The Genetics of Clan MacLeod

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First I have to thank all of the volunteers who participated in the study by giving a sample of their DNA, and Dr Alex McLeod for first bringing to my attention the history of the clan MacLeod (for brevity I will refer to both McLeod and MacLeod as MacLeod) and subsequently coordinating sample collection with myself and the numerous National Societies. DNA collection kits were sent out to over 500 volunteers, complete results were obtained from over 80% of the returned kits and these results were included in the study. Most of the remaining samples yielded partial results; whilst these cannot be included in the study it is still possible to give these volunteers some information about their genetic type. Given this huge response from the MacLeods, they form a large part of a study that I conducted at University College London (UCL) with my Ph.D supervisor Prof D Goldstein to look at the genetics of several paternally inherited surnames. The research at UCL, along with a similar project being conducted concurrently at the University of Leicester, was the first large scale study to look at surnames and genetics. A few smaller studies existed, for example in Oxford Prof B Sykes carried out research into his surname, but because this only provided information about one name the results couldn't be extrapolated to surnames more generally.

So, what kinds of questions about the history of the MacLeods can genetics help answer? At a very basic level it is possible to test whether there has been a common origin for the clan, then with further analysis we can see how closely related individuals are within the clan, and potentially identify a geographic location(s) where the members of the clan came from. The most pervasive theory about the clan's origins is that it was founded by Leod, son of Olaf the Black a Norse King and ruler of the Isle of Man and the Western Isles, although there is disagreement about whether a link with the Isle of Man can be substantiated. A large caveat also has to be inserted at this point: although the number of MacLeod DNA samples I have is very large, it is still a small sample of the total number of men called MacLeod (I only considered men in this study for reasons discussed below). Whilst I hope it is a representative sample of all of the male MacLeods alive today it is possible that if I analysed another batch of different samples of male MacLeods I would find different genetic results, leading to an alternative set of conclusions. Thus the results that I will be discussing here are only true for the sample of MacLeods I have studied, whilst one obviously extrapolates to all male MacLeods, this caveat, called Sampling Error, must always be borne in mind.

How can genetics answer these questions? The first step is to decide what type of test is suitable. As the inheritance of the MacLeod name behaves in the same way as that of other surnames in our society by being passed on paternally from father to son – daughters inherit the name but their children (usually) inherit their father's surname. The Y chromosome is also passed on from father to son only. Thus the Y chromosome is a perfect part of the human genome to study MacLeod history because the inheritance of Y chromosome genetic types should mimic that of the MacLeod surname, assuming that the name has been passed on from father to son since the progenitor of the clan MacLeod. Any lack of a correlation between the inheritance of a specific Y chromosome type and the name MacLeod could be due to one, or a combination, of several factors: multiple origins of the MacLeod name; random adoption of the name; or non paternity. Conveniently we also know a lot about the human Y chromosome!

We use two types of tests on the Y chromosome both of which look at part of the chromosome that contains so called junk DNA, DNA that has no known function. For this reason, difference, or mutations can accumulate relatively freely because there aren't any mechanisms to stop them appearing as the DNA doesn't code for anything, it doesn't tell "cell A" that it's an eye cell and "cell B" that it's a brain cell. The first test that we use allows us to cluster the DNA samples into genealogically related groups, called *haplogroups*, these are discrete groups of individuals who at some point in time shared a common ancestor, as recently (in genetic terms at least) as 10,000 years ago, or as far back as 100,000 years ago, when modern human populations migrated out of Africa. Thus for a collection of DNA samples to be genetically related they have to fall within the same haplogroup. Some of these haplogroups have widespread geographical distributions, for example in Europe a particular haplogroup ("haplogroup 1") is usually the commonest group found in most populations, particularly those in the west. Whereas other haplogroups have more restricted distributions, such as haplogroup 3 which is generally rare in Europe but relatively common in Scandinavian and central European populations.

The second test allows us to differentiate between DNA samples within the same genealogical group, by looking at so called *haplotypes*. Closely related individuals such as a grandfather, father and son will have exactly the same haplotype because the short period of time separating them means there hasn't been enough time for mutations to accumulate, whereas distantly related individuals will have very different haplotypes, because a longer period of time separates them allowing for more mutations to accumulate. Therefore DNA samples from men with the same surname are expected to fall within the same genealogical haplogroup and have identical or very closely related genetic types because the hypothesis is that these men share a recent common ancestor.

The last 5 to 6 years has seen a boom in research focussing on European patterns of Y chromosome diversity. We know in which populations certain haplogroups and haplotypes are commonest, which haplogroups are associated with historical events, such as the spread out of Africa by Anatomically Modern Humans 100,000 years ago (approx), or the apparent Neolithic Expansion westwards by farmers from Anatolia starting around 10,000 years ago. Prof Goldstein's team recently looked at Y chromosome genetic diversity in Britain specifically, and identified certain haplogroups and haplotypes associated with historical invasions, for

example the Anglo Saxons and Vikings. Thus we know in British populations the presence of a certain haplotype within haplogroup 3 is indicative of a genetic influence of the Vikings. With this information we were able to ascertain which British populations have most evidence for a lasting genetic legacy of these historical invasions, as well as those populations which appear to be composed of predominantly “indigenous” Y chromosome types, types which are proposed to represent the Palaeolithic inhabitants of Europe.

The MacLeod results are very interesting. Figure 1 shows a pie chart of the haplogroups found in the MacLeod sample. Each colour on the pie chart relates to a different haplogroup.

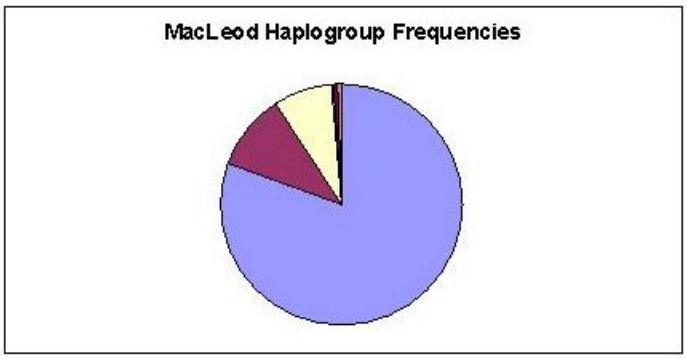

Figure 1 shows a pie chart of the different haplogroups (see text for definition) found in the MacLeod DNA samples studied here. Each colour refers to a different Y chromosome haplogroup. Hence the light blue section of the pie chart refers to the proportion of the MacLeod DNA samples belonging to haplogroup1, and the red/brown section to the number of MacLeods who belong to haplogroup 2 etc. There are three other haplogroups just about visible at the top of the pie chart; their names have not be included because they are so rare in the collection of MacLeod DNA samples. The first clear finding is that more than one haplogroup is present, therefore not all of the DNA samples investigated can be related to the same ancestor.

The first obvious finding is that more than one haplogroup is present, therefore not all of the sample can share the same ancestor – some of the samples belong to men who have acquired the MacLeod surname either because there have been multiple founding events for the name, random uptake of the name throughout its history, or non paternity. However 32% of the total sample of MacLeod DNA samples not only belongs to the same haplogroup (haplogroup 1, the most common haplogroup seen in the MacLeods as seen in Figure 1) but also has the same or a closely related haplotype, meaning that these individuals are very closely related. Using two mathematical models I was able to date how long ago this 32% of the sample shared a common ancestor – i.e. how many generations back we would have to go to find the last time two individuals in the sample had the same father and I found it was around 1000 years ago. This is slightly further back than the founding of the clan MacLeod posited by clan history, but given that there is always some statistical uncertainty in the exact dating of such events, and historical accounts are always subject to some uncertainty, an estimate of ~1000 years ago is a good match between history and genetics. I also performed a statistical test to estimate how likely or unlikely it would be to find 32% of the MacLeod sample sharing this haplotype by chance. The results showed that it was very unlikely to find such a high percentage of the haplotype in the MacLeods by chance. These results taken together suggests that this high frequency haplotype shared by 32% of the MacLeod sample represents the clan MacLeod founding lineage - the lineage that was created by the original progenitor of the clan and which has subsequently been inherited by a fair proportion of future generations. Figure 2 shows a pie chart of this high frequency haplotype in relation to all other haplotypes.

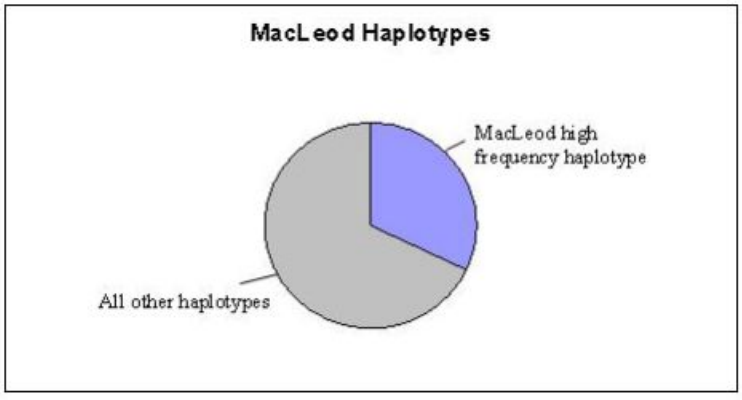

Figure 2 shows a breakdown of the haplotypes (see text for definition) in the DNA samples studied here. The section of the pie chart in blue refers to all of the individuals who share the same high frequency haplotype hypothesised to be the MacLeod founding lineage. This comprises 32% of all the haplotypes encountered. The grey section refers to *all* other haplotypes found in the MacLeod DNA samples.

The next step in the analysis was to identify where else in Britain and several European populations (Norway, Denmark, Germany, and Basques) this exact haplotype is found. Any population(s) where this type was found at a particularly high frequency are statistically more likely to be “source” populations for the MacLeod lineage – population(s) where the progenitor probably came from. Despite being quite common in several Scottish populations (Shetland, Western Isles and Stonehaven), the haplotype is not at a particularly high frequency in any one population, including the European populations, although it is quite common in several Scottish populations, making it very difficult to identify where the clan progenitor originated from. This does not exclude the chance that the clan progenitor was of Norse descent, it simply reduces the probability that this is the case. However, I also statistically examined the similarity between the whole of the MacLeod sample and the British and European populations. Intriguingly this showed that statistically, the male MacLeod sample is indistinguishable from two Scottish populations, Shetland and Oban, and the

Isle of Man, confirming the strong tie Clan MacLeod has with Scotland and the Isle of Man. Indeed it suggests that the present day collection of MacLeod Y chromosomes has been formed by men that originated in Scotland or the Isle of Man.

Conclusions

The research into Clan MacLeod genetics has shown that there is good evidence for the Clan predominantly sharing the same common ancestor around 1000 years ago. Unfortunately it is difficult to identify the geographical origin of this male progenitor by simply looking at the frequencies of the genetic type in other populations. However the statistical similarity between the MacLeod sample and Shetland, Oban and the Isle of Man is strong evidence for the Clan as a whole having its origins in Scotland or the Isle of Man. But it is important to remember that the DNA samples used in this study *may not* be a representative sample of the male Clan members, although we hope it is. Also, even if the sample we have today is representative of male Clan members today, it may not fairly represent the genetic makeup of the Clan 100 years ago, or 200 years ago, and so on. For example, the last several hundred years since the clan is thought to have been founded may have seen a large number of males randomly choosing to adopt the MacLeod surname. These men would likely introduce new and different Y chromosomes into the MacLeod gene pool, reducing the proportion of male MacLeods who are descended from the original progenitor. Nonetheless, the results are extremely interesting given the correlation they show with history.

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