2020 December 01
Redacted: 2024 July 23

BigY 700 Test Results Analysis For An O'Conor Don Descendant

I. Summary

Your previous Y-DNA test results from 2006 showed you were R1b-M222+, that is, you belong on the R1b-M222 branch, or clade, of the human male Y-Haplotree. This clade probably arose more than 2500 years ago and appears to be the genetic signature of many of the kindred groups in Northwest Ireland, which is in keeping with the known genealogy of the O'Conor Don. As you may know, a paper published by Trinity College (*A Y-Chromosome Signature of Hegemony in Gaelic Ireland*, Laoise T. Moore, Brian McEvoy, Eleanor Cape, Katharine Simms, Daniel G. Bradley) proposed a link between a large cluster of men who shared a common group of Y chromosome mutations (subsequently identified as the R1b-M222 clade) and surnames that are associated with the Uí Néill in the medieval genealogies. This was further discussed by Dr. Catherine Swift and Dr. Bart Jaski in separate essays in a collection of essays in honor of Dr. Katherine Simms (*Princes, prelates and poets in medieval Ireland: essays in honour of Katharine Simms*, 2013). Dr. Jaski mentions in his essay that some of the surnames included in the original Trinity College paper that fell into the cluster are Uí Briúin surnames such as O'Connor, O'Reilly, O'Rourke, and McGovern.

Around the time that these two essays were published, advances in the genetic sequencing of the Y chromosome resulted in the discovery of new mutations which subdivided the R1b-M222 clade into a number of distinct subclades. Often some of these subclades (distinguished by newly discovered Y chromosome mutations) had specific surnames in them that were historically linked together into kindred groups. One of these mutations is called A259 and it was observed in a number of genealogy mailing lists that this mutation occurred in men bearing surnames from the province of Connacht; specifically, to surnames which are associated with the Uí Briúin in medieval genealogies.

The meaning of all these mutation and clade names will be discussed in the appendix. What is important to know is that your new BigY 700 test utilizes an even more advanced technology that produces results that are significantly refined from your previous results and even from the results mentioned above. The technology in this test verifies

every known subclade of the R1b-M222 clade that an individual might belong to. In your specific case you follow the trend seen in men with origins in Northwest Ireland and Uí Briúin surnames since you also belong to the R1b-A259 subclade of the R1b-M222 clade. More specifically, your BigY 700 test results show that you are R1b-A21774+, that is, you are a member of the R1b-A21774 clade of the Y-Haplotree. This clade was formed by a descendant of the original R1b-M222 ancestor, so it is younger than or downstream of R1b-M222. The sequence of clades that leads from R1b-M222 to R1b-A21774 is as follows: R1b-M222 > R1b-S658 > R1b-DF104 > R1b-DF105 > R1b-A18726 > R1b-A259 > R1b-BY18120 > R1b-BY18115 > R1b-A21774.

What is significant about your new test result is that the R1b-A21774 clade is a subclade of the R1b-BY18115 clade that has been identified or associated with the Dál Cuinn, Uí Briúin Aí, Síl Muiredaig, Ó Conchobair sept. This identification was performed by using modern surnames in combination with the Y-DNA test results and correlating their relationships with the traditional Irish genealogies and annals. Most of the men who are part of the R1b-BY18115 clade have either an O'Conor, McDermott, or McManus surname, or a variant thereof.

II. Y-DNA And The Traditional Genealogies

It is unlikely that all the R1b-M222 and R1b-S658 clades will be clearly identified with a specific clan from the traditional genealogies due to their age and the uncertainty of the records. It is also currently uncertain if the individuals in the earliest genealogies actually existed. Nevertheless, it is possible to make some correlations between some of the subclades of the R1b-M222 clade and the medieval genealogies. For example, the current data makes it feasible to propose a mapping as shown below:

1. R1b-DF104 - Dál Cuinn
2. R1b-DF105 – Clanda Eóchada Muigmedúin
3. R1b-A18726 – Clanda Duach Galaig
4. R1b-A259 – Clanda Eógain Sríab
5. R1b-BY18120 – Clanda Indrechtaig
6. R1b-BY18115 – Uí Conchobair

These are our working hypotheses based on the goal of synchronizing the traditional genealogies with the Y-DNA data that is currently available. The data supporting an association with the more recent clades is stronger than that for the earlier clades. For example, we see men with Uí Bríuin surnames showing up in various subclades of the R1b-A259 clade:

- Uí Briúin Bréifne: O'Rourke, O'Reilly, Ford, McGovern
- Uí Briúin Seóla: O'Flaherty, McDonough, McHugh, O'Halloran
- Uí Bríuin Aí: O'Connor/O'Conor, McManus, McDermott, O'Flanagan

In comparison, some of the surnames associated with the Uí Néill often show up in subclades parallel to R1b-A18726 under the R1b-DF105 clade. The R1b-DF85 subclade contains large clusters of Cenél Conaill surnames and the R1b-S588 subclade contains significant clusters of Cenél nEógain surnames. Each of these subclades contains men who have undergone advanced Y-DNA testing. The parallel nature of these lineages can be appreciated by listing the sequence of subclades for each of them:

- R1b-DF105 > R1b-A18726 > **R1b-A259**: Surnames of possible Uí Briúin origin.
- R1b-DF105 > R1b-ZZ87 > **R1b-DF85**: Surnames of possible Cenél Conaill origin.
- R1b-DF105 > R1b-ZZ87 > **R1b-S588**: Surnames of possible Cenél nEógain origin.

To be absolutely clear, we are not saying that the putative progenitor of a particular group had the corresponding Y chromosome mutation occur **in him**; instead we are saying his descendants seem to have the indicated Y chromosome mutation. In other words, while not all members in a particular Y-Haplogroup clade are descended from the associated progenitor, all descendants of the progenitor are members in the clade.

Unfortunately, the formation of a clade by a mutation of the Y chromosome did not necessarily correspond with the progenitor that was selected as the founder of a particular *cland* by his descendants. So, for example, it is possible that not all R1b-DF104 descendants are Dál Cuinn, but all Dál Cuinn descendants are R1b-DF104+, that is, members in the R1b-DF104 clade.

This means that the man named as Cond Cétchathach for centuries must have had the DF104 mutation in his Y chromosome, whether it occurred in him or one of his patrilineal forefathers; and **all** of his patrilineal descendants have inherited this mutation. It is very possible that his brothers and patrilineal cousins also had this mutation which they passed on to their patrilineal descendants. So again, while all patrilineal descendants

of Cond Cétchathach must be R1b-DF104+, not all R1b-DF104+ men are necessarily his patrilineal descendants. They could be from nephew and cousin lines.

III. R1b-BY18115 Haplotree

Figure III-1 shows the R1b-BY18115 section of the Y-Haplotree based on publicly known data. Each brown rectangle is a called a phylogenetic node and represents a mutation or group of mutations that caused a new clade on the Y-Haplotree to be formed. Each phylogenetic node is comprised of the Y chromosome mutations that define the new clade. Ideally, each phylogenetic node would consist of a single Y chromosome mutation.

However, the available Y-DNA data is limited to those men who have voluntarily tested and does not represent every man who has ever lived. So the Y-Haplotree cannot represent all branches, but only those branches we have data for. That is why the Y-Haplotree is constantly growing as more men test and more branches are discovered.

Further, some lines do not have sons to propagate that line's Y-DNA sequence. There is either no issue at all, or there were only daughters, who do not carry the Y chromosome. So these lines either die out or daughter out. As a result, there is no way to test for these lines and any clades they represented.

All of this is why some phylogenetic nodes have multiple mutations that define them. We just have not discovered any branching lines yet that would allow us to split the phylogenetic node, or such lines no longer exist. As a result, rather than encompassing a single generation of one man who had a Y chromosome mutation, these multiple mutation phylogenetic nodes encapsulate multiple generations; not only of men who had a Y chromosome mutation, but also of the generations in between that had no mutations.

IV. R1b-BY18115 Cladogram

When we add individuals/men to the Y-Haplotree, it becomes a Cladogram, as exemplified in Figure IV-1. Your position on the Cladogram is indicated by the red box. **Now** we can start analyzing modern surnames and their Y-DNA genetic connections and compare that to the traditional genealogies and texts. In the Cladogram below, there are 5 men with non Uí Conchobair related surnames: Snipes, Wilson, Stagpoole, Stack, and Johnson. These men are referred to as likely SCEs (Surname Change Events); that is, men whose surname was changed from the ancestral surname to some other surname. This may arise for various reasons such as adoption, fosterage, deliberate name change, etc.

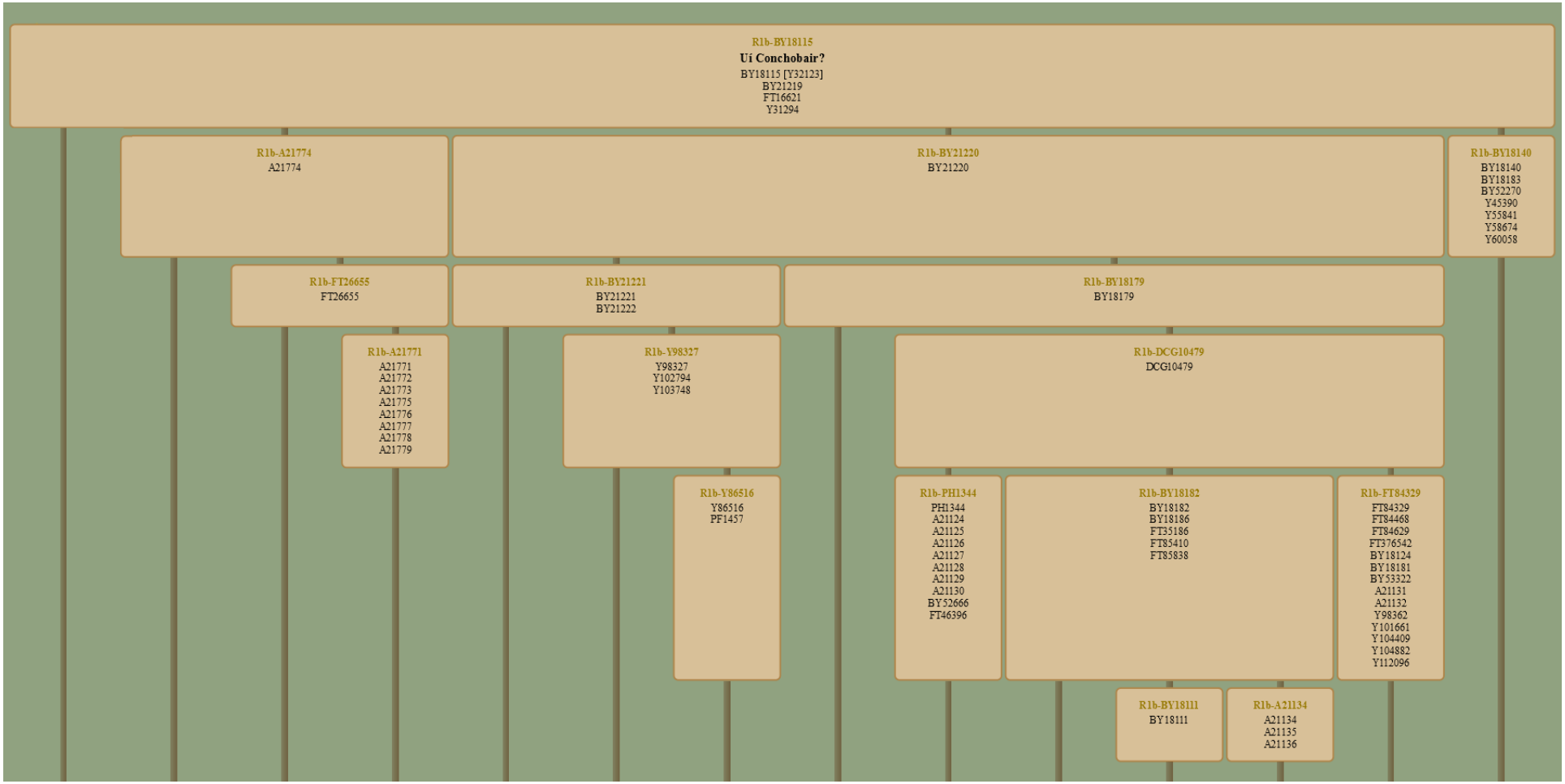

Figure III-1. Rib-BY18115 Y-Haplotree

[https://genelach.org/R1b-BY18115/]

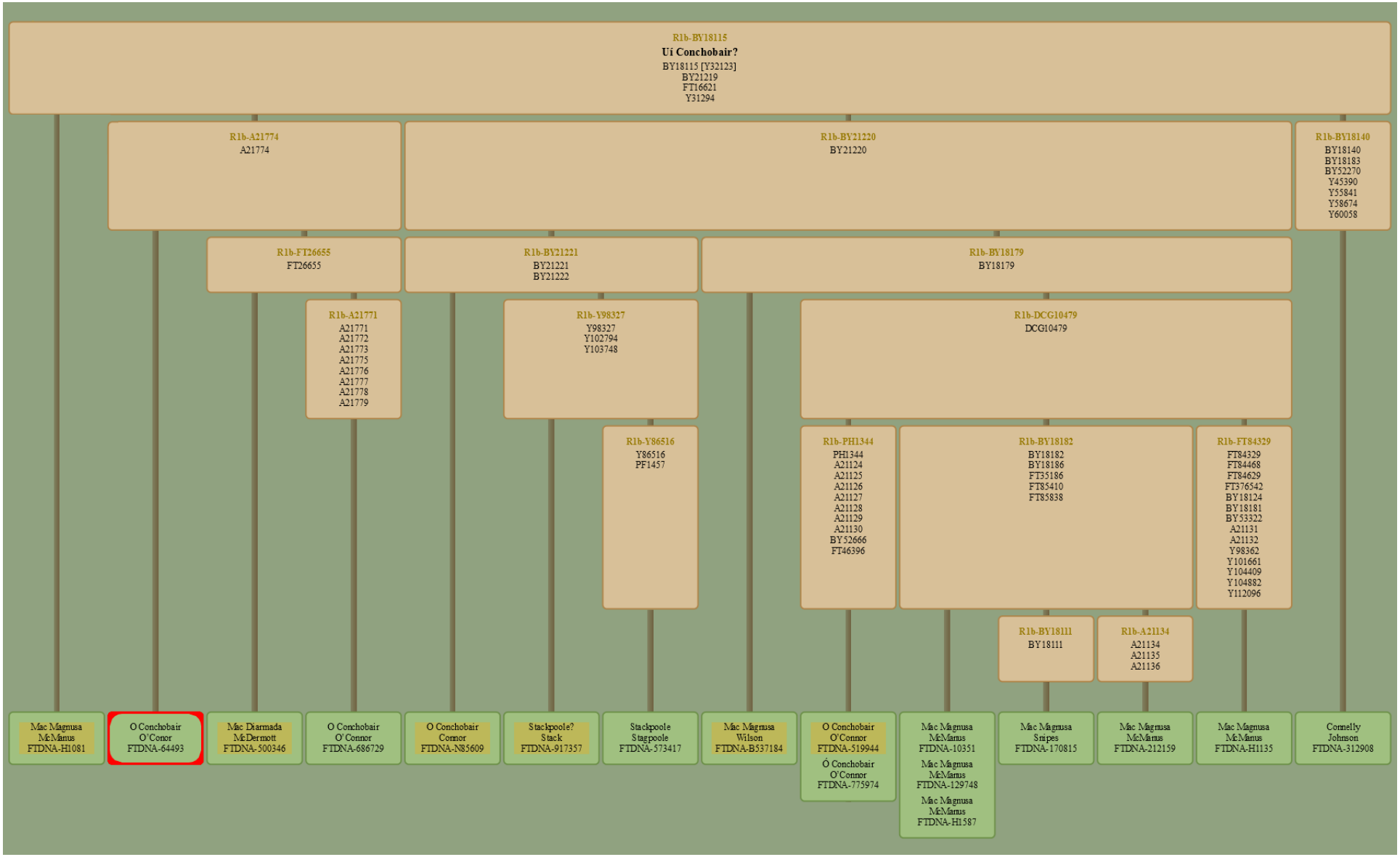

Figure IV-1. Rib-BY18115 Cladogram

[https://genelach.org/R1b-BY18115/]

The Snipes gentleman had traced his genealogy to a McManus ancestor. His Y-DNA results completely corroborate that finding, based on all the surrounding McManus surnames. The Wilson gentleman is similar although not as definite in his research as the Snipes gentleman. The Stagpoole and Stack gentlemen share a common ancestor and original surname: Stackpoole. The Y-DNA results clearly indicate the common ancestor of these men was an Uí Conchobair scion, again, based on the preponderance of the surrounding surnames. Stackpoole is, of course, one of the known Norman Viking invader surnames. How this SCE happened we will probably never know.

The fifth man is a Johnson whose research indicates his MDKA (Most Distant Known Ancestor) was a Connelly. How accurate his research is remains uncertain. It is possible his ancestral surname was originally Ó Conchobair. Regardless, the Y-DNA suggests his family came from an early split from the main Uí Conchobair line. The rest of the men all have definite Uí Conchobair surnames.

Figure IV-2 is a table of the early Uí Conchobair genealogies compiled by Dr. Bart Jaski in his work *Genealogical Tables Of Medieval Irish Royal Dynasties*. Based on this genealogy, we know the Mac Magnusa line split from your Ó Conchobair line after Tairdelbach Már Ó Conchobair (d. 1156 AD) with his sons Magnus and Cathal Crobderg. Apparently the Mac Magnusa surname was not adopted until circa the 14th century AD, another century or so after the split. It would not be unreasonable to think that some branches retained the Ó Conchobair surname rather than adopt the Mac Magnusa surname. So it is not surprising to see the Ó Conchobair surname appear under the R1b-BY21220 clade, which initially appears to be the descendants of Magnus. Again, we cannot say at this point whether the BY21220 mutation occurred in Magnus himself, or one of his early descendants.

The same uncertainty applies to your R1b-A21774 clade. From your genealogy, it initially appears that it represents the descendants of Cathal Crobderg; although the mutation did not necessarily occur in him, as discussed previously. If the split between yourself in the R1b-A21774 clade and the large McManus cluster in the parallel R1b-BY21220 clade did indeed occur after Tairdelbach Már Ó Conchobair, we can initially surmise that he was only R1b-BY18115+.

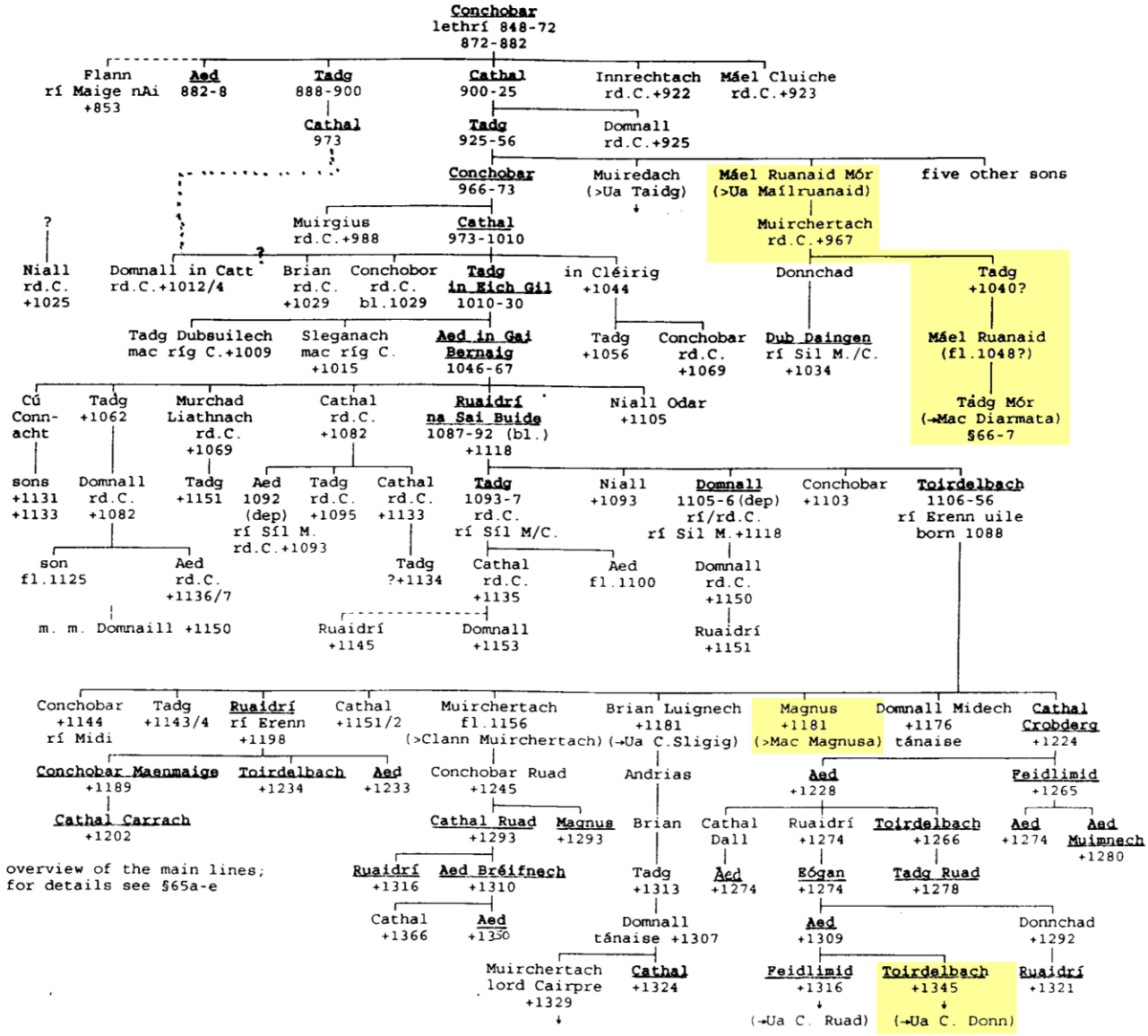

FIGURE IV-2. UÍ CONCHOBAIR, 9TH – 12TH CENTURY

This presents an interesting anomaly with the McDermott gentleman in your R1b-A21774 clade. According to most of the traditional genealogies the split between the Ó Conchobair and Mac Diarmata branches occurred circa 900 AD with Tadc in Dúr's sons Conchobar and Máel Ruanaid Már. This is well before the formation of your R1b-A21774 clade and most likely occurred sometime before or within the formation of the R1b-BY18115 clade.

With only data from the one McDermott gentleman, it is impossible to say whether this represents the actual Ó Conchobair/Mac Diarmata split, or whether this is an SCE of some type. We need more McDermott men to test in order to resolve this question. Again,

most of the traditional genealogies indicate that McDermott men will be positive for some, but probably not all, of the mutations within the R1b-BY18115 clade. However, verifying all of this thoroughly will depend on 1) having sufficient numbers of male descendants from each sept being tested, and 2) such men being tested to the necessary level of detail, e.g., the BigY 700 test.

What the Cladogram does show now is a distinct group of McManus and O'Connor individuals who fall under the R1b-BY21220 clade (recall the Snipes and Wilson gentlemen are likely SCEs from their genealogy and Y-DNA). Then there is yourself and the other O'Connor gentleman in the R1b-A21774 clade, with the McDermott gentleman being anomalous currently. Overall, this pattern is consistent with the genealogical documentation as shown in Dr. Jaski's table above.

V. Conclusion

What your Y-DNA test results confirm beyond reasonable doubt is that the R1b-BY18115 clade of the Y-Haplotree is associated with the Uí Conchobair lineage. This is a fantastic result and despite the current McDermott anomaly lends strong support to the veracity of the traditional Uí Conchobair genealogies.

Prepared by:

David Mc Daniel — Administrator, Genelach Dáil Cuinn Project Website

On behalf of:

Paul Duffy — Administrator, FTDNA Ireland yDNA Project; Co-administrator, FTDNA Ancient Breifne Clans Project

Maurice Gleeson — Co-administrator, FTDNA Sons of Aodh Project; Co-administrator, FTDNA McDermott Project

Tim McEvoy — Administrator, FTDNA Sons of Aodh Project

Gráinne Ní Fhlannagáin — Administrator, FTDNA Sons of Aodh Project

Appendix

A. Y-DNA – A String Of Beads

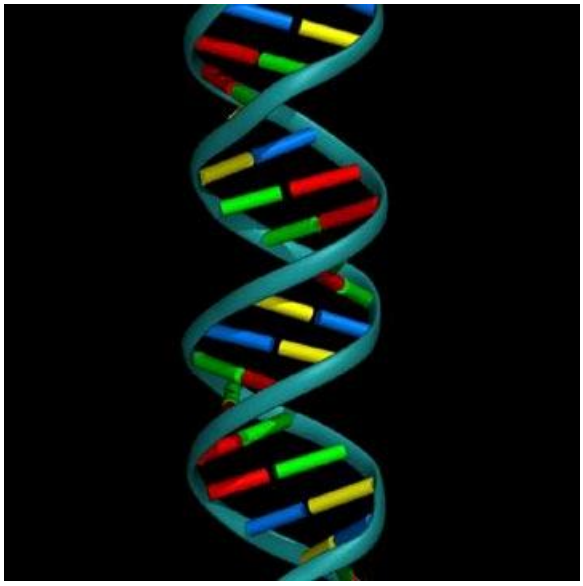

Figure A-1. DNA Double Helix

This is the familiar DNA double helix. The Y chromosome has this same structure. When we untwist the helix, we have something like the following.

Figure A-2. Y Chromosome Untwisted

There are two parallel "strings of beads". Each "bead" is called a nucleotide and there are only four different nucleotides, or only four different colors of "beads". The colors are given letter designations: A, C, G, and T. The two parallel strings or strands are

complementary to each other because each color can only pair with one other specific color: A with T and C with G. The corresponding “beads” on each strand are called a base pair.

One strand of the “string of beads” of the Y chromosome is approximately 59 million “beads” long, so the Y chromosome has approximately 59 million base pairs. As a result, there are plenty of places for mutations to occur, and the mutations are typically unique.

The “knots” on each end of the string are different so we always know which end is the “left” end and which end is the “right” end. And since the two strands are complementary to each other, we only need to examine one strand to understand the Y chromosome’s sequence of “beads”.

Since only men have a Y chromosome, a son can only inherit his Y chromosome from his father. There is no contribution from his mother, unlike with the other chromosomes in human DNA. In a perfect world, the same sequence of “colored beads” would be passed on from father to son, so **all** men everywhere would have the exact same “string of beads” for their Y chromosome passed on from the first man.

However, the copy process sometimes hiccups and a change or mutation is introduced that causes the son’s “string of beads” to be different from the father’s. Some generations later, a different hiccup occurs that introduces a second mutation; and so on through the ages. As stated previously, each mutation is retained and passed along to all male descendants in that line.

In the example below, the son has a change which is passed to the grandson, so the son and grandson have the same “string of beads” for their Y chromosome. But there is another hiccup in the great grandson, who now has TWO changes or mutations compared to the original father: the one introduced in the son and now the new one introduced in him.

These types of mutations are called SNPs (Single Nucleotide Polymorphisms). There are other more complex mutations that occur as well, but the effect is the same. The addition of a new mutation causes a branch point on the Y-Haplotree which defines a new clade. If one son has a new mutation, but another son does not, we can determine from which son a man descended by looking at his Y chromosome and seeing which "beads" have mutated.

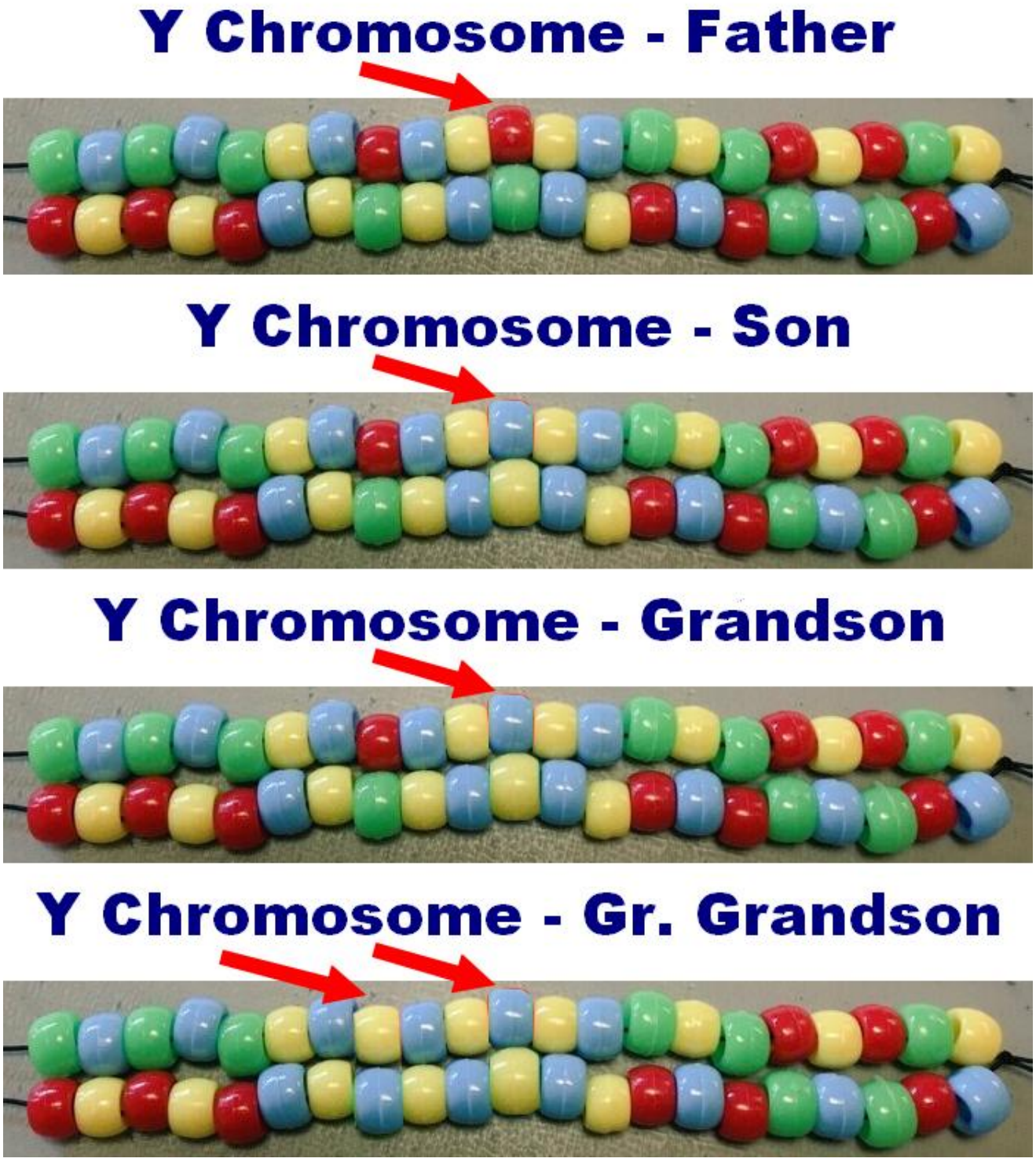

Figure A-3. Y Chromosome Mutation Example

B. The Y-Haplotree

As stated previously, all these mutations form the Y-Haplotree, and every man can be assigned to a particular clade of the Y-Haplotree based on which mutations he has in his Y

chromosome. This makes the Y-Haplotree similar to a normal family tree, but with one significant difference: while a normal family tree shows every generation of every descendant line, the Y-Haplotree can **only** show those generations/men and descendant lines that had a Y chromosome mutation occur in them.

So each clade represents an individual man in which that particular mutation of the Y chromosome occurred, and thus formed a new branch of the Y-Haplotree. Again, these mutations of the Y chromosome are permanent, except in extremely rare circumstances, and are inherited by **all** male descendants of the original ancestor in which the mutation occurred. This fact is what has allowed the Y-Haplotree to be built. It is constantly growing as more men do Y-DNA testing and new clades are discovered and existing clades are expanded.

These clade and mutation names may appear to be confusing, but they have no intrinsic meaning. When we say that you belong to the R1b-M222 clade, for example, the leading R1b indicates this mutation belongs to the very early R1b clade that a significant percentage of the European male population belongs to. The trailing M222 indicates which particular subclade of R1b that you belong to, and that this subclade is characterized by the M222 mutation of the Y chromosome. M222 itself merely indicates that this particular mutation of the Y chromosome was discovered by the M code laboratory, and it was the 222nd Y chromosome mutation that the M code laboratory discovered.

Similarly, A21774 merely indicates that the particular mutation of the Y chromosome that characterizes the R1b-A21774 clade was discovered by the A code laboratory, and it was the 21,774th Y chromosome mutation that the A code laboratory discovered. So there is **no** correlation between a mutation or clade name and the chronology of when it occurred and where it appears on the Y-Haplotree.

Recent statistical analysis of the Y chromosome mutation process has shown that for a BigY 700 test such as you took, a new Y chromosome mutation occurs at a rate of once every 83 years on median. There is a wide margin of error around this figure, so it is only good for rough estimates. In conjunction with this mutation rate, the current evidence indicates that any individual man only has one Y chromosome mutation occur in him.