

H11 Newsletter



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1. FT – DNA mitochondrial (Mt) DNA tree

FT DNA has now provided the Mt-DNA Haplotree on their homepage. Scroll down to the bottom of the homepage and under Community you find a link to this site.

For the H11 mitochondrial line navigate starting at the top working down from L0 to L123456 to L23456 to L2346 to L346 to L34 to L3 to N to R branch and moving to R0. Then expand and choose HV and expanding it choose H and there are 976 branches under H. Go right to the bottom and choose H-T195C! and expand it. Then choose H11 which has 16 branches under it. At this point, I followed my own branch H11a2a1 and will demonstrate as follows:

Choose H11a with 13 branches. The variety of countries at this level is large:

Germany 54, Ireland 34, England 30, USA 27, Sweden 21, Scotland 14, United Kingdom 11, Poland 10, France 8, Finland 8, Canada 7, Norway 6, Italy 5, Czech Republic 4, and Austria 3.

H11a expands and choose H11a2. There are four more branches under H11a2 and expanding gives H11a2a and it has three branches beneath

it. Expanding gives H11a2a1 which is my haplogroup with countries being:

USA 14, England 14, Ireland 10, Scotland 10, United Kingdom 7, Germany 4, Canada 3, Northern Ireland 2, and Wales 1.

This, one would surmise, is a predominantly British Isles group.

My maternal grandmother was born in Birmingham, England and her mother was also said to be born in Birmingham, England. My closest matches tend to be Northern Ireland or South-west Scotland (namely Argyllshire or Ayrshire). I have communicated with several of the USA members (four to be exact) of this group and they were descendant of a group from County Antrim who traveled with the Rev William Martin in 1772 to the Carolina Colony. Some members of this group were descendant of Planters from Argyllshire/Ayrshire sent to Northern Ireland by Cromwell in the 1600s. The descendants in the United States tend to refer to this group as Scot-Irish.

The nomenclature for my line is H11a2a1.

The results for country of origin given above are interesting - they total 65 individuals within the FT DNA database that have agreed to have their results used in a research project. Of that group of 65, there are only 17 in this research project (26%) so I must admit that I am perhaps not really adding much to knowledge of this haplogroup with such a small representation in the study.

Of the group in the H11 project there are:

USA 9, England 3, Ireland 2, Scotland 0, United Kingdom 1, Germany 0, Canada 2, Northern Ireland 0, and Wales 0.

I happen to know 2 of the members from England are my brother and myself. All of these individuals are listed in my matches one might think and indeed I have 105 matches between 0 and 3 steps away. I consider 3 steps away to not even be meaningful looking at

mitochondrial DNA and actually even 2 steps away does not really entice me to look at the match. I have 1 at a genetic distance of 0 and 23 at a genetic distance of 1. I had not really thought to look at this before. All of the 105 matches belong to H11a2a1 which means to me that only 62% have agreed to have their results used in a research project. Of the 23 that are a genetic distance of 1, 20 have taken the Family Finder Test. None of these 20 individuals match me on Family Finder.

The 23 matches to me are a genetic distance of 1 meaning that our common ancestor could be a thousand years ago or more. That does tell me that although the number of people who agree to be part of the research project is only 62%; there isn't likely anyone that is related to me in a reasonable time frame in this group of matches.

Looking at DNA Painter there are 13 individuals who share a length of DNA on Chromosome 23 with me. Of this group of 13 only two share greater than 15 cM on Chromosome 23 hence I do not really look at this particular set of matches unless they are sharing larger amounts on other chromosomes.

Other members of the group may find more success with their H11 subclade.

2. FT DNA Project:

There are now 317 members in our H11 project. Full sequence results are completed on 277 members of the group. Interestingly 220 members of this group have also done Family Finder. Unfortunately it is not possible to visually look at the Family Finder results as that would compromise the privacy of individuals. However, you can look at your matches in Family Finder.

3. Project Statistics (yDNA statistics removed):

Combined GEDCOMs Uploaded 49

DISTINCT mtDNA Haplogroups	16
Family Finder	220
Genographic 2.0 Transfers	20
Maternal Ancestor Information	269
mtDNA	288
mtDNA Full Sequence	277
mtDNA Plus	285
mtDNA Subgroups	22
Total Members	317
Unreturned Kits	12

4. The latest release of the phylotree used by FT DNA was dated 18 Feb 2016:

H11 breakdown in the PhyloTree mt:

H11	T8448C G13759A T16311C!
H11a	T961g A16293G
H11a1	C8898T C16278T!
H11a2	A14587G (T16092C)
H11a2a	T16140C
H11a2a1	A3145G
H11a2a2	G5585A T15670C A16265G
H11a2a3	C9521T
H11a3	T16243C
H11a4	5899.XC C16111T
H11a5	C15040T
H11a6	G1719A G5979A A16525G
H11a7	T152C!
H11a8	C9911T
H11a8	T14325C
H11b	T13572C
H11b1	T7645C

Within the study group we have members in every sub-haplogroup except H11a5 (and it can be seen in the chart above that the mutation C15040T marks this subgrouping). I have written to Dr van Oven several times but he is likely too busy to respond. H11 is a very small subclade of H. In time, he may have time to review H11 once again as I have created more subclades within the breakdown he currently he has for the H11 project. I will not do any of this new expansion in this newsletter but hope to look at that for the next issue when, hopefully,

more members of the project have given me permission to look at their presumed/known country of origin.

<http://www.phylotree.org/tree/R0.htm> *

*van Oven M, Kayser M. 2009. Updated comprehensive phylogenetic tree of global human mitochondrial DNA variation. *Hum Mutat* 30(2):E386-E394. <http://www.phylotree.org>.

[doi:10.1002/humu.20921](https://doi.org/10.1002/humu.20921)

5. Changes in how a project administrator can view your results

FT DNA has upgraded their access to accounts so that the default is Group Access only. If you wish to have your results included in the project then you must grant Limited Access to the Administrator.

Any submissions to this newsletter can be submitted to Elizabeth Kipp (kippeeb@rogers.com).