# H11 Newsletter

**Background:**

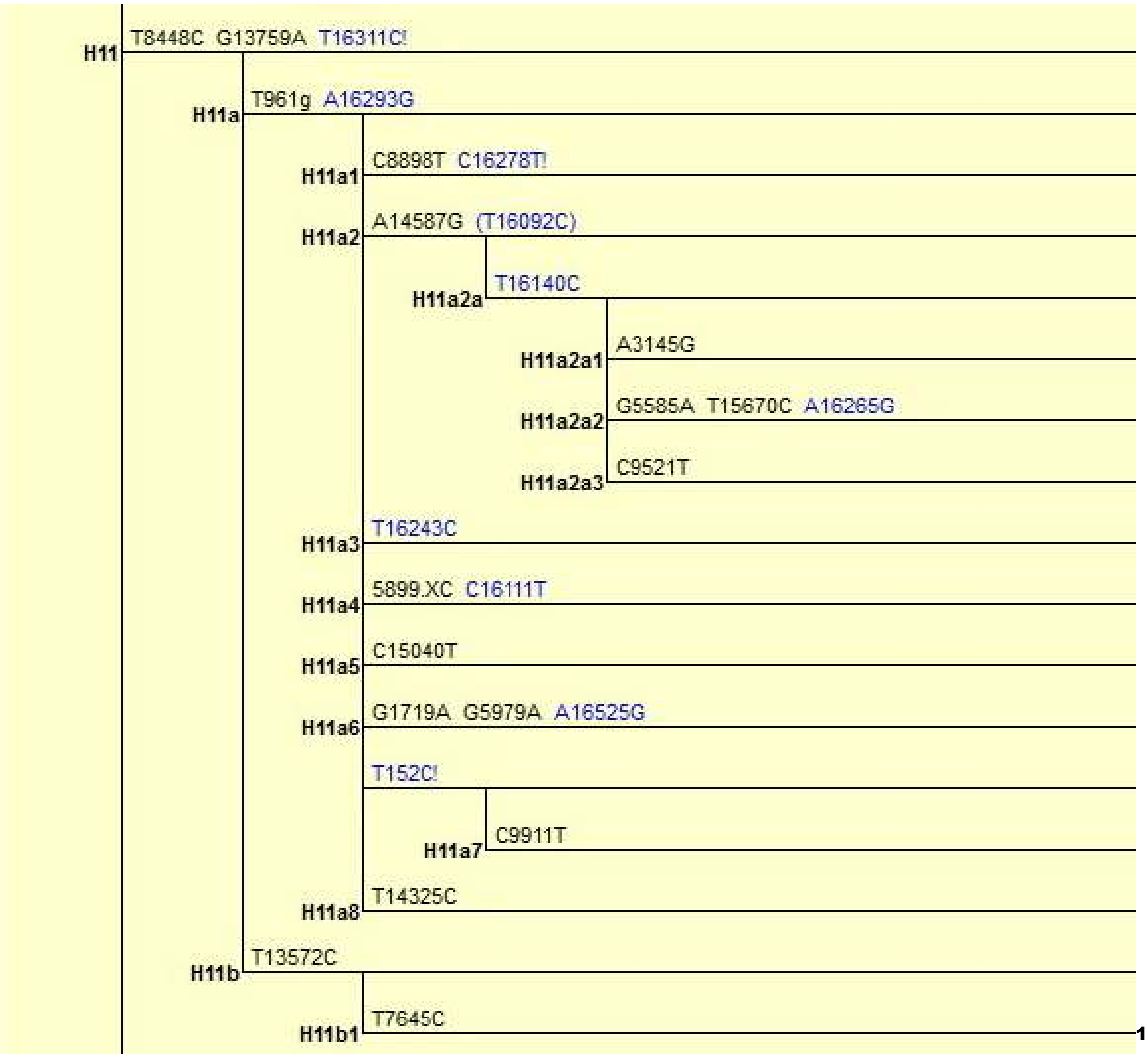
**This first issue is meant to just let me try out this new idea. I like the idea; I already have two newsletters for my two one name studies and find them very useful to just get my ideas out of my head and onto paper and share them with like-minded people.**

**I have now gone through every project in the study and extracted whatever "resting spot" information is available. If there are any changes from what is currently in your study I would appreciate it if you would now let me know as well as changing it within your project as our project is now over 200 members (kippeeb@rogers.com ).**

**I first tested my mtDNA in 2006 and H11 had very little information attached to it. The comment at that time was made that the haplogroup was approximately 50,000 years old and had likely wintered at Ukraina Ice Refuge during the Last Glacial Maximum 15,000 to 20,000 years ago. Placing this group in that particular area is rather interesting given the migration routes that appear to follow once the ice retreated. A paper published by Dr Behar does have a much shorter time frame for the age of the haplogroup and I am still reviewing it.**

**The information on H11 has increased in terms of the subgroups that are now part of this umbrella subhaplogroup of haplogroup H. We are the older sister of H haplogroup but definitely only a tiny portion of that haplogroup and estimated at 1 to 2 % of H.**

**The Phylo Tree was originally produced by Dr Kayser M van Oven in 2009 and is currently in its 17th Build as of the 18th of February 2016. Members of this study belong to every named subclade with the exception of H11a5.**



[1]

**There are some interesting mutations that are shared by members of the group and will perhaps form a new subclade at the next build of the Phylo Tree.**

**Resting Areas:**

**Resting areas are the furtherest back known locations of our female ancestor. Many of the members of the project have been able to add this interesting information.**

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[1] http://www.phylotree.org/tree/R0.htm , accessed 5 Feb 2017

## Haplogroup Subclades:

**H11b1 has twelve members and five have a particular mutation which will perhaps lead to a further defining of this particular subclade.**

**Locations for H11b1 (4 members do not know the location of their ancestor except in North America):**

**Eastern Europe – 4**

**Central Europe – 2**

**Scandinavia – 1**

**North West Europe – 1**

**H11b has two members and both have an extra mutation that could also lead to a further defining of this group that lacks the defining mutation of T7645C. Neither can trace their ancestor outside of North America**

**H11a8 has four members with the defining mutation of T16368C.**

**Location for 2 of the 4 members is Ireland and the remaining two are unable to trace their line out of North America.**

**H11a7 has two members with the defining mutation C9911T. They both share two further mutations which may be useful in the future with this haplogroup.**

**Location for both traces back to Northwestern Europe (British Isles).**

**H11a6 has just one member with the defining mutations A16525G, G1719A and C9911T.**

**H11a4 has five members with the defining mutations C16111T and 5899.1C.**

**Location for all four traces back to the British Isles and Scandinavia.**

**H11a3 has two members with the defining mutation T16243C.**

**Location for one member tracing back to the British Isles and the second is unable to trace out of North America.**

**H11a2 with mutation T16092C but lacking T16140C has seven members. I find this group to not be as cohesive as other groups and suspect it will be divided up differently in the future (the distinction is made by FT DNA).**

**Location for 3 members tracing back to Scandinavia, 2 to Eastern Europe, 1 to Central Europe, 1 to Southern Europe and 1 to northwestern Europe.**

**H11a2a3 has six members with the defining mutations T16092C, T16140C, C9521T and A14587G. Two of the members have a mutation which may further subdivide this group.**

**Location for just two members tracing back out of North America. One traces back to Scandinavia and one to northwestern Europe.**

**H11a2a2 has fourteen members with the defining mutations T16092C, T16140C, A16265G, G5585A, T12235C, and T15670C.**

**Location for ten members of this group tracing back to Eastern Europe, one member tracing back to Central Europe and one member tracing back to Scandinavia.**

**H11a2a1 has fifteen members with the defining mutations T16092C, T16140C, A3145G, and A14587G. Three members of this group have a defining mutation but two of them are siblings (one includes me) so is possibly not significant.**

**Location for six members is northwestern Europe (all British Isles), one member is from Eastern Europe and the other eight members are unable to trace their line out of North America.**

**H11a2a has three members with defining mutations T16092C, T16140C, and A14587G.**

**Location for one member is Scandinavia and the other two are unable to trace their line out of North America.**

**H11a2 has eight members with defining mutation A14587G. I find this group to also be very weakly put together under this classification. Two of the members share a mutation that could put them into a new subclade.**

**Location for 2 members is northwestern Europe, two members are from Scandinavia, 1 is from southern Europe and three members are unable to trace their line out of North America.**

**H11a1 has 47 members with defining mutations C16278T and C8898T. Several members of the group share further mutations in common and it may be that at the next release of a new phylo tree there will be further subdivisions of this group.**

**Location for 16 members is eastern Europe, for 15 members it is Scandinavia, for 5 members it is northwestern Europe, for 4 members it is central Europe and one member it is southern Europe. Six members are unable to trace their line out of North America.**

**H11a includes members who have not done further testing and can be a little confusing because of that. Looking only at members with a full genetic scan, there are 53 members in this group with defining mutations T961G and T8448C. There are several groups that have shared mutations that may lead to further subdivision of this group.**

**Location for 14 members is northwestern Europe, for 10 members it is Scandinavia, 6 members it is central Europe, 5 members it is eastern Europe and 1 member it is southern Europe. Seventeen members are unable to trace their line out of North America.**

**H11 also includes members who have not done further testing. Looking only at members with a full genetic scan, there are 13 members in this group at the top of the H11 haplogroup with no further defining mutations than T8448C.**

**Location for 4 members is Scandinavia, for 3 members it is northwestern Europe and for 1 member it is central Europe. Several of these members share mutations so there could be a further subdivision different from H11a and H11b perhaps in the future. Five members are unable to trace their line out of North America.**

**Overall location irrespective of subclade:**

**Central Europe – 18 members**

**Eastern Europe – 37 members**

**Northwestern Europe – 51 members**

**Southern Europe – 5 members**

**Scandinavia – 41 members**

**Not specified – 57 members**

**There are ten members only who have not completed the full genetic scan.**

**Any submissions to this newsletter can be submitted to Elizabeth Kipp (kippeeb@rogers.com). I am considering publishing this twice a year (February and August) or four times per year (February, May, August and November. By May I will have made my decision.**