What can Y-DNA tell us about the Ewings?

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Summary

The majority of the Ewings have a distinctive DNA profile. Variants of the same profile are present in perhaps 20% of Irish descent males, especially those found in the North West of Ireland. This profile can be determined in using markers called STRs, but recently the group can also be more easily detected using a SNP called **M222**. This group has been labeled haplogroup **R1b1c7**. The origin of this group is under intensive study, but the evidence to date is consistent with being derived from the original hunter-gatherer population that settled Ireland after the last ice age ended 9000 yrs ago. In part, this group may have achieved its current high frequency, because it appears to be associated with the **Ui Neill** dynasty founded by **Niall Naoighiallach** an Irish king who died in 405 AD. This connection is consistent with the **Dal Riadic** oral history of the origin of the Ewing's, who are reputedly descended from **Ui Neill** descendants that settled in Western Scotland about 1000 AD, specifically the **MacEoghainn** clan who settled in Argyll. Thus it appears that the Ewings' history can be traced back to the prehistoric hunter-gatherer period in Ireland, they then moved to Scotland sometime in the first millennium, then moved back to northern Ireland again in the 17th Century as Scots-Irish, and then finally shifted to the USA.

Introduction

In some situations Y chromosome markers can provide interesting information about your likely ancient origin as well as identifying close paternal relatives. In the last 2 years sufficient information has become available for this to be done with some confidence for a group of people whose origins are clustered mainly in North West Ireland. We will first quickly review these markers and their properties.

The Y chromosome is only inherited by males, and as such follows surnames since they became prevalent and also oral genealogies kept by Scottish and Irish bards. There are two types of markers or variants on this chromosome STRs and SNPs.

STRs and SNPs

The standard Y chromosome DNA test measures repetitive DNA markers that vary in length called STRs. These have a relatively high mutation rate changing in length on average every 500 generations. Usually these changes are single steps and they take what is called a "random or drunkards walk". Normally, around 37 of these markers are used so there should be a mutation in at least one of these markers every 24 or so generations. Since you have to count from both relatives back to the common ancestor, typically 12 generations will separate individuals that have a mutation. Over a longer time period these mutations can also occasionally revert to their original state. This variability makes them very useful for genealogy, which typically is looking for relatives in the last 10 generations. They also have another benefit as they can provide an estimate of the age of the group. This is done by examining the variability seen around the original ancestor's values and using some mathematics based on the estimated mutation rate to calculate the number of generations to a common ancestor for the entire group. However, it does make it difficult to identify distant pre-historical relatives.

Another type of variant is a SNP. This is where a specific base in the DNA is altered; these changes are at a very much lower rate, on average once every 50,000,000 generations. Fortunately, there are many base pairs that can change making them reasonably frequent. For the cases we discuss here though they can be considered unique events. A person with the variant will with a very high chance be descended from the male in which the variant first appeared. SNPs can be combined and form a tree structure called haplogroups all descended from the last common male ancestor at the dawn of time.

Combining data from SNPs and STRs provides the most informative results. The SNPs track deep ancestry many thousands of years, and the STRs identify recent branches within SNP defined groups, and based on their diversity the age of the SNP group itself. SNP results also have another use, they can also help exclude STR results of unrelated ancestral lines that now look similar "just by chance." This is particularly valuable for borderline cases and when not enough STRs are used.

R1b, the North West Irish Variety and M222

The latest Y chromosome tree is available at ISOGG (www.isogg.org/tree) and is shown in Figure 1 (see next page). We will start with haplogroup **R1b** which is defined by a SNP variant called **M343**, which first appeared in a male perhaps 30,000 years ago. These people migrated into Europe prior to the start of the last ice age and have been associated with Cro-Magnon man and are best exemplified by cave paintings in Southern France. During the height of the last ice age from 24,000 to 10,000 years ago people in Europe retreated to several refugia probably located in Spain (Iberia), South Eastern France, Italy and the Balkans. By this time another mutation had occurred called **M269** and this distinguished them from people now located primarily in the Middle East. It is now thought the people located in South Eastern France, Italy and the Balkans can

be identified by two further mutations **S21** and **S28** respectively. However, the exact history of these groups is not clear; what is known is that **S21** is now frequent in a band through Northern Germany, North Holland and Scandinavia. In contrast, **S28** is widespread, but seems to have a focal point in southern Germany near the head of the Danube and some have speculated that it is associated with the La Tène Celtic culture.

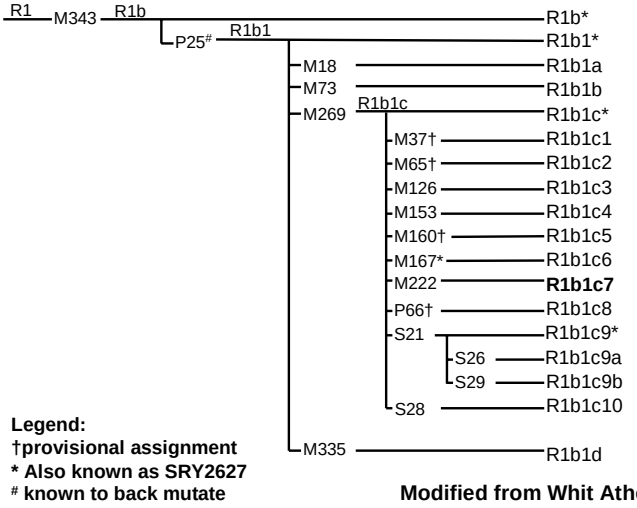

Figure 1. Summary of the current 2006 YCC R1b haplogroup tree, based on SNP results available to date, with the **R1b1c7** group in bold type.

It is thought that during this period, due to small population size and relative isolation, a very distinctive STR haplotype emerged and either during the same phase or just prior to its creation a SNP mutation also appeared called **M222**. The **M222** variant appeared in individuals that had the **M269** mutation, but not the **S21,** or **S28** mutation. Some have speculated that this group emerged elsewhere and moved to Ireland. If they did they have left little trace in their homeland. Until such evidence is found we are better off assuming the mutation and distinctive STR haplotype emerged in Ireland.

This group was initially identified and described by David Wilson based on STR profile alone as the Northwest Irish haplotype. The expanded group was defined by myself based on a different STR results as **R1bSTR19 Irish**. The different names are used to remind people how they have been estimated.

These variants probably only initially accounted for several clans or tribes in Ireland, but they were successful and subsequently expanded to represent 10-20% of the Irish population. This expansion could have occurred at any time, but most likely during periods of rapid change such as during the introduction of agriculture around 3500 BC or later during the bronze or iron ages. However, by the iron age the population was already several hundred thousand people and rising so any later emergence or expansion of this variant would have required a marked and sustained advantage extending over perhaps 20 or 30 generations. Later dates require even more improbable scenario's. There are only two potential candidates for such an event, virtual elimination of opponents by warfare or their decimation by disease. The figures in large STR databases suggest this groups make up 20% of R1b haplogroup with Irish male ancestors, 9 percent of Scots, and close to zero in the rest of Britain and Europe.

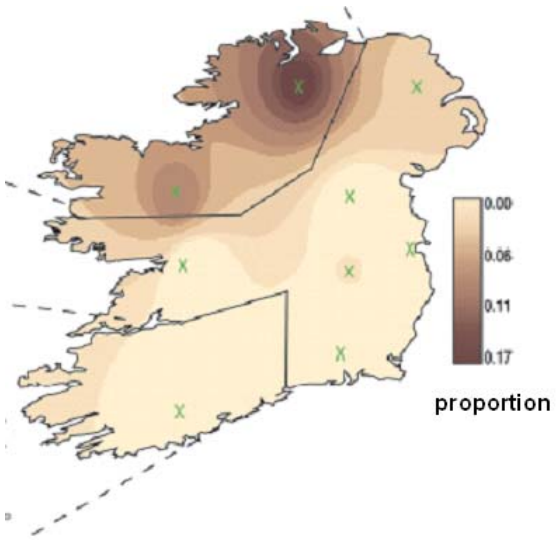

Figure 2. Distribution of the **IMH** across Ireland from Moore et al (2006), note it peaks in North West Ireland at close to 17% and is lowest in the south and west of Ireland. They also noted it was relatively frequent in Western and Central Scotland based using 6 marker STR profiles published by previous workers using 6 marker STR profiles published by previous workers.

Recent Irish Study

Recently a group of Irish researchers based in Trinity College in Dublin published a very interesting paper (Moore et al. 2006[1]) looking at SNP and STR profiles of 796 Irish males based on their surname and origin. They did not use the **M222** SNP, but used 17 STRs and were able to distinguish a portion of those with the distinctive haplotype described previously which they called **IMH**. Figure 2 is the distribution they observed across Ireland. Further study by this group found that it was particularly associated with those who claimed **Ui Neill** ancestry. In fact they suggested that the modal haplotype was

[1] L. Moore, B. McEvoy, E. Cape, K. Simms and D.G. Bradley. A Y-Chromosome Signature of Hegemony in Gaelic Ireland. *Am J. Hum. Genet.*, Vol. 78 (February 2006), pp. 334-338. www.journals.uchicago.edu/AJHG/journal/issues/v78n2/43032/43032.html

the same as **Niall Naoighiallach** whose descendants subsequently became the ruling elite in Irish history for nearly 700 years. They also suggested that the current frequency of this haplotype group was due to a reproductive advantage enjoyed by this clan due to their status since that time. This **Ui Neill** dynasty was discussed in my previous article[2]. In practice many in the group are unlikely to be direct **Niall Naoighiallach** descendants, but a fraction certainly is.

Now while extremely exciting, this study now has to be examined in light of other evidence described above. First they could only classify the group with some difficulty having neither SNP nor extended STR profiles. Secondly, their results were limited to Irish samples. Thirdly they knew nothing of the **M222** SNP association with this group. Therefore while the results certainly stand some care is required comparing their results with others. It is likely that the group they defined is only a fraction of the larger group David Wilson, myself or the **M222** SNP define.

The Ewings

So where do the Ewings fit? If a dendrogram (relationship tree) is drawn of all **R1b**, which shows the major groups as well as all the individuals within the **R1bSTR19 Irish** cluster then almost all Ewings fit in a compact group by themselves. The group is located within the **R1bSTR19** cluster, and to date this is also 100% equivalent to having the **M222** SNP variant (see Figures 3, at right, and 4, on nthe next page). The Ewings are at some distance from the R1bSTR19 modal (or most common value) suggesting they branched off at an early date to many in the group; specifically, the Ewing modal is genetic distance seven from the **R1bSTR19** modal. You can see how Ewing values compare with the **R1bSTR19** modal by having a look at the Ewing Surname Project Results tables on the website of Clan Ewing at www.clanewing.org, where the **R1bSTR19** modal is referred to as "UiN." TD is within the same Irish cluster, but in an unrelated region. SL matches a group that is very prevalent in Scotland and almost absent in Ireland. DS, JM and JMc inhabit another extended group. Note that a dendrogram shows relationships, and those with the shortest and closely joined branches more closely related. The technique used here is best for relationships that are hundreds to thousands of years old, as there

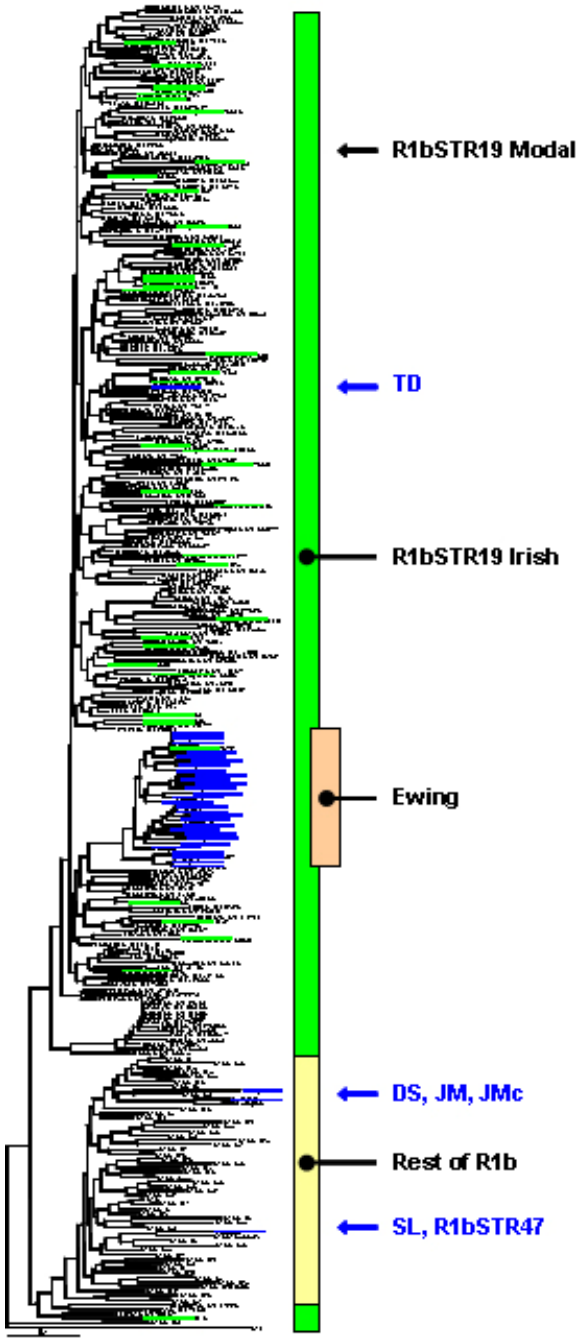

Figure 3. Diagram showing relationships between the R1bSTR19 cluster individual haplotypes (group identified by the long bar) and the "large group of related Ewings" (group identified by the short bar). The location of some "unrelated" Ewings on the chart are shown with arrows. WM does not appear on this chart because he is unique among Ewings so far because he is in haplogroup G, and on a chart at this scale he would be several pages away. The original chart is large and color coded such that one can see which individuals have had SNP testing, and can see the initials of individual Ewing project participants. For a version which can be viewed at any resolution visit www.geocities.com/mcewanjc/ewing.pdf.

[2] J. McEwan. Origins of the MacEoghainn Clan: What Information Can Y Chromosome Markers Provide. *J. Clan Ewing*, Vol. 11 No. 3 (August 2005), pp. 23-29. http://www.clanewing.org/DNA_Project/DNA_Articles/Origins_MacEoghainn_Clan.pdf

are better methods for recently related individuals. Therefore some care should be exercised assigning degrees of relationship within the major Ewing group. The companion article[3] by David Ewing provides a more in depth summary of the likely recent genealogical relationship.

In theory you can also identify families within the **R1bSTR19 Irish** group that are closely related to the major Ewing group, the **McCracken's** and **McGhee's** for example. These may be pre-surname relatives. However, at this stage we still do not have enough information from Irish and Scots families to be able to easily track the various lineages within the group. I also suspect that to do this reliably will require at least 67 STR markers.

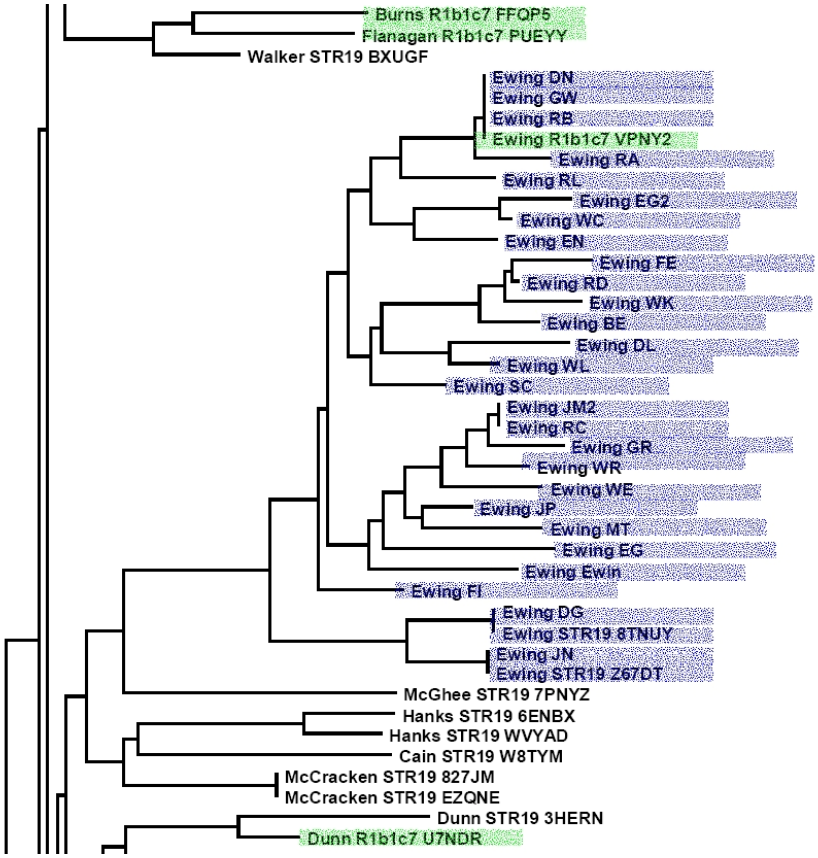

Figure 4. Magnified view of the diagram in Figure 3 showing the core Ewing group, individuals labeled green have been SNP tested all are positioned based on STR haplotypes.

This **R1bSTR19 Irish** connection is consistent with the **Dal Riadic** oral history of the origin of the Ewing's, who are reputedly descended from **Ui Neill** descendants that settled in Western Scotland about 1000 AD, specifically the **MacEoghainn** clan who settled in Argyll. The DNA evidence to date is inconclusive as to whether the Ewings are descended directly from **Niall Naoighiallach** himself or his extended Irish "clan relatives", but it is most likely the latter based on their relationship with the modal value of **R1bSTR19 Irish**. However, the evidence is sufficient to suggest that it is now unlikely they originally had a Cymric origin. What is currently lacking in the chain of proof is a sufficient number of tested individuals descended from **Aodh Anrathan** to tie the Ewings to a sub branch of **M222**. This includes other variants of the Ewing name.

Thus it appears that the Ewings' history can be traced back to the prehistoric hunter gatherer period in Ireland, they then moved to Scotland around 1000 AD, then moved back to Northern Ireland again in the 17th Century as Scots-Irish, and then finally shifted to the USA.

How believable is the evidence?

This interpretation of the **R1bSTR19 Irish** cluster and **M222** is based on extremely new information and is still subject to very robust debate among DNA genealogists. It is so new in fact that only one scientific publication has appeared and it did not use the **M222** SNP and extended STR profiles. Like all interpretations it is based on weaving numerous strands of evidence each by themselves of little value and subject to differing interpretations into a solid rope of circumstantial evidence. In short it depends on the following elements:

- The variability of the cluster and its distinctiveness, confirmed by SNP testing, means that almost all individuals can be identified based on STR profiles alone. This allows the much larger quantity of STR data to be examined in confidence.

[3] D. N. Ewing.. Ewing Surname Y-DNA Project. *J. Clan Ewing*, Vol. 12 No. 3 (August 2006)., pp. 17-25. http://www.clanewing.org/DNA_Project/DNA_Articles/060717_CEJ_Y-DNA_WebSite.pdf

- There is very little evidence for this STR group on the European continent, including Iberia, and no SNP evidence to date. It has its highest concentration in Ireland and those whose ancestors can be traced to Ireland. This suggests Ireland is where it originated, and it is very unlikely that it was part of a ruling elite that conquered Ireland in one of the Celtic invasions.
- The STR variability suggests an age of the larger group that is at least thousands of years old, and when coupled with known population dynamics it suggests an origin prior to the beginning of agriculture.
- Its geographic and surname distribution suggest an origin prior to **Niall Naoighiallach**. When this is combined with estimates of the variability of the **Ui Neill** it is consistent with an origin much earlier than when **Niall Naoighiallach** was alive.

What still needs to be done?

Like many things it is very difficult to get certainty with these studies. Here are some areas where we lack knowledge.

- *Profiles on surname variants*. There are few tested Ewing or **McEwen** surname variants and no **McKeown's** from northern Ireland. If 10-20 individuals were available from each of these we would be able to identify whether these surname variants are related, or represent unique surname origins. Given that the Ewings represent a broken clan unique surname origins would not be unexpected.
- *More profiles on supposedly related families*. These include the **Lamonts** and other **Dal Riadic** group families. If they are truly related, they should each have a family branch that is more closely related to the Ewings than just the **R1bSTR19 Irish** group as a whole.
- *New SNPs*. A current problem is that at least 50% of **R1b1c** individuals that have no defining **R1b1c** subgroup SNP. This unclassified group probably consists of several disparate strands perhaps up to 15,000 years old. A SNP that included all those that also had **M222** as well as other individuals would more definitively identify the origin of the group prior to the emergence of **M222**. Currently, we cannot exclude that **M222** originated somewhere entirely different than Iberia in some rare or unknown refugia.

Conclusion

The majority of the Ewings are closely related to one another and reside within a Y chromosome group that most likely originated in Ireland at the end of the Ice age. As more evidence is gathered we will be able begin to discern pre-surname relationships, particularly as they relate to the **Dal Riadic** migration and its relationship with the **Ui Neills**.