

The Jewish Genealogical Society of Great Britain



Genetic Genealogy – Expanding the Jewish Family Tree



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Genetic Genealogy – Expanding the Jewish Family Tree

1. What is Genetic Genealogy?

Genetic Genealogy is an additional tool available to the family historian, and it can be especially useful for Jewish genealogists, where written resources may be limited. Genetic genealogy can show who you are related to over time, allowing the tracing of historic population movements which provide a window into the past. With genetic genealogy, you may be able to expand your family tree by finding hitherto unknown branches, and you may be able to join up gaps by finding lost relations. Genetic genealogy is helpful for solving family mysteries –some relationships may only be solved conclusively through genetic testing.

There are a number of reasons why you may want to do genetic testing – these include;

- Make matches that go back beyond the adoption of surnames – before the late 18th century or early 19th century, Ashkenazi Jews used patronymics
- Check family movements – finding the mother country of the most recent ancestor, or to trace divergence of family branches across different continents
- Find links where there are few or no written records, or records were destroyed in wars, fires etc
- Connect aliases and surname changes in families e.g. where brothers may have taken different names, or names became anglicised
- Incidences of those marrying out/converting, or false paternity - adoption or illegitimacy
- Find female lines of descent, where the woman has taken her husband's name and moved to her husband's place of origin

DNA testing can provide that “eureka” moment and link the disparate strands together. But it may also provide more queries than answers – as this is a science in its infancy, it is not foolproof and there are new developments all the time.

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2. Some basic biology

DNA stands for deoxyribonucleic acid. DNA stores the hereditary information that is passed on from one generation to the next. All body cells except red blood cells contain a copy of our DNA.

At conception a person receives DNA from both the father and mother. Each human has 46 chromosomes, which come in two sets of 23, one inherited from each parent. Of these, 22 are single chromosomes, whilst the 23rd is the sex chromosome. A woman has two x chromosomes inherited from each parent, and a man has one x chromosome (inherited from the mother) and one y chromosome (inherited from the father). The male chromosome ydna is located in the cell nucleus, whereas the maternal sex chromosome Mtdna is located outside the nucleus of the cell in the mitochondria.

Each chromosome contains tightly coiled threads of DNA. A DNA molecule comprises two strands wrapped round each other like a twisted ladder (the double helix), where the rungs consist of bases. These bases are called Adenine (A), Guanine (G), Thymine (T) and Cytosine (C) – which fit together in pairs (C with G and T with A). Genes are discrete stretches of these bases that code the instructions for the body. There are around 24,000 genes in the human genome, and each gene has a fixed position on a chromosome. The gene is the unit of heredity whilst DNA is the recipe or blueprint. Scientists have discovered that there are more than 1,000 genes on the X chromosome but only 27 on the Y chromosome.

However, there are long stretches of DNA with no known function – 95% of the genome does not code for anything. Non coding DNA is known as “Junk DNA”. Junk DNA does not affect traits, reveal medical conditions or affect survival – it records our ancestral history. Mutations accumulate in Junk DNA preserving evidence of past events going back thousands of years ago. Mutations, or changes in DNA which have an indifferent effect on the body, are found in specific places on non coding DNA, and provide markers that indicate specific differences between humans. Most mutations are spontaneous, and represent copying errors in cell reproduction, once in every 50 million bases.

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3. Ydna and mtdna and your line of descent

Genetic testing reveals your direct line of descent – if you are a woman the line is through your mother's, mother's mother and so on back through time (called mitochondrial dna or mtdna). If you are a man it is through your father's, father's father and so on back through time (called ydna). A woman can only be tested for her mtdna line of descent, which she will pass onto her daughters. But a man can be tested for both his mtdna and ydna, through each x and y chromosome he inherits. However, although he can receive his mtdna from his mother, he cannot pass this onto his children. A man can pass on only his ydna but to his sons alone.

In the case of males, the direct line of descent is more obvious because the surname will be passed down from father to son, and records can be traced to some extent (more likely in recent times for most Jews). With females, the surname in the past has been changed upon marriage – mtdna testing will give you information about your mother's mother's family that you may not be able to obtain through other means. It is important to understand that dna inheritance is through the direct male or female lines only. Thus the only way you can test on your mother's father's side or your father's mother's side is to find individuals who can prove a direct line of descent, and who would agree to undertake a dna test.

4. Autosomal dna

Parental genetic material is shuffled or reassembled at conception, so that children will receive part of their mother's and part of their father's dna, making them unique individuals. The shuffled dna material received from both parents is called autosomal dna – you will receive half from each parent, and therefore a quarter from each grandparent. The markers present in your autosomal dna can indicate geographical origins, through comparisons with populations which also share those markers. Autosomal dna testing is a particular form of genetic testing, which is being refined but is not yet of great use in Jewish genealogy, but may be so in the future. To date it has been used to estimate proportions of a person's background that may be, for example, Chinese, Native American, or Black African. Gradually it is proving possible to narrow down ethnic groupings, for example, one company claims to match to Hungarian Ashkenazi, though this may be more a reflection on its sample make-up, i.e. it had not apparently used any other Ashkenazi populations for comparison to date.

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5. What markers show

Examination of mutations or markers has shown that our most recent common ancestor (MRCA) hailed from Africa about 130,000 years ago, and genetic studies trace the path out of Africa to the Middle East and from there into Europe, Asia, Australasia and the Americas. This has recently been shown in more depth through genetic tests of native and aboriginal ethnic groupings in Africa and elsewhere undertaken through the National Geographic Project led by Spencer Wells.

Concentrations of mutations in particular populations/geographical areas are called Haplogroups. This allows us to ascertain the geographical origins of individuals, where they have migrated from and to over time, and increasingly the length of time ago the mutation was likely to have occurred (through examination of historical, anthropological and archaeological records). Categories of mutational changes for both mtDNA and YDNA are given letters of the alphabet, followed by a number, to denote their differences – African ancestral Adam is A and Ancestral Eve is L.

6. Haplogroups

Early on human numbers were small and tended to be concentrated in isolated pockets – this was true in the European ice ages where the cold destroyed human populations – it is estimated that the 730m people in Europe today (and 27.5m in AD 500) are descended from no more than 30,000 individuals at the end of the last ice age, about 17,000 years ago. Professor Brian Sykes of Oxford University has identified their maternal origins as the “Seven Daughters of Eve” (in reality there are about nine, if you include small haplogroups), showing how the gene pool had been reduced. These individuals lived mainly in three European ice age refuges – one at the foothills of the Pyrenees, another in the foothills of the Italian Alps and the third in Ukraine. This isolation allowed particular mutations to be passed on in these geographical areas and their descendants’ movements tracked across Europe and beyond.

The commonest Haplogroups in West Europe are H for women and R for men accounting for half of the present day population, but H can be broken down into at least 18 different sub groups, and R is split into R1a for Eastern Europe and R1b for Western Europe, with many sub groups or clades. Today we can track the passage of members of haplogroups by examining mutational differences between them. This is likely to be more difficult with the more common haplogroups, but can be of immense benefit with rarer haplogroups, for example, a number of Jewish groups exhibit unique markers, not found in other populations.

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Where there are more mutations, this shows greater genetic variation, an older genetic line (African genes have the most variation), or a greater inflow into the gene pool. Because Jewish populations were frequently isolated through the effects of the diaspora, (being expelled from one country to another), and also intermarried within the group, Jewish mutations are fewer and less varied. This makes them easier to track. Jewish populations frequently experienced ancient bottlenecks (where the population decreased or stayed the same), but modern population surges, again giving rise to specific mutations which survived the bottlenecks and grew as the population grew. This is why both geneticists and genealogists are very interested in Jewish lines of descent – the very history of the diaspora makes them ideal subjects of study for genetic genealogy.

7. Jewish mtDNA Haplogroups

In Jewish Ashkenazi women the most common haplogroups are K, H, and N1b (Hammer et al 2004). N1b, making up 10% of female Jewish mtDNA, was known to be of non-European origin. However, in 2005, Doron Behar, an Israeli scientist, was able to show that the most common Jewish female haplogroup K sub groups, shared by about 32% of Jewish Ashkenazi women, may originate in the Middle East. Taking K and N1b together, over 40% of Jewish women may have a maternal origin in the Middle East, and are descended from just four founding mothers (3 K and 1 N1b), sharing markers unique to people of Jewish origin (non Jewish K groups do not have these marker motifs), indicating specific founder events. The K sub groups are called K1a1b1a (the most common), K1a9, and K2a2a, and are commonly found in people of recent Polish Jewish origins.

Apart from a small number of women identified as being of African origin, the remaining 60% of Jewish Ashkenazi women are most likely primarily of European descent (although further studies may yet identify other Middle Eastern strands amongst the predominantly European H and HV groups). H, which is the most common haplogroup amongst non Jewish European women (about 50%), accounts for about one quarter of Jewish Ashkenazi women, and HV groups (its related or predecessor haplogroup) about 10%. A significant minority are to be found spread amongst all the other common European haplogroups, namely, U, J, T, and the smaller Eurasian groups of I, W and X – in many cases the haplotypes or subclades are unique to women of Jewish origin indicating further founder effects.

It has been hypothesised from this that the female mtDNA was largely of local origin – this means that as the Diaspora spread into Europe, Jewish men took local wives and then their mtDNA was passed down in isolated and dispersed communities, with little inflow of genes from outside. An analogy could be made with the Vikings who travelled from Norway and Denmark to the British Isles and onwards to Iceland and Greenland. They took local wives – most female mtDNA in Iceland is of Celtic (not Scandinavian) origin, matching with Irish and Scottish mtDNA.

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A current 2007 study, has shown that the genetic make-up of Ashkenazi Jewish women varies significantly between those of different geographical origin. Mishmar et al compared the mtDNAs of samples of women whose ancestors came from Poland, Romania and Russia (including Ukraine). This showed varying percentages of those with K, N1b, H or HV origins. (See table below). Further assessment of different groups (e.g. German, Lithuanian, Belarus, Hungarian etc.) may help to explain population movements in due course. See Table 1 below.

	Hammer et al 2004	Feder, Ovadia, Glasser & Mishmar 2007		
	All AJ	Pol AJ	Rom AJ	Rus AJ
No	554	192	104	150
	%	%	%	%
K	33	38	31	17
H	21	14	26	27
HV*	12	11	9	17
J	12	9	9	10
N1b	10	6	11	7
T	5	5	3	7
U	4	6	5	7
W/X/I	3	5	3	3
L/M+	4	4	4	1
K and N1	43	44	42	24

HV group including HV, HV, HV1, pre HV, and V
+ African haplogroups

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Set below is a case study comparison of Jews in the mtdna HV1 haplogroup. Table 2 shows the markers for twelve members of this group, whilst tables 3 and 4 show full genome results for those members sharing close results in table 2.

Table 2 – Case Study comparison of twelve low and high resolution mtdna results

Haplogroup HV1	Person											
HVR1 Mutations	A	B	C	D	E	F	G	H	I	J	K	L
Low resolution												
16067T	x	x	x	x	x	x	x	x	x	x	x	x
16183C	x	x	x	x	x	x	x	x	x	x	x	x
16189C	x	x	x	x	x	x	x	x	x	x	x	x
16519C	x	x	x	x	x	x	x	x	x	x	x	x
HVR2 Mutations	HVR2 Branches of Haplogroup HV1											
High resolution	1	2						3	4			
152C	x	x	x	x	x	x	x	x	x	x	x	x
263G	x	x	x	x	x	x	x	x	x	x	x	x
309.1C	x	x	x	x	x	x	x	x	x	x	x	x
309.2C	x	x	x	x	x	x	x	x				
309.3C	x											
315.1C	x	x	x	x	x	x	x		x	x	x	x

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Table 3 - Full Genome Mtdna results for B and C above – HV1a exact match

Haplogroup	HV1	Control Region differences from CRS (Mutations indicating closer relationships within branch)				
HVR1 differences from CRS (Low resolution mutations showing haplogroup)	16067T	750G	1438G	2706G	3547G	4769G
	16183C	6023A	7028T	8014T	8860G	12696
	16189C	15218G	15326G			
	16519C					
HVR2 differences from CRS (High resolution mutations showing branch within haplogroup)	152C					
	263G					
	309.1C					
	309.2C					
	315.1C					

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Table 4 - Full Genome Mtdna results for D above – one mutation away

Haplogroup	HV1	Control Region differences from CRS (Mutations indicating closer relationships within branch)				
HVR1 differences from CRS (Low resolution mutations showing haplogroup)	16067T	750G	1438G	2706G	3547G	4769G
	16183C	6023A	7028T	8014T	8860G	12696
	16189C	13434G	15218G	15326G		
	16519C					
HVR2 differences from CRS (High resolution mutations showing branch within haplogroup)	152C					
	263G					
	309.1C					
	309.2C					
	315.1C					

CRS refers to the Cambridge Reference Sequence (in H haplogroup) which is used as the benchmark for comparison of mutational differences.

8. Mtdna HV1 Case Study - What do these results mean?

Table 2 shows the test results for twelve Jewish people - a mix of men and women from Europe, USA and South Africa. Mtdna markers mutate slowly over time and there are only a limited number of markers that can be tested in mitochondrial dna. If you have a relatively rare mtdna, this means that broad family relationships are easy to spot. With common mtdna like haplogroup H, this needs to be broken down into the subgroupings, or clades, such as H1 etc. The HV1 group is shown here, which is relatively rare in the European population, but occurs at a rate of 1 in 50 people of Jewish origin, amongst both people of Ashkenazi or Sephardic origin (it is slightly more common amongst the latter). The origin of HV1 is disputed – it could be either European or Middle Eastern.

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In this sample of twelve, we can see that all share the common HV1 markers of 16067T, 16183C, 16189C and 16519C - this shared inheritance is called HVR1 (the hyper variable segment is tested) or low resolution, as the common ancestor will be way back in time. HVR2 is called the high resolution, as this starts to break down the haplogroup into branches, depending on which mutations are present. In the sample there are four different marker variations (or branches), but all twelve share 152C, 263G, and 309.1C. Eight share 309.2 C, but only one has 309.3C. Four people have neither 309.2 C nor 309.3C. One person has neither 309.3C nor 315.1C, but all the other eleven have 315.1C.

Three of the group who have all the markers except 309.3C belong to the same branch, but in order to find out if they are more closely related, they need to take the full genome test (see table 3). Persons B (in the UK) and C (in the USA) find they have exactly the same set of markers, therefore they must be related within the last 300 years, although neither have known about each other before. Both can trace their families back to great grandmothers on the border areas of SW Lithuania and NE Poland (but the surnames are different), therefore the relationship must be in the generation before, or even further back. Their great - great grandmothers could have been sisters, or possibly great-great-great grandmothers.

Person D's test results (see table 4) show that he is one mutation away from persons B and C, but photographs show his family bear a strong resemblance for facial, hair and eye colouring characteristics to person B. His family also come from the same geographical area as persons B and C, within about 30 square kilometres. Clearly, this mutation does not stretch back too far to when it separated from the other line, or it could even be a more recent mutation in the present or immediate past generation.

9. Jewish ydna Haplogroups

Behar in 2004 looked at the origins of the Ashkenazi Y chromosomes, based on ten European communities. The results showed that Ashkenazi Jews fell into 19 haplogroups, but that 7 haplogroups accounted for 84.5% of Ashkenazi Jewish chromosomes. In comparison just 5 haplogroups accounted for 88.7% of non Jewish chromosomes. See Table 5 below.

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Haplogroup	Marker	% Ash Jewish	% Non Jewish
J1	12f2*	19	
J2	M172	19	6
All J		38	6
E3b	M35	16	
E	M78	3	5
All E		19	5
R1b	M343/P25	10	31
R1a1	M17	8	26
All R		18	57
G1	M201	8	
G2	P15	2	
All G		10	
Q	P36	5	
I	P19	4	20
K	M9*	2	
Q/I/K		11	

The study concluded that the major Ashkenazi founding populations were J1 and J2, E3b, G and Q.

J is the most commonly occurring Jewish male haplotype shared by 38% of Ashkenazi. *Note; there is less information on Sephardic Jewish haplotypes, due to the fewer numbers who have been tested to date.*

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Jews share haplogroup J with other Middle Eastern populations such as Druze, the Samaritans and Palestinians, indicating a common heritage going back thousands of years. However, because of the diaspora, and centuries of isolation in Europe, Jewish J haplotypes (sub groups) are quite distinct from other non Jewish J haplotypes.

The **Cohen Modal Haplotype (CMH)** is a specific set of twelve Y STR marker values that occurs in J1 (See *Wikipedia for more details, which uses FTDNA data*). See Table 6 below showing the 12 markers. Amongst all Jews who have the CMH, 52% are Sephardi and 47% are Ashkenazi.

DYS 393	DYS 390	DYS 19	DYS 391	DYS 385a	DYS 385b	DYS 426	DYS 388	DYS 439	DYS 389i	DYS 392	DYS 389ii	Ash %	Sep %
12	23	14	10	13	15	11	16	12	13	11	30	47	52

The Cohen Modal Haplotype has been found amongst the Lemba of South Africa who descend from ancient Jewish Yemeni traders.

See the G5 case study on the succeeding pages for information about this group. This seeks to compare markers for 9 Jewish men from the newly discovered G5 haplotype, which is also likely to be of Middle Eastern origin. The G5 group exhibits the M377 marker.

One study by Karl Skorecki et al in 2003 found that 30% of Ashkenazi men from Poland and Belarus were R1a, and that this figure rose to 60% amongst Ashkenazi Levites from this area. This was taken as a signal of the ancient Khazar kingdom, between the Black Sea and Caspian Sea, which converted to Judaism, and whose descendants settled in the Baltic region.

Behar found that the levels of admixture with the European host populations were about 5 to 8% amongst all Ashkenazi except the Dutch, which was over 25%. Admixture populations were likely to be R1a, R1b and I.

For more information on Y chromosome haplogroups see <http://www.isogg.org/tree/index.html>

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Table 7 – Case Study comparison of 37 markers for nine men in ydna group G5 (G SNP = M201, G5 SNP = M377)

		A	B	C	D	E	F	G	H	I
Locus	DYS	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles
1	393	13	13	13	13	13	13	13	13	13
2	390	23	23	23	23	23	23	23	24	23
3	19	15	15	15	15	15	15	15	15	15
4	391	10	10	10	10	10	10	10	10	10
5	385a	13	13	13	13	13	13	13	13	13
6	385b	16	16	16	16	16	16	16	16	15
7	426	11	11	11	11	11	11	11	11	11
8	388	12	12	12	12	12	12	12	12	12
9	439	11	11	11	11	11	11	11	11	12
10	389-1	14	14	14	15	14	14	14	14	14
11	392	11	11	11	11	11	11	11	11	11
12	389-2	32	32	32	33	32	32	32	32	32
13	458	18	18	19	18	18	18	18	18	18
14	459a	8	8	8	8	8	8	8	8	8
15	459b	9	9	9	9	9	9	9	9	9
16	455	11	11	11	11	11	11	11	11	11
17	454	11	11	11	11	11	11	11	11	11
18	447	24	23	24	24	24	24	24	24	24
19	437	16	16	16	16	16	16	16	16	16
20	448	21	21	21	21	21	21	21	21	21
21	449	28	28	28	28	28	28	28	28	28
22	464a	13	13	13	13	13	13	13	13	13

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		A	B	C	D	E	F	G	H	I
Locus	DYS	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles
23	464b	14	14	14	14	14	14	14	14	14
24	464c	15	15	15	15	15	15	15	15	15
25	464d	15	15	15	15	15	15	15	15	15
26	460	10	10	10	10	10	10	10	11	10
	GATA									
27	H4	11	11	11	11	11	11	11	11	11
	YCA									
28	11 a	20	20	20	20	20	20	20	20	20
	YCA									
29	11 b	20	20	20	20	20	20	20	20	20
30	456	17	16	17	17	17	16	17	17	17
31	607	15	15	16	15	16	16	16	16	15
32	576	15	15	15	15	15	15	15	15	15
33	570	16	16	15	17	16	16	16	16	16
34	CDYa	34	34	34	34	34	34	34	34	34
35	CDYb	34	34	35	35	35	35	36	35	35
36	442	12	12	12	12	12	12	12	12	12
37	438	10	10	10	10	10	10	10	10	10

Information available on Ybase and collected by the author

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10. YDNA G5 Case Study -- what do the results mean?

Men's ydna has two sorts of markers, slow and fast. Slow markers are called Single Nucleotide Polymorphisms (SNP's) which denote haplogroup or sub haplogroup membership – those with the same markers will share a common ancestor. Slow markers are given a letter and a number. In the example given, the nine men belong to the very rare and recently discovered G5 group. G is denoted by the SNP M201, whilst the G5 men all share the M377 marker.

Fast markers are called Single Tandem Repeats (STR's) where short units of DNA (alleles) are repeated several times (e.g. 8,9,10 etc) at specific locations which are given numerical identifiers e.g. 393, 390 – the pattern of STR's helps to reveal family branches within the sub-haplogroup - some markers are more stable than others and so a range is given.

Different bodies test for different numbers of STR's – some will only test for smaller numbers like 12 or 25 (which are not so reliable). Here 37 markers are shown – amongst a group of men some of whom have had 67 markers tested. In the future, even greater numbers of markers will be tested, in order to refine the exact nature of a relationship. It should be noted that different bodies test for different markers and these are not always the same or comparable – you should always check if you wish to compare the results from different companies (e.g. at the ybase website).

The 37 markers here show the mutational differences between the nine men in the G5 ydna group. This group is almost exclusively Jewish (a few have ancestors who were likely Jewish), and is thought to descend from a single founder who came to Lithuania somewhere between the ending of the Black Death in the 14th century and the beginning of the 18th century. G5 is a haplogroup that possibly originates in the Fertile Crescent.

Person A and person B share a common great grandfather in the UK. Their ancestor came from the Polish/Lithuanian border region. Person A is thought to represent a typical G5, by the FTDNA G5 group. Person B differs from person A by two mutations at 37 markers (and by three mutations at 67 markers). Normally, three mutations (at 67 markers) is taken as evidence further back than great grandfather, but mutations can arise randomly and may be more likely where fathers are older. In person B's case his father and grandfather were older when the son in question was born. However, both Persons A and B match with another person at 3 mutations away (results not shown) – no connections can

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be made with this person whose immediate ancestors come from Ukraine. It is likely the relationship here IS further back than great grandfather. Because events are random, 3 mutations may represent quite different timescales for different relationships.

Returning to the table, persons A and B are very similar to the other men for 25 markers, but significant differences start to show between 25 and 37 markers. In fact, persons E, F and G have identical profiles to person A at 25 markers. Between 26 and 37 markers, A and B share differences from the others at locations 31 and 35. At points 30 and 35, F and G show differences from E. Crucially, the 67 marker results (not shown) further differentiate the group members, to see who is closer to whom, within the overall family relationship. Note; Persons C to I are all based in the USA. This information comes from the FTDNA G5 group.

11. Which company to use? How does DNA testing work?

Family Tree DNA is recommended by JewishGen, as it specialises in Jewish Genetics, and is run by a board, which is mostly Jewish. Its founder Bennet Greenspan speaks at Jewish Genealogy events. Family Tree DNA is involved in the National Genographic DNA project to test people from all over the globe, run by Spencer Wells, author of “The Journey of Man.” Ftdna will run mtdna and ydna tests for you – see www.familytreedna.com.

Other UK companies that offer mtdna and ydna testing include Oxford Ancestors run by Brian Sykes at Oxford University and EthnoAncestry run by Jim Wilson at Edinburgh University. Oxford Ancestors specialises in Western European ancestry, and tends to offer fewer markers than other companies at a higher price. Although EthnoAncestry specialises in Celtic and Scandinavian backgrounds, it markets some sophisticated tests at reasonable prices, and you can tailor make your markers if you know which ones you want. There are also a range of other companies based in the UK and USA offering similar services. Two companies specialise in autosomal testing, Trace Genetics and DNA Tribes.

Testing is easy, but it is not cheap. However, when you consider how much accumulating certificates and subscribing to on line databases can cost, it is not too large an investment to make. You will need to choose the type of test you require – mtdna (female) low and high resolution, and full genome tests (there is no point just having the low resolution test, you need the high resolution test as well to prove close relationships), and ydna 37 or 67 marker tests for men. You may need to upgrade to 67 later on, if you match with someone reasonably closely at 37. (Note; other companies may only offer e.g. 43 markers).

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The test simply involves using a swab to collect cells from the inside of your cheek. Two samples are taken, to alleviate any problems or errors that could arise. You are given a test tube and packaging in which to return the samples. Results are emailed back to you and you are sent to your own place on the Family Tree DNA website.

In the case of men, you may be part of a Surname grouping or specialist FTDNA group such as;

- Jewish DNA project
- Belarusian Jewish Polesie DNA Project (open to both men and women)

There are also haplogroup specific interest group pages on FTDNA, such as one for the G group. FTDNA results are given on three pages; –

- **Who you are related to**
- **Where your matches' ancestors places of origin were**
- **Your actual DNA results** showing your mutations/markers and haplogroup/ haplotype (subgroup) (where appropriate).

In the case of Mtdna, your results are compared to the Cambridge Reference Sequence (after the British scientist at Cambridge University whose Mtdna was an ubiquitous H), showing where your mutations vary from the norm.

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Sources/Further Reading

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