New Y-DNA Evidence for Norse Descent of Leod

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The authors have dedicated this article to the memory of the late Ian Fraser Macleod of Christchurch, New Zealand, a stalwart and devoted clansman who was committed to the concept of Clan MacLeod as a worldwide organization based on family, fellowship, friendship and love.

Traditionally Clan MacLeod has claimed Norse descent through its progenitor, Leod. However, over the past quarter century qualified genealogists have questioned the details of that descent. This has been nicely summarized by Andrew MacLeod in an earlier article in this periodical.[1] While it should be noted that none of these genealogical deliberations have questioned the Norse descent per se, they have untied the traditional claim of Leod's descent from Olaf the Black, King of the Isle of Man. To a certain degree, this has left the entity of Norse descent in the male line itself clouded. During this same time frame new tools have been developed to further trace ancestral linkages through DNA. Several studies that will be referenced subsequently in this article have been undertaken utilizing these tools relative to Clan MacLeod. Although the initial results of these studies brought further into question the case for Norse descent, recent findings have now essentially confirmed the Norse descent of Leod, as this article will demonstrate.

Genetic Genealogy

One particularly useful genetic genealogy tool is Y-DNA testing, since Y-DNA is passed down from father to son and can thus be tied to a surname. These tests evaluate specific locations in a DNA strand that are identified by DNA Y-chromosome Segment (DYS) numbers such as DYS390. The number of Short Tandem Repeats, or STRs, within the segment are counted to come up with a numerical value, for example DYS390 = 25. The number of DYS locations tested can vary considerably, from six in the original Clan MacLeod study up to the 111 that are available in the current study. An individual's specific set of test results is called a haplotype, and comparison of two haplotypes can indicate whether the two are related and share a common ancestor. The comparison may show either an exact match or some differences where mutations have occurred. Groupings of related haplotypes are called haplogroups, which are identified by alternating letters and numbers, such as R1b.

STR testing usually provides enough information to allow prediction of an individual's major haplogroup. However, to pinpoint the subdivision of a haplogroup to which an individual belongs often requires a different type of testing. Single Nucleotide Polymorphisms, or SNPs, are

locations with very slow mutations that occur only once, unlike STRs, which can show multiple mutations. SNPs are designated with a letter and a number, such as L165. Variations in SNP terminology sometimes occur when the same SNP is identified by different researchers working independently. By noting which SNP mutations are present, geneticists can track an individual's line to its most recent branching, which can be an important tool in charting the emergence of population groups like Clan MacLeod.

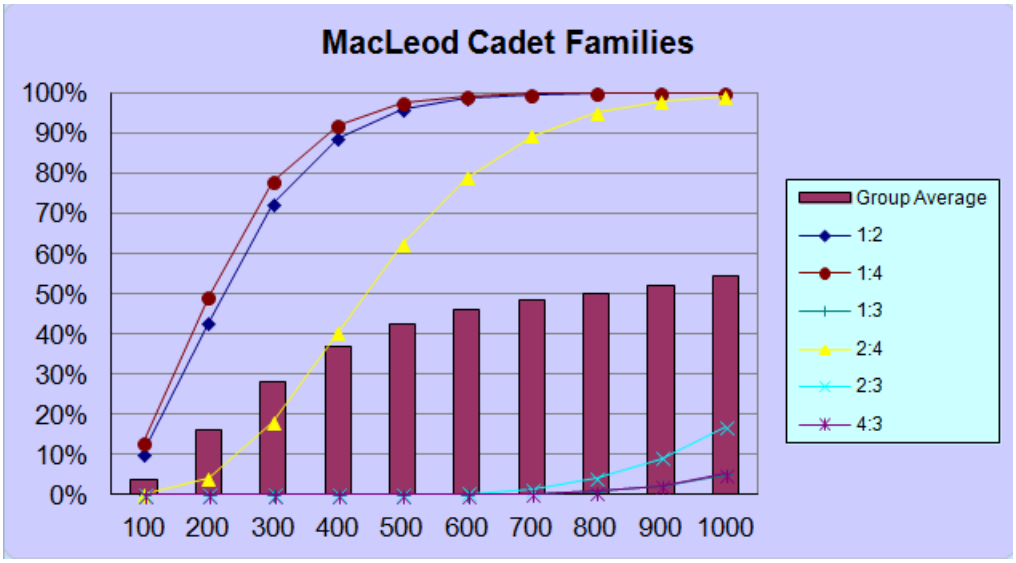
Clan MacLeod Studies

As is often the case in emerging scientific studies, one encounters terminology variations. This has been the case in Clan MacLeod Y-DNA studies. Initial studies, undertaken in 2003, revealed a dominant haplogroup for MacLeods. The first study was performed in laboratories at University College London (UCL).[2] Of the some 500 male MacLeods from around the world who agreed to test, ultimately 367 samples were tested, almost 75 percent of the entire group. For the purposes of this study, only six markers were tested and non-standard names were used to identify the haplogroups and haplotypes. Although it proved impossible to obtain the actual results identified by specific individuals, enough results were made available for later identification of the two main haplogroups using standard nomenclature: R1b and R1a. R1b is the most prevalent haplogroup in Western Europe. This raised questions concerning a Norse origin for Leod, this particular haplogroup not being typically Scandinavian. While this study showed a secondary haplogroup, R1a, which is typically Scandinavian, the R1b haplogroup was by far the most frequently found in that study.

Because the results from the UCL study were so strongly definitive in determining that there did indeed exist a "MacLeod" haplogroup, it was decided to continue the study through a corporation in the United States of America, Family Tree DNA (FTDNA). This company is located in Houston, Texas, and uses the laboratories of the University of Arizona in Tucson, Arizona. A Clan MacLeod Group Project was formed in 2003 and continues today. At the present time 224 persons have ordered Y-DNA testing through the Project. Another 70 persons have ordered similar testing through an associated project, the MacLeod Septs Project.[3] Of the 224 current participants in the MacLeod Project, the haplogroup distribution of the 181 with MacLeod surnames[4] is as follows:

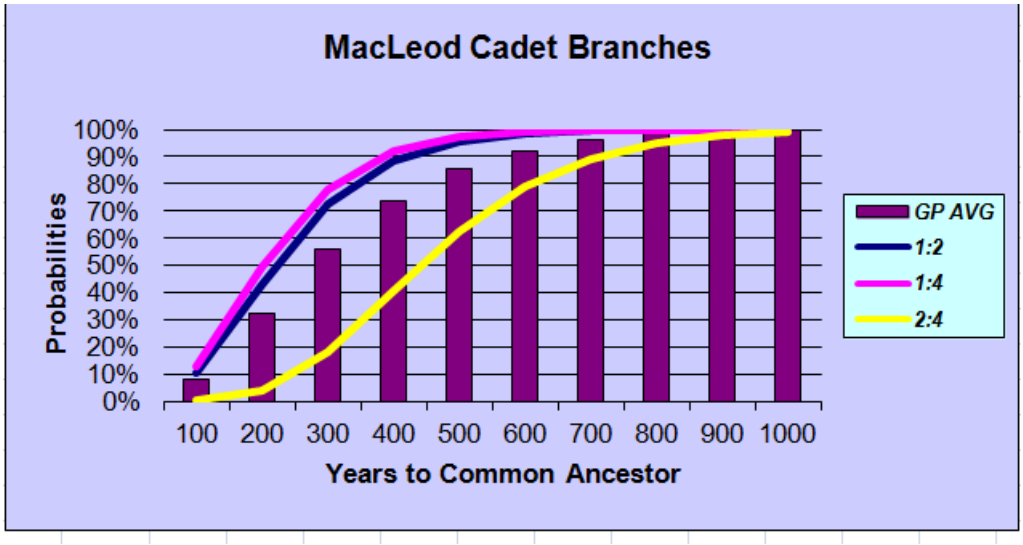
HAPLOGROUP	PARTICIPANTS	PERCENT
E1b	4	2.2
I	16	8.8
R1a	17	9.4
R1b	144	79.6

The UCL study and the final paper previously published in this periodical[5] considered the haplogroup findings in Clan MacLeod. Two other studies were individual case studies,[6] and another presented an overview of genetics and Clan MacLeod.[7] The study with pertinence to the present study involved five individuals claiming descent through specific Cadet branches of Clan MacLeod.[8] A Cadet branch consists of a family or families descending younger sons other than the Chiefly line, e.g., second, third, fourth, or fifth sons, and so on. In this study three of the five individuals showed definite close relationships compatible with the timing of Leod's lifetime, but two did not. The following illustrations are from that study. The first chart compares each of the five individuals to one another; only three approach the 90 percent statistical significance line needed to assure relationship. The low Group Averages indicate that the five are not closely related as a group.



The second chart compares these three individuals to one another, removing the two non-matched individuals. This shows the close relationship between the three individuals, with the Group Averages climbing to significant percentages rapidly when compared to the first chart.

The Cadet families designated "1" and "2" descend through the Harris and Dunvegan branch, and the Cadet family designated "4" descends through the Lewis and Raasay branch. The difference in the curve for 2:4 and the other two closely connected curves is probably the result of Cadet family "2" being a Cadet family of more recent origins. In all three families, the time to nearest ancestor is compatible with the time of Leod.



This study revealed that there were at least three Cadet branches, two from the Harris and Dunvegan line and one from the Lewis and Raasay line, which show a Y-DNA significant match compatible with the lifetime of Leod. This is confirmatory of their traditional genealogy, which has been documented in *The MacLeods: The Genealogy of a Clan.*[9]

Viking DNA and Clan MacLeod

Listed by the International Society of Genetic Genealogy (ISOGG) in their Web site, ISOGG Wiki,[10] as a New Project in 2010 is the following:

> R1b-P312 L165 project established December 2010.
> Administrators: Lori McLeod Wilke, Timothy McLeod and Alasdair Macdonald. L165/S68 is currently known as R1b1b2a1a2e according to the 2011 ISOGG Y-SNP tree. The SNP was discovered in 2007 by Dr. Jim F. Wilson of EthnoAncestry and has been designated L165 by Family Tree DNA. This subclade is heavily populated by families from the

> Western Highlands, but is believed by Jim Wilson to be Norse Viking.

Dr. James Wilson is a Senior Lecturer in the Centre for Population Health Sciences at the University of Edinburgh, where his group studies population history and structure and the genetics of complex disease. Thomas Krahn is the Technical Laboratory Manager of FTDNA's Genomics Research Center in Houston. He specializes in complex kinship testing and family reconstructions and is an expert in developing new molecular biological methods and assays to resolve questions of biological heritage. Wilson, as noted, discovered the SNP in 2007 and named it S68. Shortly thereafter Thomas Krahn independently discovered the same SNP in another sample, and it was named L165 to be compatible with FTDNA terminology. The ISOGG now uses the combined terminology, L165/S68, to designate the SNP.

In their recently published book, *The Scots: A Genetic Journey*, Wilson and his co-author, Alastair Moffat, write:

> Clan MacLeod traditionally recognized their Norse ancestry and an analysis of their DNA is rewarding. From a sample of 45 Macleod Y chromosomes, almost half—47 per cent—clearly show social selection at work in that they descend from one individual. . . . Theirs is a recently discovered subgroup labeled S68. It is found in Lewis, Harris and Skye, core Macleod territory, but also in Orkney, Shetland and Norway, with a few examples in Sweden. Despite extensive screening, S68 is very specifically located, showing up only once in the east of Scotland and once in England. This is a classic pattern for a Viking marker in Britain but one much rarer than M17. MacLeods determinedly claim descent from a common name-father, a Norse aristocrat called Ljot, a relative of Olaf, King of Man. They are probably right to continue to claim that—science, for once, is supporting tradition."[11]

The R-L165 Project noted above, based on FTDNA with Wilke as Group Administrator and McLeod, Macdonald, and Conrad Terrill as Co-Administrators, has done a great deal to study and publicize the L165 terminal SNP.. The full haplogroup designation used on FTDNA's phylogenetic tree is R1b1a2a1a1b5b. The group encompasses L165+ individuals regardless of

surname; out of 112 members, 26 have MacLeod surnames.[12] The R-L165 group has used modal haplotypes to evaluate which individuals are likely to test positive for L165. By early 2011 they had identified three markers that were probable indicators, as follows: DYS390 = 25, DYS464a = 14 (the most important indicator), and DYS534 = 16. They had also determined two markers as possible indicators, as follows: DYS449 = 31 and DYS570 = 16. These values differ from those of P312, the R1b subgroup from which L165 branched off, thus providing a means of potentially identifying individuals belonging to the L165 branch.[13]

These indicators have remained fairly constant with the addition of new participants except for DYS570. For that marker, the MacLeods who have tested positive for L165 show a mode of 17 rather than the 16 shown when all surnames are included in the calculation. According to Wilke, predicting L165+ results using the MacLeod modal haplotype has been very successful when the individual matches the haplotype within allowable distances for the number of markers tested. Successful prediction has also occurred with individuals who tested outside the matching distance to the haplotype, but within an allowable distance to another individual who matched the haplotype. Successful prediction at greater distances has been more problematic since other sub-branches share some of the same modals with L165.[14]

Thus far 26 R1b participants, or 14.3 percent of those with MacLeod surnames, in the Clan MacLeod Group Project have tested for L165 and are positive. Twenty-three of these are the same individuals as in the R-L165 project; they have joined both projects. The R-L165 group has 3 other MacLeods that are not in the MacLeod Study, and the MacLeod Study has the 3 Cadet branch participants who are not in the R-L165 group. Most of the R1b MacLeod-surnamed participants in the Clan MacLeod Group Project have not tested to determine their terminal SNP. Comparing the results of these individuals with the DYS predictors described above highlights the likelihood that a substantial portion of these are L165+. The modal values for this group as a whole exactly match those of the predictor DYS numbers when 17 is used for DYS570. The table below shows the percentage of individual participants whose results exactly match the predictors by test level. Since the five predictors are not all included until one reaches the 67 marker test level, some test levels show no results for certain DYS numbers.

TEST LEVEL	NUMBER	DYS390	DYS464a	DYS534	DYS449	DYS570
12 Markers	34	65%				
25 Markers	3	0%	33%		33%	
37 Markers	43	60%	53%		47%	65%
67 Markers	34	59%	47%	62%	35%	56%
Total	114	60%	50%	62%	41%	61%

These results reflect only exact matches; other participants who are close but not exact matches could still test positive and increase the percentages in actual as opposed to predicted results. However, a larger portion of MacLeod R1b participants will need to be actually tested for L165 to validate these predictions.

Validating Leod's Norse Descent

With the earlier Y-DNA studies in Clan MacLeod we were left with a dominant haplogroup, R1b, that is known as the major European haplogroup, with no definite Norse connection to our traditional history and with three of five Cadet families tested showing evidence of a common ancestor compatible with Leod. With the discovery of the R1b SNP, S68, known as L165 among the geneticists in the United States, as a unique Scandinavian marker, the possibility of linking our traditional history to haplogroup evidence for our Norse ancestry became possible. Some existing participants in the ACMS Clan MacLeod Project, hearing of the L165 marker, undertook to test for that marker additionally. Those who tested positively could say they were of Norse descent, and while that give statistical evidence to suggest that Leod's marker was also positive, it was not definitive because of the general lack in solid standard genealogy. When it was realized that we had three individuals from Cadet branches who were proven to have a common ancestor compatible with Leod, and who had solid standard genealogy, it was evident that by testing them we might be able to confirm much more definitively that their modal was that of Leod's and that he was, indeed, Norse, as Clan tradition has always held.

The three individuals were notified of the additional test, and it was ordered. The results are positive for L165/S68 in all three. In the earlier study, the identities of the five individuals

tested were kept confidential for obvious reasons. It now seems reasonable to identify these three Cadet branches that have allowed us to more solidly prove the traditional Norse descendent of Leod. They are Talisker and Glendale from the Harris and Dunvegan line and Raasay from the Lewis and Raasay line. In recent correspondence, Wilson made the following comment:

> I think what is quoted in The Scots is simply a quick analysis of MacLeod men at ysearch [sic] some years back. It is quite easy to predict who is in the S68 group from 37 or indeed fewer STRs. To this I added some MacLeods sampled in some projects of mine, in particular for the BBC Alba series On the Ocean, who had both STRs and S68 tested. This is where we first became aware of the high frequency in the Western Isles. So the sample was not huge, n=45, and there appeared to be at least 14 independent Y lineages present, each typically accounting for 1-5% of men, while the S68 lineage accounted for 47%. The largest descent group by a clear mile and thus almost certainly the founding Leod lineage, as you have now verified.[15]

Where does this lead our study? Now knowing that the SNP, L165/S68, is found not only in 47 percent of an independent study, i.e., Wilson's, and found in the three authentic Cadet family individuals that we have tested, we can further define the dominant MacLeod line by testing for the L165/S68 SNP. We need to encourage any participant who has been found to have the R1b haplogroup to sign up for further L165/S68 testing. Additionally, other male MacLeods, however spelled, who have not participated in the FTDNA Study, are encouraged to join and after finding out their haplogroup, if appropriate, then effect the additional L165/S68 test.

In closing, we should reiterate that Clan MacLeod is <u>not</u> a Clan with only R1b subclade L165/S68 positive individuals. As noted above, there are several other haplogroups represented: non-L165/S68 positive R1b individuals, R1a individuals, E individuals, I individuals and others. All of these are true and valued members of Clan MacLeod.

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[1] Andrew P. MacLeod, *Clan MacLeod Magazine*, no. 91, November 2000, pp. 262-270.
[2] Julia Abernethy, "The Genetics of Clan MacLeod," *Clan MacLeod Magazine*, no. 98, April 2004, pp. 760-763.
[3] The Clan MacLeod Project is located at www.familytreedna.com/public/ACMS_MacLeod/default.aspx and the MacLeod Septs Project is located at www.familytreedna.com/public/MacLeodSepts/default.aspx.

[4] The current 43 participants with surnames other than MacLeod have been omitted for this count.
[5] "Haplogroup Studies in Clan MacLeod," *Clan MacLeod Magazine*, no. 107, October 2008, pp. 51-58.
[6] "McLeod Lines: A Genetics Project Case Study," *Clan MacLeod Magazine*, no. 101, October 2005, pp. 182-186, and "Sandhills Streams and MacLeod Genes," *Clan MacLeod Magazine*, no. 106, April 2008, pp. 495-506.
[7] "Clan MacLeod and Genetics: Past, Present and Future," *Clan MacLeod Magazine*, no. 100, April 2005, pp. 118-121.
[8] "Genetic Studies in MacLeod Cadet Families," *Clan MacLeod Magazine*, no. 102, April 2006, pp. 244-250.
[9] Donald MacKinnon and Alick Morrison, *The MacLeods: The Genealogy of a Clan [Sections Two and Three and Four]*, Clan MacLeod Society, Edinburgh: 1968, 1970, and 1974.
[10] International Society of Genetic Genealogy, ISOGG Wiki, http://www.isogg.org/wiki/New_DNA_projects, accessed 11/27/2012, 9:30 am.
[11] Alastair Moffat and James F. Wilson, *The Scots: A Genetic Journey.* Birlinn, Edinburgh: 2012, pp. 191-192.
[12] R-L165 Project, www.familytreedna.com/public/R-L165Project/default.aspx, accessed December 6, 2012.
[13] Personal Communication, E-mail from Lori McLeod Wilke to R-L165 Project participants, April 1, 2011.
[14] Personal Communication, E-mail from Lori McLeod Wilke to James B. MacLeod, November 20, 2012.
[15] Personal Communication, E-mail from James F. Wilson to Alexander C. McLeod, November 15, 2012.