosphate molecules forming the vertical sidepieces of the ladder.

An important property of DNA is that it can replicate, or make copies of itself. Each strand of DNA in the double helix can serve as a pattern for duplicating the sequence of bases. This is critical when cells divide because each new cell needs to have an exact copy of the DNA present in the old cell.

Strands of DNA are organised into genes. A gene could be defined as the shortest string of DNA that actually does something useful in our development. However between the genes are strings of useless or junk DNA that do nothing (maybe they did once in earlier stages of evolution). These useless strings of bases are important for genealogy but I will come back to that later.

Genes and their attendant junk DNA are organised into chromosomes (so called because scientists use coloured dyes to identify them). The human genome (i.e. our DNA) consists of 46 chromosomes, or rather 23 pairs. We inherit one set of 23 from our father and one set from our mother. When we come to pass on 23 chromosomes to our children each chromosome is a composite containing some DNA from each partner in the original chromosome pair. Thus the DNA we pass to our children is a mixture, some from our father and some from our mother. The mixture is different every time.

However one of the pairs of chromosomes is different. This is the pair of so-called sex chromosomes, the X and Y-chromosomes which determine the sex of a child. A female has 2 X-chromosomes, one from each parent. However a male has an X-chromosome from his mother and a Y-chromosome from his father. It is a gene on the Y-chromosome that causes a baby to be a boy. In the absence of this gene the default is always to produce a girl.

The significance of this is that (unlike all the other chromosomes) the Y-chromosome is never mixed with a copy from the mother. It passes unchanged from father to son through the generations.

Now the body is very good at faithfully copying DNA from generation to generation, but it is not perfect (otherwise evolution wouldn't work). Very occasionally a copying mistake occurs. For example an adenine (A) base may become a thymine (T) base. If it happens in a gene it may cause disease, or rarely it improves the gene. But if it happens in junk DNA it has no effect and so the mistake continues to be copied from generation to generation. It is these differences that make DNA useful in historical and genealogical studies.

There is one other piece of DNA that is passed unchanged from generation to generation. It is in addition to the 46 chromosomes and acts as the energy source for a cell. It is called mitochondria and is only passed down the female line. Males do have it, inherited from their mother, but don't pass it on.

DNA Testing for Genealogy

There are currently three categories of DNA test marketed for people interested in their genealogy or genetic history. These are Y-chromosome tests, mitochondrial tests and autosomal tests. **The Warburton DNA Project** focusses on Y-chromosome tests because, like a surname, they pass from father to son, and so fit neatly with a one-name study. I will discuss mitochondrial and autosomal tests briefly at the end.

Y-Chromosome Tests for Genealogy

There are three types of Y-chromosome test used in genealogy. These are Short Tandem Repeat (STR) tests, specific Single Nucleotide Polymorphism (SNP) tests, and next generation sequencing tests.

The DNA test itself is the same in all cases and is actually very simple. The test kit is mailed to you. It consists of a couple of cotton buds and a return envelope. You wipe the inside of your mouth with the cotton buds and mail them back. This sample can then be used for any or all of the tests described. Results are returned within a few weeks. The sample may be retained by the testing company so that additional tests can be ordered without the need for a new test kit.

Single Nucleotide Polymorphism

I mentioned above that very occasionally a DNA letter is copied wrongly e.g. an A becomes a T. This is known as a Single Nucleotide Polymorphism or SNP. So a SNP is when a letter is copied wrongly.

SNPs occur very rarely. A specific letter may have only changed once in the whole of modern mankind's existence (150-180,000 years). The global population can therefore be divided into those who have the SNP and those who don't. Of those who do, a proportion will have a later SNP, and so on. Haplotrees are charts that map the sequence of these SNPs. By relating the current geographical spread of the SNPs, archaeological evidence, and the amount of change at various locations, researchers have been able to piece together ancient human migration patterns.

There are currently about 70,000 known Y-chromosome SNPs. Recently **Family Tree DNA** have developed a Y-DNA haplotree (Y-Tree) containing 70,000 SNPs, and as new ones are discovered they will be added to that haplotree. Other organisations are also working on all, or parts of the tree.

The SNPs have been organised into a number of major haplogroups based on their inter-relationships and geographic spread. These haplogroups are indicated by a letter, and specific positions within the haplogroup were defined originally defined by a complex series of letters and numbers. However recently the convention is to define your position in the haplotree by your haplogroup letter followed by your most recent shared SNP. My position is R-FGC17094. FGC17094 is a SNP that occurred since the Warburton name was adopted, and is probably about 500 years old. Thus anyone sharing that SNP is a Warburton (or descended from one) and shares a common ancestor with me.

Y-chromosome Short Tandem Repeat Tests

When Y-chromosome testing for genealogy began in earnest, comprehensive SNP testing was expensive. Fortunately there was another test that was much cheaper, and can be used to determine matches that denote a common ancestor, particularly if supported by a shared surname, or other historical evidence.

It so happens that there are some short DNA sequences that are repeated several times. Whereas with SNPs we were dealing with a change to a single base or letter in the DNA sequence, you can think of these sequences as words that are repeated several times. Every now and then the number of copies of the word changes. For example one may be added so, whereas there were 10 repeats before, there are now 11.

These strings of words are called Short Tandem Repeats (STRs), so a test for them is an STR test. There are a number of locations where they occur on the Y-chromosome. These are called markers in STR tests. There are tests available for different numbers of markers, and different testing companies test different markers.

Since its inception the **Warburton DNA Project** has been based on STR tests, beginning with a 43 marker test from **DNA Heritage**. However **DNA Heritage** ceased trading in 2011 and I switched to the **Family Tree DNA** 37 marker test, of which only 32 makers are common with the original 43 marker test. **Family Tree DNA** offer tests for 37, 67, and 111 markers. Some participants (including me) have taken these more extensive STR tests, as well as SNP tests, as described below.

The objective of STR tests is to compare results to determine if the persons tested are sufficiently matched to have a recent common ancestor. When two STR results are compared the number of markers with different values are counted. This number is known as the genetic difference . For example, the only difference between my profile and that of my genetic cousin Clive is that at marker DYS458 I have 16 repeats and he has 17, so our genetic distance is 1.

The genetic distance is used in conjunction with mutation rates to calculate the number of generations since a common ancestor lived. These are called Time to Most Recent Common Ancestor (TMRCA) calculations.

A mutation is a change in the number of repeats at a particular marker. Research is continuing on just how often these mutations occur. It seems some markers mutate more frequently than others, and maybe they vary for a single marker between families.

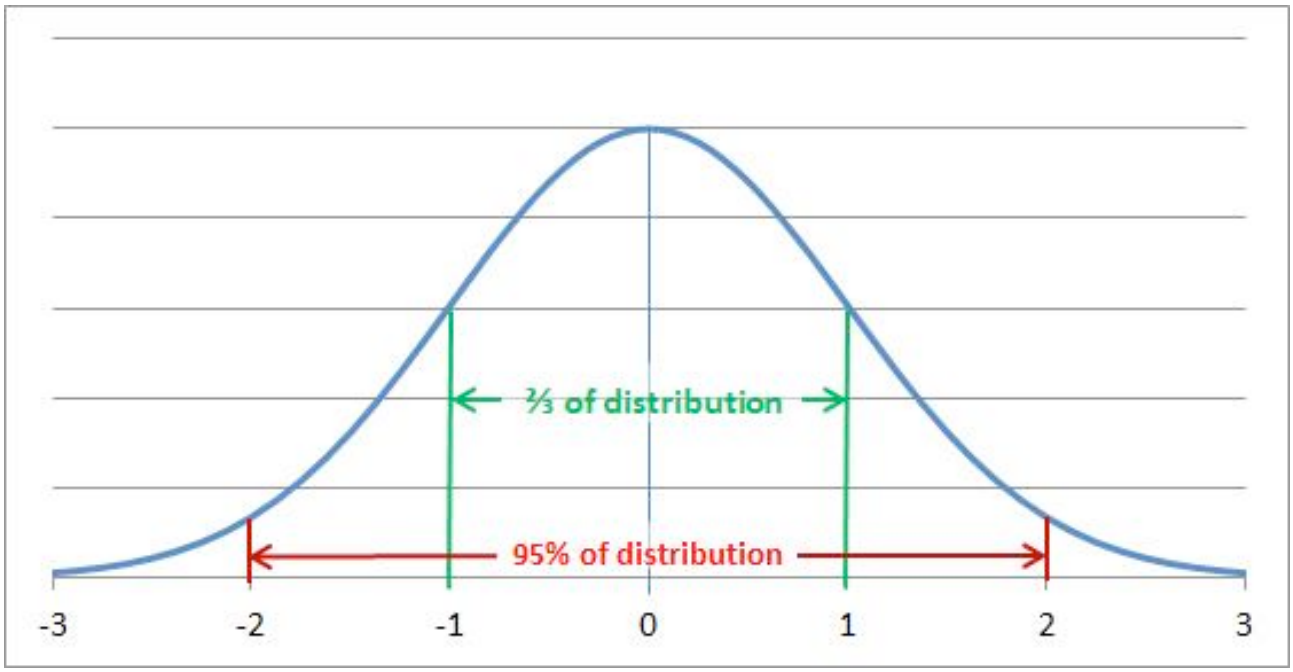
To put mutation rates into perspective, a marker with a mutation rate of 0.3% will, on average, change its number of repeats once in every 333 transmissions of the marker from father to son. If there are 33 markers with the same mutation rate, a change should occur in one of those markers, on average once in every 10 transmissions of the Y-chromosome from father to son. This is one mutation in 10 generations, or if a man had 10 sons, one son would have a mutation at one location.

For many markers there is also documentation on the frequency at which each possible result occurs. Each possible value is known as an allele. Each allele will occur at a different frequency. A match with an allele that has a low frequency may be particularly significant. See my **Mutations Table** for details and sources on mutation rates, and allele distributions.

TMRCA calculations produce a range of probabilities for the time to the most recent common ancestor. For those of you with no background in statistics here is a (hopefully) simple explanation. Suppose I have a bag containing 500 balls, of which 50 are blue and the rest red. I now select 10 balls at random. What are the chances of me getting 1 blue ball? If I kept repeating the test I should get 1 blue ball more frequently than any other result, but on occasions I will get no blue balls, and on other occasions two, three, or rarely even more blue balls. By repeating the test many times the frequency of each result can be determined and plotted on a graph.

This will tell me what are the chances (the probability) of any given test returning just one blue ball, or any other number of blue balls. Of course there are mathematical formulae to work out the results without having to keep testing it.

So for any combination of the number of markers tested, the genetic distance, and the average mutation rate it is possible to calculate a probability curve for the number of generations to the most recent common ancestor. The curve would look like the one below with frequency on the vertical axis, and number of generations on the horizontal axis. The chart shows that two thirds of possible values lie within one standard deviation of the mean, and 95% within two standard deviations. Standard deviation is a calculation of the variability in the possible values.



If two results are from cousins who share a common ancestor five generations ago there are 10 Y-chromosome transmissions between them, five on each line, and this must be taken into account in the calculations. Time to Most Recent Common Ancestor (TMRCA) calculators have been developed to perform the calculation, and several are available on the web.

The following table shows the probability for the number of generations to the most recent common ancestor given the genetic distance between 2 results on the **Family Tree DNA** 37 marker test.

Probability	**10%**	**25%**	**50%**	**75%**	**90%**
Genetic Distance	**Generations to Most Recent Common Ancestor**				
0	1	1	2	5	8
1	2	3	6	9	13
2	4	6	9	13	18
3	6	9	13	17	23
4	9	12	16	22	27
5	11	15	20	26	32

For example I have a genetic distance of 4 from Mark. There is an 80% chance that our most recent common ancestor lived between 9 and 27 generations ago, with mean at 16 generations (480 years). However there is still a 20% chance he lies outside these boundaries.

This table, and similar tables for 2 **DNA Heritage** results, and the common marker set between **DNA Heritage** and **Family Tree DNA** results, can be found in the **Mutations Table** document on the Warburton website.

To convert generations into time it is necessary to multiply the number of generations by the average length of a generation. There are references to a generation being 20-25 years but these are focussed on inheritance and the first born. In my own line the average of the last ten generations is over 37 years, with one of my ancestors being born when his father was 59 years old. There is probably considerable variation from line to line but I use an average of 35 years per generation to calculate the time to the most recent common ancestor.

The number of repeats for a marker can change up or down, and occasionally by more than one. It could be that, due to these changes cancelling each other out, two people who are unrelated finish up with the same profile. The probability of a random match is low, but in a large population some random matches are inevitable. Therefore matches are only considered meaningful when there is additional evidence, such as a shared surname, to link two people. This is why most STR studies are surname studies, though there are some locational ones.

Surnames were introduced around 12-1300 AD, when feudal estates needed them for record keeping. In fact it was nearly 700 years before my own birth that Sir Piers de Dutton built a manor house at Werberton and began to style himself de Werberton, At 35 years per generation this works out as 20 generations. Two modern day descendants of Sir Piers de Werberton would be 40 transmissions apart so we might expect a 37 marker test with a mutation rate of 0.36% to produce a genetic distance of slightly over four.

STR results come with an estimate of your SNP based haplogroup, but they cannot identify your more recent SNPs. My result indicated that I have SNPs at markers M207 (which defines me as haplogroup R), M343, and M269.

Using the Results in the Warburton DNA Project

The **Warburton DNA Project** uses the Y-chromosome 37 marker STR test from **Family Tree DNA**. This provides sufficient markers to be able to determine matches in a surname study.

A result consists of a string of numbers, one for each marker, and a prediction of the haplotype that would result from a Y-chromosome SNP test. Each of the markers has a name, such as DYS19. The associated number is the number of Short Tandem Repeats at that location, and is typically between 8 and 30.

The first step is to look for matches with previous results. Most results are either clear matches, with a genetic distance of 5 or less from another result, or a mismatch with a genetic distance of 9 or more from all other results. I refer to a group of matched results, or a single unmatched result, as a DNA profile.

Y-chromosome SNP Tests

There are two types of SNP tests. The first is to test for specific known SNPs, either singly or in groups. Without some prior indication of the SNPs you are likely to have, this is a hit and miss approach akin to searching for a needle in a haystack. However this approach is useful if your match has determined his SNPs in detail and you wish to know which of his more recent SNPs you share.

Determining those SNPs in detail requires the second type of test, known as a next-generation sequencing test. Such a test will trawl through a large part of the Y-chromosome checking you against all the known SNPs in that part of the Y-chromosome, and looking for new ones unique to you. There are several suppliers of these tests, testing greater or lesser parts of the Y-chromosome. Obviously the more they test the higher the cost.

The **Family Tree DNA** version of this test is the Big Y test. Big Y-500 covered roughly 12 million base pairs of the Y-chromosome and checked 70,000 known SNPs. It is one of the smaller and cheaper versions of next generation sequencing test, but still relatively expensive. Also it was originally only available as an upgrade to an STR test.

It was by taking this test that I discovered my most recent shared SNP is R-FGC17094, and I have more recent ones unique to me. It has been calculated that SNPs uncovered by the Big Y-500 test, occur on average, every 125 years, giving another method for calculating the time to the most recent common ancestor.

The test also showed I have SNP U106 which is the subject of a major project at **Family Tree DNA**, and SNP R-DF98 which identifies me as belonging to a clade called **The King's Cluster** within the R-U106 project.

My direct ancestors were in modern Western Germany about 5,000 years ago. They disappeared a thousand years later only to re-emerge in Britain following the Norman conquest. As there has been little DNA testing in France I presume this is where they spent the missing period.

My more recent SNPs confirm an earlier STR match with a group of Duttons. History records that it was a descendant of a Norman knight, Odard de Dutton, who first adopted the Warburton name after building a manor house in the village of the same name.

In the last 12 months there have been some significant developments. Firstly a new version of the Big Y test, Big Y-500, was introduced, and then upgraded to Big Y-700 in January 2019. The upgraded test includes the 111 STR markers of the most extensive STR test, plus at least 589 further STR marker results, and can be ordered directly. This large number of STRs should enhance STR based calculations of time to most recent ancestor (TMRCA) considerably.

In parallel the development of **Family Tree DNA**'s Y-Tree means that a Big Y-700 tester can be placed quite easily on his twig of the world haplotree. Indeed literally as I have been updating this article (January 2019) **Family Tree DNA** announced a Big Y Block Tree Matching Tool which allows every Big Y tester to see precisely their position on the Y-Tree, along with their matches, neighbours, and the sequence of SNPs which lead them there.

The difference between STR matches and SNP matches is that SNP matches are definitive whilst STR matches are only indicative. My most recent shared SNP, FGC17094, like all SNPs, occurred once in a particular individual. My match John and I are his descendants. FGC17094 is at the end of a long list of SNPs which define our history. Others, like Mark Warburton, the Duttons and the Howells separate from this line at earlier stages. Another cousin, Clive did a specific SNP test for FGC17094, and was positive, proving he shared our history.

John and I had an earlier STR match. This indicated we had a common ancestor, but because STR mutations are bi-directional it was only the additional fact of our common surname that verified this. The test only indicated our earliest SNPs. The dates of common ancestors can be estimated from the genetic distance between two STR tests, and patterns of mutations can give some idea of when related clans diverged, but SNP sequences and matches give a more precise picture.

The Big Y-700 test is still not cheap compared to a Y-37 test, but during **Family Tree DNA**'s last sale Big Y-500 cost less than $500, and it is likely Big Y-700 will be available at a similar price in future sales. At this price it is coming within range of many testers. As it produces a definitive result in terms of your position on the Y-Tree, encompasses available STR tests and more, and is probably all the Y-chromosome testing most people will ever

need, it should now be the first consideration for anyone who is not closely related to a previous tester. It is a cheaper option than starting with an STR test and then upgrading.

Unmatched Results

To date the success rate in finding matches is about 70%. This leaves about 30% of results with no match. There could be many reasons for this, We don't know how many people just adopted the name in feudal times. Many lines will have died out, and others could have few descendants today, even though they are old. Other lines will have started later as a result of adoption, illegitimacy, or infidelity, but may still have had time to grow into significant clans. Bancroft Warburton was illegitimate when he was born in 1738 (though his parents did later marry) but his descendants include over 170 Warburtons.

These later events are referred to as non-paternal events. Whereas DNA profiles always pass from father to son, there are occasions when a male receives the Warburton name from someone other than his biological father. The rate of such events is apparently about 2% per generation.

Even a small number on 'non-paternal events' in each generation will add up over several generations and many of us will be affected by them somewhere in our family tree, if not in our paternal line. We all have 32 great great great grandparents. Add in parents, grandparents etc. and there are 62 individuals we are directly descended from in a tree that goes back just 200 years. The law of averages says at least one of these will be the result of a 'non-paternal event'. I know I have one illegitimate great grandmother, and a great great grandmother I'm not sure about.

I have also uncovered, and written about, a case in the Warburton Village clan where matches show that early 18th century two cousins have different DNA profiles. This means a non-paternal event must have occurred, but there is no evidence of it in the parish record.

Of course by definition every Warburton line must have started with a 'non-paternal event'. The first Warburton in the line must have had a father whose name wasn't Warburton. Except where we have documented history, like the baptism record of an illegitimate child, or the evidence that Sir Piers de Dutton adopted the Warburton name when he built a house at Warburton, we may never be sure of the exact details in many cases.

There are a number of reasons why a son might not take his natural father's name. Infidelity and illegitimacy are obvious reasons, but it isn't unheard of for a family to take the wife's name if she brings a considerable inheritance to the family. For example the Egerton family who inherited Arley Hall in 1813 from Sir Peter Warburton through his niece, changed their name to Egerton Warburton.

Also a name might simply be adopted, for example because it is a step-father's name, or it is politically expedient. There is a case documented in the London Gazette of 1792 of a Charles Terence Mongon adopting the name Warburton (the name of his maternal cousins) apparently because it would aid his preferment in the protestant Church of Ireland.

Unmatched profiles could still belong to sizeable clans and have ancient origins so there is a chance they will be matched in the future. I've found a couple of new matches in the past year.

There is also the possibility of identifying links to other surnames and uncovering clues as to your true biological origins. For example I have one project member who discovered he had matches with a number of Stewarts. With the advent of the Y-Tree and the Big Y Block

Tree Matching Tool such matches will become much easier to find because you can be sure SNP matches are real and not possibly just random results.

Triangulation

When the results of two participants in the **Warburton DNA Project** match, this identifies a triangle with the participants' common ancestor is at the apex, and the participants at the base. All the other male Warburton descendants of the common ancestor are contained within this triangle, and will have the same DNA profile as the first two participants, unless of course there was a 'non-paternal event' in their line from the common ancestor.

In the **Warburton One-Name Study** I am using traditional genealogical research to build a series of family trees. These family trees are the inverse of a traditional family tree in that they follow multiple lines of descent from a single common ancestor, so I refer to them as clans. As such they mirror the triangles produced from DNA matches. I have traced my own line back to an earliest ancestor called George who died in 1639. My clan tree (the Hale Barns clan) traces all known lines of descent from George. Of course there may be more lines I have yet to uncover.

My aim is to assign a DNA profile to each of the Warburton clans, that I document. A single Y-chromosome DNA result will link a DNA profile to a Warburton clan, but it will give no clue as to how long the profile and the clan have been linked. The only way to determine at least a minimum time of association is to find a matching profile, and build a triangle.

Where a match is found and a triangle created, this triangle can be fitted onto the Warburton clan family trees. A triangle may only cover part of a clan, with its common ancestor being a descendant of the clan's earliest ancestor. We would not be certain at this stage if we had found the DNA profile of the whole clan. I have one clan, the Warburton Village clan, which contains two triangles with different profiles, and where the common ancestors of the triangles are cousins who lived in the early 18ty century. At least one of these profiles must result from a 'non-paternal event' though nothing untoward is documented in the parish records.

When the match is with a member of a different clan, the two clans are linked by a common DNA profile. The common ancestor may be within the clan with the deepest known history, making the younger clan a new branch of the older one. We believe this to be the case with my genetic cousin Clive. His ancestors are now considered to be a branch of the Hale Barns clan.

However it might be that the two clans are descended from an earlier common ancestor who pre-dates the earliest known ancestor in each clan. This would be the case if the earliest known ancestors of each clan were contemporary, and clearly not related.

Where a match indicates a high probability that a most recent common ancestor lived since 1600 AD then it is worth using genealogical tools such as parish records to find a link. Even when the actual links cannot be determined there may be geographic links. For example the Hale Barns clan and its associated clans seem to have origins in North Cheshire, close to the village of Warburton itself.

Once a triangle is defined there is little point in anyone else from within the triangle being tested as he should match the existing results. There might be a small benefit from refining the haplotree (see below), but this could be offset by the risk of uncovering an unknown, recent 'non-paternal event'.

Expanding Y-Tree Twigs

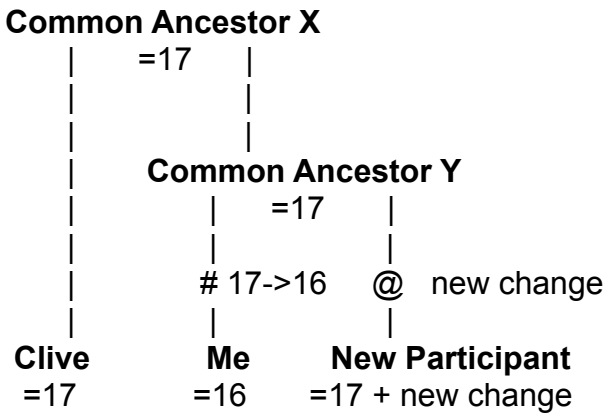
To date the **Warburton DNA Project** has has uncovered two large groups of matches across multiple clans, and a couple of smaller ones. One larger group is the Cheshire

Group, believed to be descended from the original Warburtons who in turn are descended from the Norman Knight Odard de Dutton. The second large group is the Lancashire Group, which is located in the Haslingden-Bury area. It may be particularly appealing to overseas Warburtons to see if they can link to one of these groups and so establish their geographic origins more closely.

I have produced haplotrees for the Cheshire Group, and the Lancashire Group that illustrate how the clans in these groups are related to each other. The haplotrees are extensions of the relevant Y-Tree twigs, and include known genealogical information, and the results of STR matches, and specific SNP tests not known to the Y-Tree developers.

As an example, the one difference between my genetic cousin Clive and myself in our STR tests, is that he has 17 repeats at marker DYS458 and I have 16. Subsequent matching results have also had a value of 17, indicating that 17 is probably the original value and the mutation to 16 took place somewhere in my line.

If we tested a new participant with whom I shared a more recent common ancestor, we could pinpoint where the change occurred more accurately, based on whether he had a value of 16, or 17. Furthermore, if the new participant had a different change from me, any future clan member showing the same change would be closely related to him. See the example genetic family tree below (which is based on STR results).



=17 or =16 the value of DYS458
position of change from 17 to 16 (roughly: it could be anywhere between common ancestor Y and Me)
@ rough position of new change

Subsequently I have discovered my two unique SNPs, FGC17096, and A20340. Clive has tested for these SNPs but doesn't have them, so these must also be specific to my line. Clive may have his own unique SNPs but he hasn't done the Big Y test.

Handling Grey Area Matches

Some of my results for the Lancashire Group have a genetic distance which gave a low probability of a common ancestor in 25 generations, but were both more closely matched to a third result. They also share a low frequency allele for certain markers.

An allele is one of the possible results for an STR marker, and for each marker there is a distribution curve showing the probability of each allele occurring. If a number of results show the same low probability alleles for certain markers, then the chances of a random match are reduced. This led me to include several matches in the Lancashire Group despite the genetic distance being larger than normal in some cases.

Subsequent SNP testing has verified a number of these matches, but not all. They did all share SNP S6881 which dates between 445AD and 1184AD, and all but one shared much more recent SNPs implying a common Warburton ancestor. One however was on a completely different branch under S6881, headed by SNP A11377, which is dated between 520AD and 1403AD. A common ancestor could have lived in the early years of the village of Warburton, which was founded in the 10th century. This would imply that two cousins from the village adopted the village name as their own independently. However a majority of instances of S6881 occur in Lancashire so it is also possible a non-paternal event occurred within the larger Warburton group.

Mitochondrial Tests

Mitochondrial tests are SNP tests. As mentioned above, Mitochondria is a small piece of DNA that acts a the energy source for a cell. It has roughly 16,000 bases, which means SNPs occur much less frequently than for the Y-chromosome. However, like the Y-chromosome, because it only passes down the female line it remains unchanged from generation to generation.

As we all carry mitochondria inherited from our mothers, anyone can take the mitochondrial SNP test. The small number of SNPs limits its use as a genealogical tool, though it was the test that identified a skeleton found under a Leicester car park as that of King Richard III.

It does provide an alternative view of our deep history. By performing exactly the same haplogroup analysis on both the Y-chromosome and mitochondria two separate, corroborating pictures of mankind's past can be built. The results can be fascinating. For example my mitochondria, and my Y-chromosome have completely different histories which are discussed in a companion paper **My Use of DNA in Genealogy**.

Autosomal Tests

The tests discussed so far concentrate on the DNA that comes from a single parent. Autosomal tests such as **Family Finder** from **Family Tree DNA,** and **AncestryDNA** from **Ancestry,** test DNA from the 22 pairs of chromosomes that contain a mix of DNA from all ancestors. Strings of DNA are compared either between databases of test results to seek strings that come from a common ancestor, or against reference populations to determine ethnic origins.

As a genealogical tool autosomal test can help to prove cousins with a common ancestor up to about fifth cousins. These tests are also relatively cheap leading to them being the most popular tests used today. In January 2019 it is estimated that 15 million people have tested so far, 10 million of these using the **AncestryDNA** test.

The value from these tests come from the matching databases maintained by the suppliers. There is also a cross supplier matching database at gedmatch.com, but it seems that only about 1 million results are loaded there. Matching is a more technical exercise than for SNP or STR matches. A SNP match is either positive or negative, and it is straightforward to compare two STR results and calculate genetic difference. Autosomal comparisons involve scanning large amounts of DNA from databases of results looking for strings of DNA that are common, and this can only be done by the owners of the databases.

Like all DNA tests autosomal tests face the possibility of an unwelcome result, possibly exacerbated by the fact that they concentrate on recent generations. If a Y-chromosome test indicates non-paternal event it could have occurred hundreds of years ago, unless you

test two closely related males, and this isn't usually necessary. However an autosomal test can uncover recent family skeletons. A new meaning of NPE is used; not parent expected.

Some early tests reported small amounts of Neanderthal and other pre-human DNA in most non-Africans. This is because early modern human populations met the descendants of earlier humanoid migrations from Africa and interbred. A small amount of genetic material from these earlier species is found in most non-African populations, suggesting it conferred advantages that resulted in the descendants of this interbreeding coming to dominate modern populations.

However I have noticed that results from the currently most-popular testing companies no longer show this element of our DNA.

Summary

DNA testing is best viewed as an important additional tool in traditional genealogy. The various types of DNA test can add to your understanding of where you come from. In particular Y-chromosome DNA profiles can be extremely useful in the study of family history if they are used in addition to the traditional tools of genealogical research. My objectives in the **Warburton One-Name Stud**y is to continue to exploit this synergy to develop an ever broader understanding of the various Warburton clans and what links may exist between them.

Further Reading

1. Stephen Oppenheimer, *Out of Eden: The Peopling of the World* (Robinson Publishing, 29 Jul 2004)

2. Professor Bryan Sykes, *Seven Daughters of Eve* (Corgi, 1 Sep 2004)

3. Professor Bryan Sykes, *Adam's Curse: A Future Without Men* (Corgi, 1 Sep 2004)

4. Chris Pomery and Steve Jones, *DNA and Family History: How Genetic Testing Can Advance Your Genealogical Research* (PRO Publications. Sep 2004)

5. Professor Bryan Sykes, *Blood of the Isles* (Corgi, 3 Sep 2007)

6. Stephen Oppenheimer, *The Origins of the British: A Genetic Detective Story* (Robinson Publishing, 12 Apr 2007)