# DNA for your ONS: Tips and Techniques

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## Genetic Groups

In the October 2013 Journal the topic of Genetic Groups for your DNA Project was introduced. As your project grows, each Genetic Group you establish will usually end up being comprised of participants from multiple family trees of the surnames in your ONS. This represents trees that are related in the time period between the adoption of surnames and the progenitors of the documented trees. The number of groups and the number of trees are a function of the frequency of your ONS surname, how it ramified, and the number of origins, as well as events such as illegitimacy.

In some cases a group of trees in a Genetic Group may share a mutation, such as all the Meates of Ireland sharing a mutation as compared to the result for the progenitor of the surname. This mutation indicates the Meates of Ireland all share a common ancestor between the progenitor of the surname and the start of the documented family trees.

When your project is in its infancy, and you are still building up participants, it is often difficult to determine who to group in a Genetic Group. This is especially true with haplogroup R1b. One step that is helpful is to validate each tree. This means to test a distant direct line male, who comes off the tree as close to the progenitor of the tree as possible. For example, if the progenitor of the tree had two sons, test a descendant from each son. This will validate the genealogy research, since the two results should match or be close.

If the results of the two distant direct line males are a close match, and not an exact match — there is no way to tell which man has the mutation(s), unless you have other trees that match, or you do further testing. If you reference the chart in the January 2011 Journal, on page 13 [www.one-name.org/journal/pdfs/vol10-9.pdf#page=13], you will see that by testing a descendant of a third son of the tree progenitor, the DNA Project was able to determine which of the two men had mutations, and were able to determine the ancestral result for the progenitor of the tree.

In looking at this table of results, I often get questions about the mutation for the result of a descendant of the son Jacob, the first line on the chart. The mutation occurred with marker DYS 464, which is a multi-copy marker. Most people have four, and if you have more than four copies, Family Tree DNA will report the results for each copy.

This marker is scored differently. The results are presented in order of low to high, not the actual order. So for these three men we have:

15 15 16 17
15 15 17 18
15 15 17 18

It is clear that the last two men match. In comparing the first man to the other result, the 16 is the mutation, since the other results both have two 15s and one 17. If you want to know the actual order of the results for the marker, you can order the 464x test under Advanced Tests.

Once you know the ancestral result for the tree progenitor, as shown in the above referenced example, this helps in grouping R1b results, as you compare the results of the tree progenitors, since you are eliminating some or all mutations from consideration.

With haplogroup R1b, the challenge of determining relatedness in a genealogical time frame and placing the people in Genetic Groups becomes more difficult the higher the frequency of your surname(s). A more frequent surname usually indicates more origins, and therefore usually more different R1b results.

With haplogroup R1b, it is often helpful to wait to put a participant in a Genetic Group, until you have at least two validated trees that match. The reason for this is that you can have what appears to be a match, yet they are related prior to the adoption of surnames. Haplogroup R1b comprises over 40% of Europe, and many men had the same or a close Y-DNA result at the time of adoption of surnames, and adopted different surnames. They belong to the same haplogroup, or major population group, and are related at some point, so their results tend to be close. Sometimes two men who are in the same haplogroup and related prior to the adoption of surnames, both coincidentally adopted your ONS surname, yet come from different surname origins.

The second factor impacting R1b results is convergence. An example is where there were two 37 marker results at the time of adoption of surnames which had a genetic distance of three, and over time, mutated so they are now a 36/37 match.

To handle the haplogroup R1b participants where you are waiting to find a participant for validation or participants from another tree to match, you can manage the situation by establishing some special Genetic Groups, such as:

Genetic Group 990 Needs Validation
Genetic Group 991 Needs a Match to another Tree

The problem with interpreting and putting R1b results into Genetic Groups can be addressed through various approaches, including validating trees, waiting for two or more trees to match, testing more markers, determining the ancestral result for each tree, and combining the results with surname distribution mapping and early recordings. The latter approach is an area to address when you have built up a sizable pool of participants for your ONS.

## Want to Get Started?

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