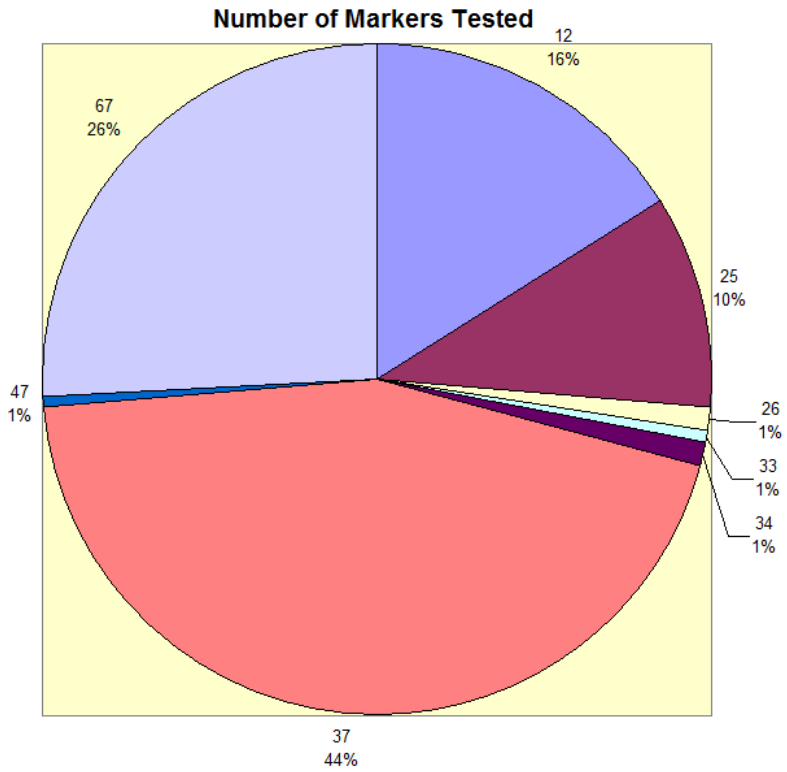
Exploring R1b Wrights: 14 May 2010

R1b is the most common haplogroup of Europeans, and Wright is one of the most common surnames in the United Kingdom, so it makes sense that most Wrights would fall within the R1b haplogroup. It becomes a challenge to sort the lines into groups that are helpful for genealogical purposes.

Today, there are a total of 186 participants who fall within the R1b haplogroup; this is about 60% of the total number of Wright participants in our Y-DNA project.

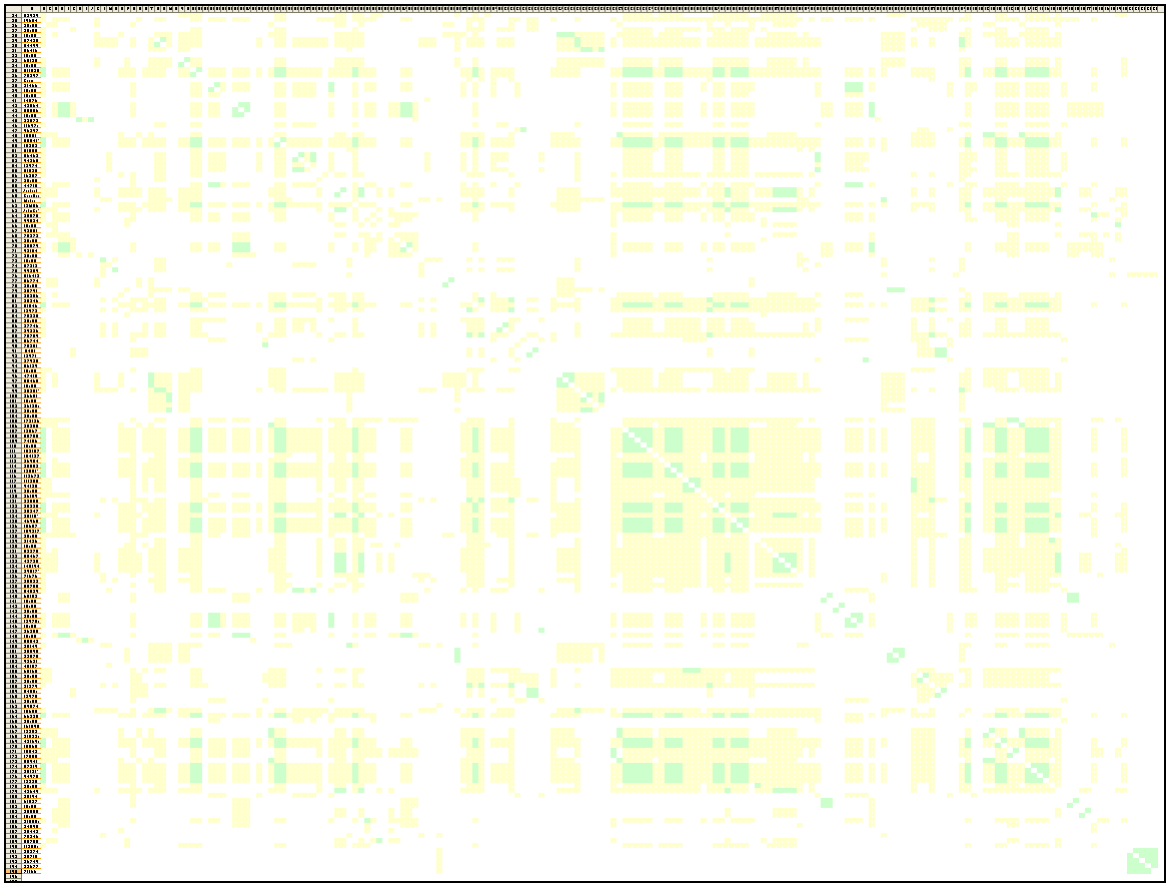
The number of markers tested by the R1b participants is shown in this graph:



There is a project run by Charles Kerchner to determine the modal haplotype (the most common value) at each marker for R1b males with any surname. This haplotype represents the "founder" or common ancestor of all R1b males. This R1b modal haplotype turns out to be exactly the same as the 12 marker R1b Wright modal haplotype (which means that Wrights represent the broad group of all European males):

Marker >>	DYS-393	DYS-390	DYS-19	DYS-391	DYS-385-a	DYS-385-b	DYS-426	DYS-388	DYS-439	DYS-389-1	DYS-392	DYS-389-2
R1b Modal	13	24	14	11	11	14	12	12	12	13	13	29
Wright R1b Modal	13	24	14	11	11	14	12	12	12	13	13	29

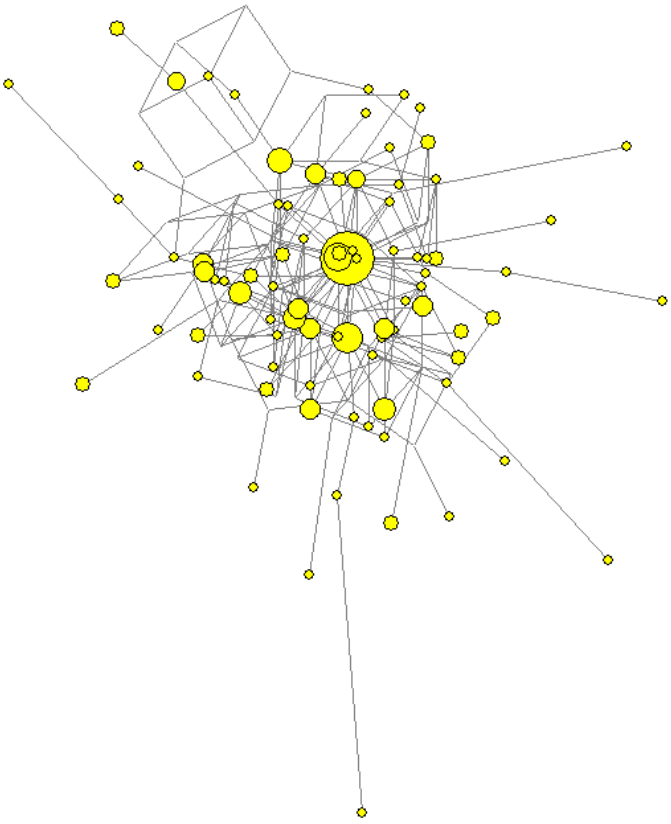
Looking more closely at the 12 marker R1b Wrights, we do see clusters and this allows some separation into individual family lines – the smaller branches off the R1b branch. The following table is a genetic distance chart comparing all the 186 participants to one another. To fit, this is shrunk down to a microscopic (unreadable) level, but the point is that anyplace you can see color, especially green, there is a family line cluster.



One can use genetic distance to calculate the time-to-most-recent-common ancestor (TMRCA). This calculation uses several assumptions, including the rate at which mutations or changes occur, and the number of years in a generation. There are also assumptions that mutations tend to occur one step at a time and that they tend not to step one way and then back again – although they could. Some rough rules-of-thumb are to expect about 1 mutation to occur in about every 500 chances, and that there is an average of 30 years per generation.

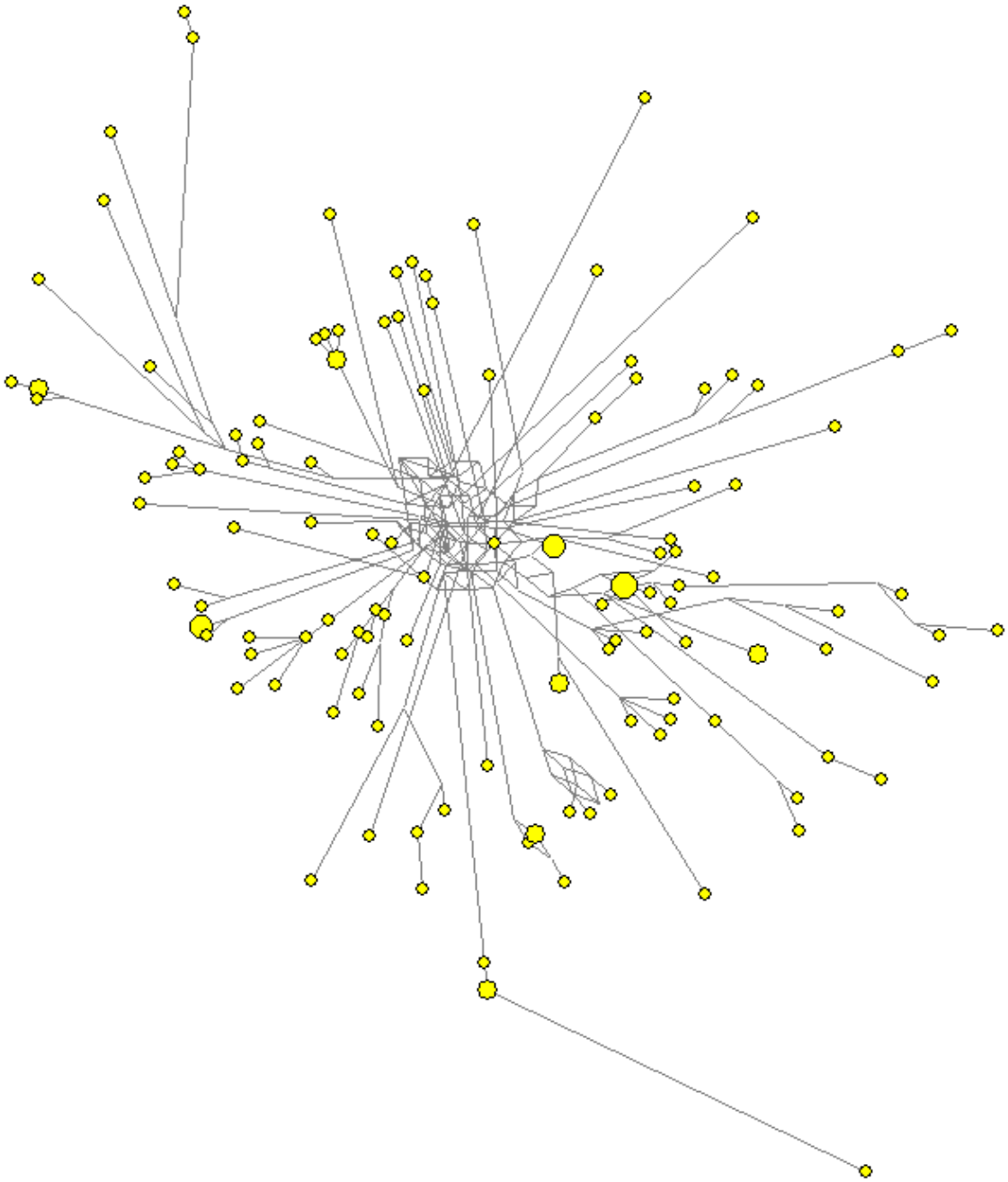
With 12 markers or genes, there are 12 opportunities for a spontaneous change to occur each generation. That means for 500 chances to take place, there would be about 500/12 or 42 generations = 1260 years. But, it turns out that each marker demonstrates a different rate of mutation – some are faster, and some are slower. It is more accurate to calculate the rate considering which markers were tested. There is a program written by Dean McGee call the Y-Utility that provides that calculation. Using this utility, the range was 450 to 7350 years from our 12 marker Y-DNA participants to the theoretical common ancestor. This is a very broad range and anything over 944 years ago precedes the use of surnames, so is not very useful for genealogical studies.

A better way to visualize the clusters is by creating a phylogenetic tree. This is a computer-generated hypothesis that looks at the steps each family line would take from the common or modal value. Assume there is one common ancestor to all R1b Wrights. Over time, small changes or mutations occur – usually one at a time in a given generation. That moves that family away from that center common ancestor. Since mutations occur at random, the movement away from the center can occur in any direction. People describe the pattern created as a "starburst" or "snowflake" pattern. It looks like a dandelion that has gone to seed – a central area with radiating lines outward. This is three-dimensional, so it is hard to show on a two dimensional surface, but looks like this for the 12 marker R1b Wrights:



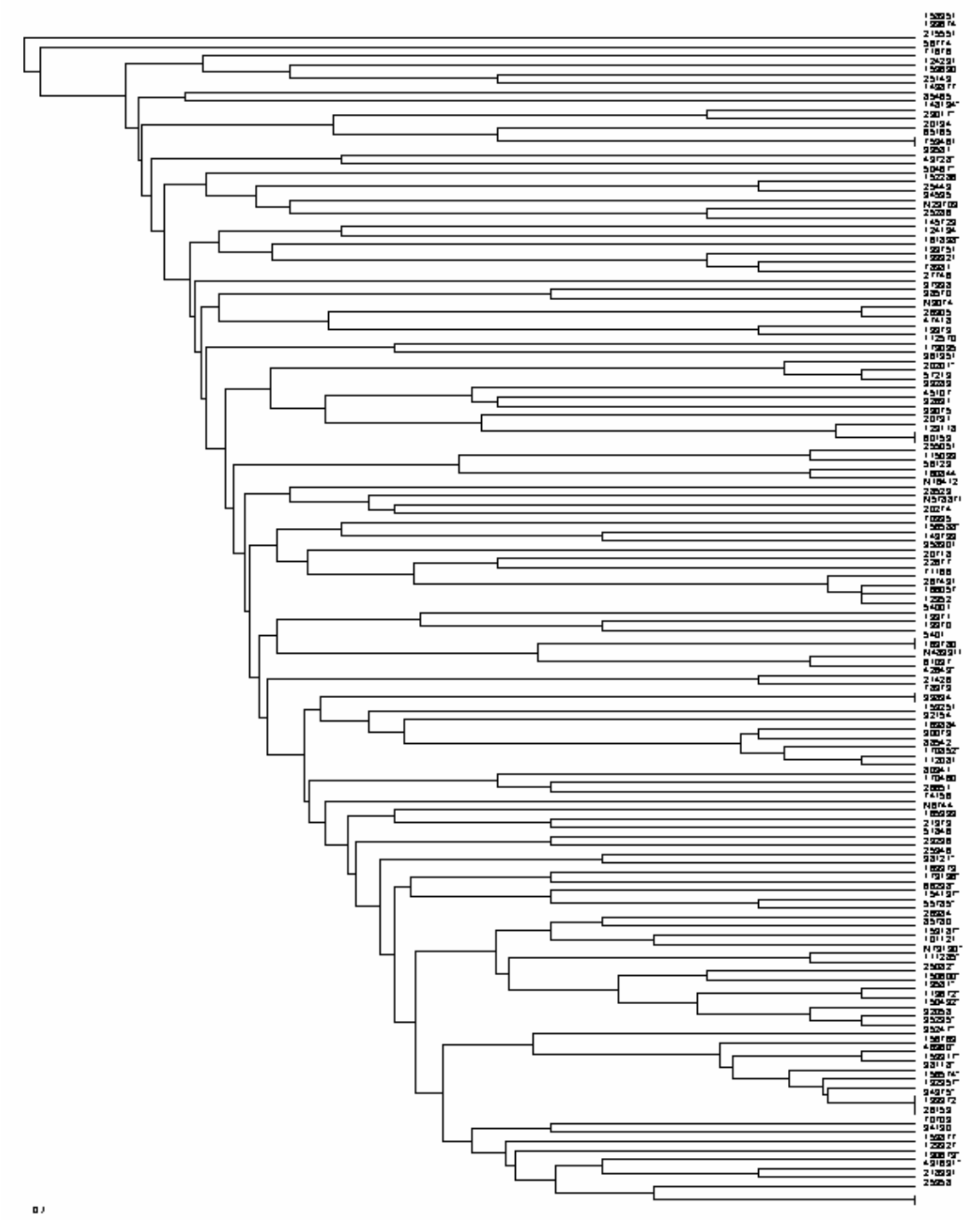
The largest yellow dot represents the most common haplotype, and dot size is proportionate to the number of participants that match that particular pattern. You can see that most are pretty close to that center dot, which is why it is so hard to tell lines apart when only testing 12 markers. Wrights within the R1b haplogroup would benefit from testing additional markers, and most of our participants have done that.

We have 132 participants who have tested 37 or more markers. This helps to spread the family lines apart to determine differences between them. This can be shown in the following phylogenetic tree:



Now you can see family lines emerging – and that there are a lot of them! Here is a link to an enlarged view with the kit numbers included. This may be helpful in trying to determine which lines are related, or which actually branched off from antecedent lines.

Another way to look at this is to use a program that generates a tree like the one we see at FamilyTreeDNA on your haplogroup page – this is called a phylogram. This can be created using another computer program. For the 37+ marker participants, one theoretical model (a guess made by the computer running through various combinations and likely branch patterns) is shown below. Here is a link to a pdf file you can magnify to find your test kit.



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