

Appendix V – High Level Analysis

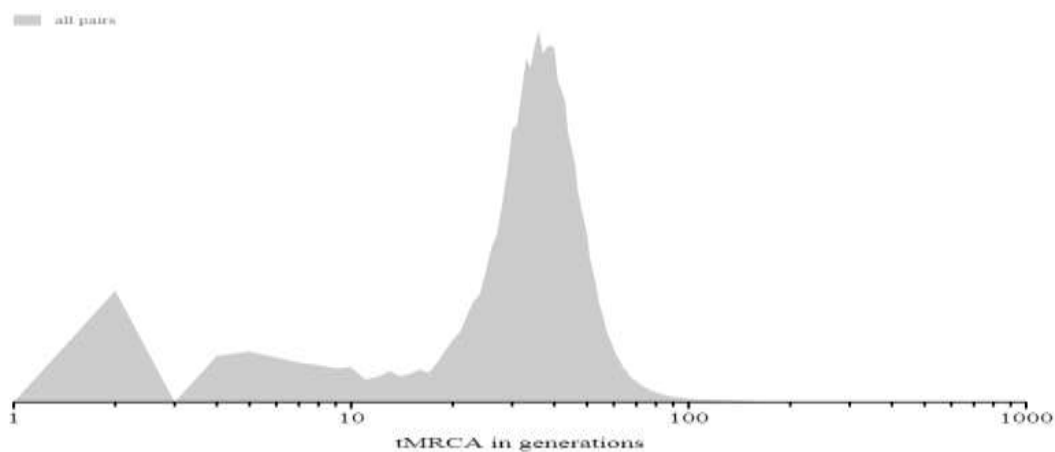
The conjunction of formal genealogy research and Y-DNA testing (Y-STR and Y-SNP) have been used to address the objectives detailed in the table below.

| Study Objectives | Y-STR testing | | | Y-SNP testing | |
|--|---------------|-------------------|----------------------|---------------|-------------|
| | Matching | Phylogenetic tree | Statistical analysis | Ad-hoc | Full/Big -Y |
| Approach used | | | | | |
| Identify Y-DNA connections between families | | | | | |
| a) within last 0-800 years, i.e. genealogical time | Yes | Yes | Yes | No | Yes |
| b) before genealogical time | No | Yes | Yes | Yes | Yes |
| Identify geographical origins before they arrived on the IOM | Yes | Yes | Yes | Yes | Yes |
| Evaluate timescale of arrival on the IOM from elsewhere | No | Yes | Yes | No | Yes |

On a family by family basis these objectives continue to be addressed and a fuller picture continues to be built up over time. With the ongoing advances in DNA testing science and the greater affordability of testing leading to an increase in the size of the tested population, a continuous improvement in the level of detail of knowledge of the male genetic tree is being gained. It is anticipated that this process will not be complete for the foreseeable future.

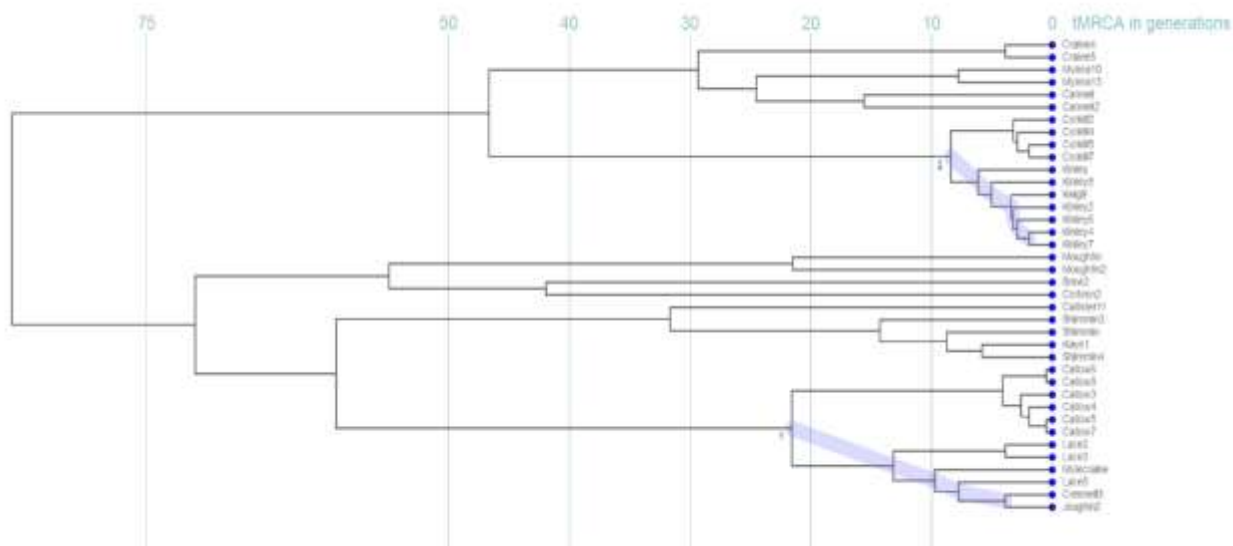
The coloured caps running along show where the analysis has identified individual clades or genetic families descended from one single founder within this population. See <http://www.scaledinnovation.com/gg/gg.html?rr=strclades>

Another view of this data shows the distribution of tMRCA²'s within this population confirming the 40 generations old figure.



Haplogroup I2 – The Mesolithic British Isles population

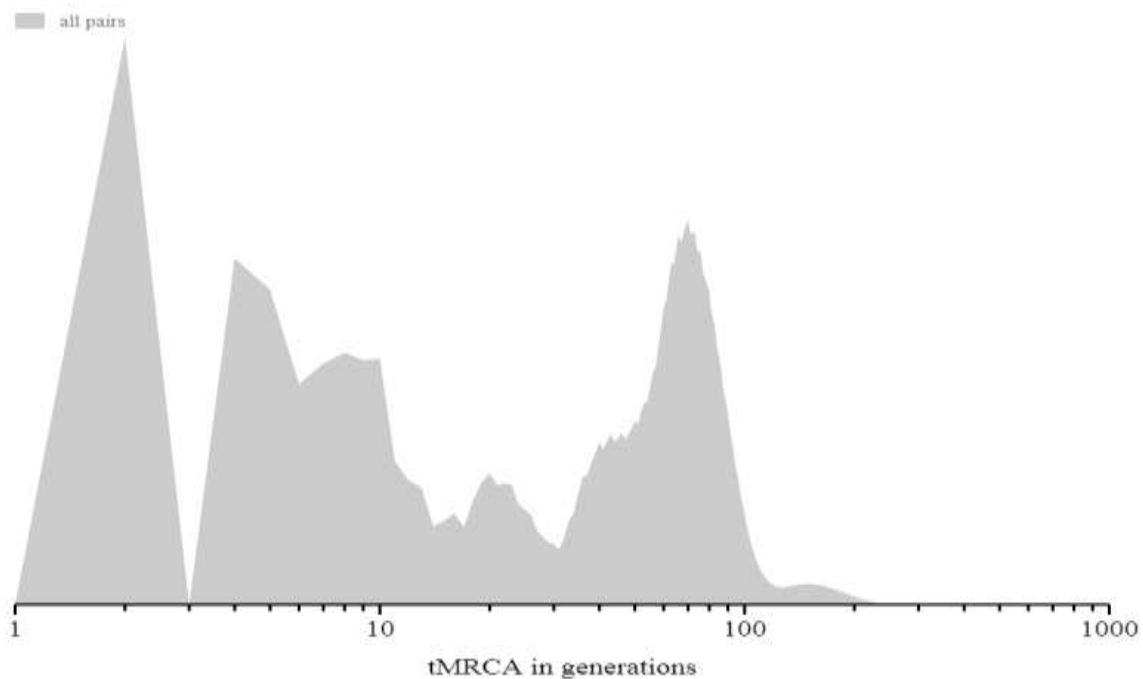
The analysis of this distance dendrogram shows that this sample of I2 men is relatively old with a founding date ca 80 generations ago, i.e. ca 2400 years ago. At ca 400BC for the period around which the first ancestor of this present-day population may have arrived, this small group represents the oldest surviving population on the Island.



We can see two distinct groups within this population as well as the identification of two distinct clades.

² tMRCA = Time to most recent common ancestor

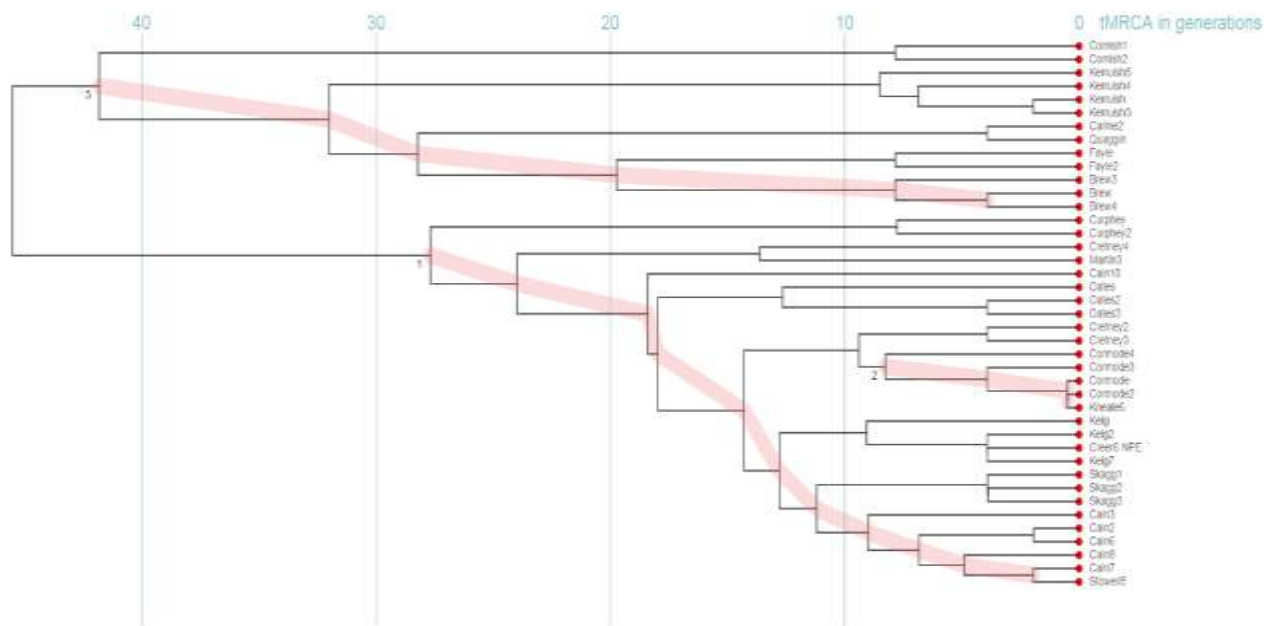
The distribution of tMRCA's shows a similar age profile.



This analysis indicates that there was a population bottleneck ca 20-30 generations ago. There being an expansion from ca 20 generations ago (600 years) until today and before then a decline from 80 generations ago.

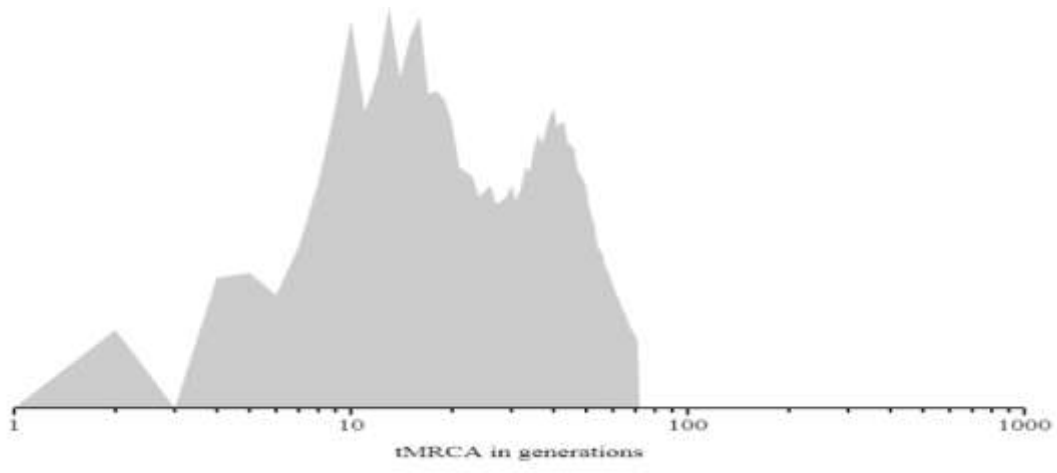
Haplogroup R1a – The second N European/Scandinavian population

This population of Manx families shows a very similar picture to that of the other Scandinavian origin group from Haplogroup I1



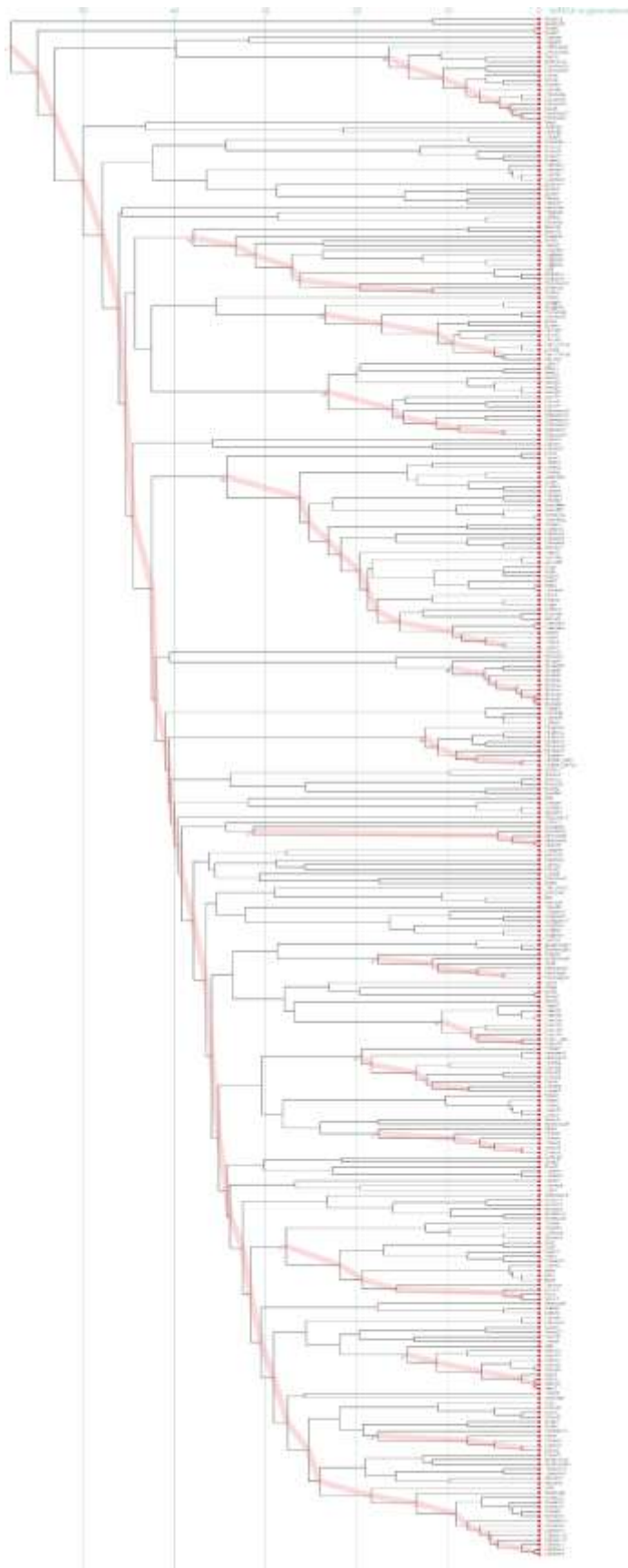
Again, this group is around 40 generations old (ca 1200 years) putting the arrival of this group of Norsemen on the Island at around 800-900AD in line with what the history books tell us. The dendrogram shows two major clades within this population. The first (upper) clade has an older founding date than the second, indicating that they were from the earliest groups of occupying Scandinavians, arriving as mentioned above, around 800-900AD. The second, larger, clade is that of the group of Manx families that are believed possibly to have descended from the family of the early Manx King Godfred Crovan. The calculated founding age of this clade at ca 28 generations old is consistent with that theory.

The analysis of the tMRCA profile confirms this picture, namely the earliest age of the group at ca 40 generations old and containing two distinct clades, the second occurring sometime after the first.



Haplogroup R1b – The predominant male (Celtic) haplogroup

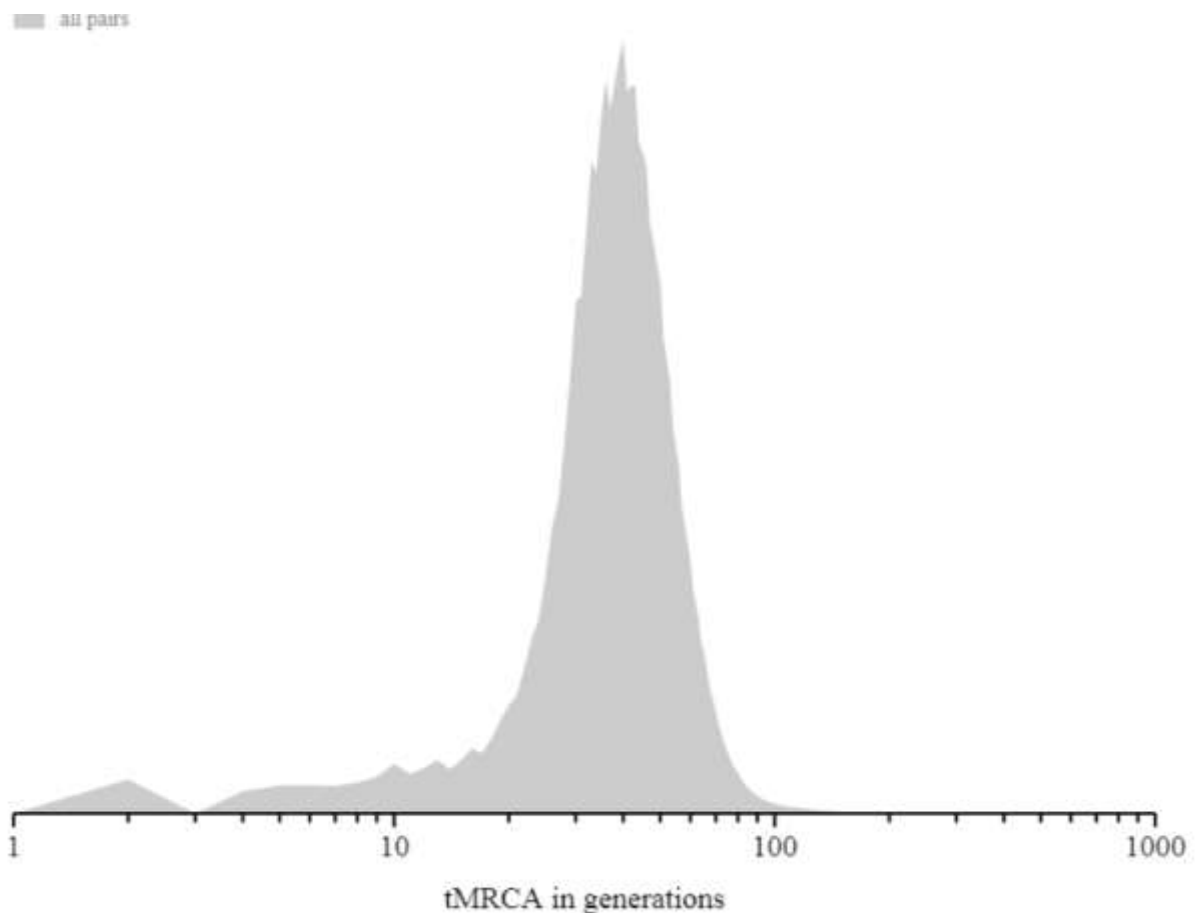
This population of Manx families is the largest in the study and the dendrogram the most complex.



The founding age of this population is around 58 generations ago or ca 1700 years ago or 300AD. This indicates that some of these R1b families are the descendants of some more of the earliest surviving male lines on the Island. Furthermore, as we know that family names became hereditary and permanent between 1050-1300AD, then we can say that the majority (at least) of these families adopted their family names on the Island.

The complexity of the clade structure within the dendrogram is similar to that found on other R1b populations in the British Isles and suggests also a diffuse and gradual process of population movement into the Island over time. (In comparison to that seen in I1 and R1a when there was a clear period of Scandinavian occupation for example).

By contrast the tMRCA profile, perhaps because of the much larger sample size, is clearer.



The mean founding age of this population is ca 40 generations ago, ca 800AD, but with some male lines going back more than 2000 years ago.

Summary

This analysis provides proof of the overall picture that we would have expected from our knowledge of the history of the people of the Isle of Man.

The earliest traces are of the I2 Mesolithic population which must have first arrived around ca 2400 years ago (400BC) on the Island, followed by the increasingly dominant group of R1b men who started to arrive around 300AD.

Finally, and more recently, the wave of Scandinavian occupation and rule from 800-1200AD follows on and is clearly shown in the two significant populations of haplogroup R1a and I1 men who arrived and settled during this time.

Y-DNA Connections Between Families

It became obvious relatively early in the project that a number of families bearing different family names were in fact genetically related on the male line within comparatively recent times, Namely, they shared a common male ancestor who lived in the period before 1050AD approximately and before family names became hereditary. Perhaps with hindsight this feature might have been predictable, but nevertheless it came as a surprise once uncovered. The following section therefore discusses these previously unknown family connections in more detail.

The technique used to recreate the genetic family tree charts (phylogenetic trees) shown later, takes the differences between the Y-STR results of these men and the relative rate of mutations for the Y-STR markers by which they differ to identify genetic relationships and the timing of when common ancestors might have lived³.

Haplogroup I1

Haplogroup I1 in a current male population is indicative of having an earlier origin in Northern Europe and/or Scandinavia. In men with ancestry on the Isle of Man over the last 8-900 years we can conclude that most probably their immigrant male ancestor came from Scandinavia with the Viking and Norse-Gael invaders.

Caley, Coole and Leece

All of these Manx family male lines are classified as haplogroup I-M253>L22>L813>P109 and analysis indicates that they share a single common ancestor in the period 850-1000AD. Supporting the view that this patriarch arrived on the Island as a member of the Scandinavian occupation and settlement.

Cowley and Kneale

The Cowley male line and the two separate Kneale lines (Manx and Irish) found on the Island are all haplogroup I1 also. Analysis indicates that all three of these lines shared a common ancestor some 1500-2000 year ago, before their respective patriarchs arrived on the Isle of Man. The Irish Kneale line, genetically distinct from the Manx Kneales, arrived on the Isle of Man with a James McKneale who came from Ireland in the late 1700's.

Others

The Casement, Corkish, Kaighin, Karran, Kinrade, Lewin, Looney, Lowey and Mylroi male lines all are classified also as haplogroup I1, but the level of analysis is insufficient to determine any earlier connections between them.

³ The software used is an online utility (SAPP) developed and made available by Dave Vance. See <http://jdvtools.com/SAPP/>. The process used to produce the phylogenetic tree chart first of all calculates the genetic distances between a group of men, predicts a time until their most recent common male ancestor (TMRCA), then uses a neighbour-joining algorithm to construct a tree and then draws that tree as a chart.

Haplogroup I2

Haplogroup I2 is the oldest Y-haplogroup of any size in Europe and is associated with the indigenous hunter-gatherer population that colonised Europe after the Ice Age. The surviving I2 in the British Isles however is a very old and diverse Mesolithic population and is the third largest population there after R1b and I1.

Corkill and Kinley

These two male lines are classified as I-M223>L161>PF4135>Y12072>A11115 and share a common male ancestor around 1300AD, before hereditary names. This male line probably came from the Cork area of Ireland to the Isle of Man.

Others

The Callow, Cannell, Craine, Moughtin and Shimmin male lines are all early British Isles origin haplogroup I2 lines, but with no obvious recent connections.

Haplogroup R1a

Haplogroup R1a in a current male population is indicative of having an earlier origin in Northern Europe. This designation in a Manxman almost certainly indicates that his ancestor came to the Isle of Man from Scandinavia and who must have arrived on the Island as part of the Scandinavian rule around 900-1250AD.

Cain (S), Cormode, Cretney, Curphey, Keig (N) and Oates

This group of families are the largest cluster found to have all been descended from one single man. The deep analysis of their Y-DNA results indicates that their common patriarch was a Norwegian Viking and there is a growing belief that these male lines all may well descend from the family of Godred Crovan, King of Mann 1079-1098. More research is ongoing. See here: <http://www.manxdna.co.uk/Manx%20Kings.pdf>

Brew and Fayle

The patriarch of the Brew and Fayle male lines was another Norwegian Viking who came to the Isle of Man during the period of Scandinavian rule. Both Manx families originated on the north of the Island and are categorised as haplotype R-M512>Z1983>CTS8277.

Haplogroup R1b

Haplogroup R1b is the dominant male genetic haplogroup in the British Isles and it proves to be similarly so for the Isle of Man, but at a lower level than in the neighbouring areas. It is commonly presented as signifying an earlier Celtic origin. The patterns of early population movement into the Isle of Man from surrounding regions were much more diffuse in number and timing than those, for example, from Scandinavia, and so where common ancestors for various R1b male lines have been identified, they generally occurred earlier and before the family lived on the Isle of Man.

[Caine \(Lonan\), Clucas, Howland and Quine \(Santon\)](#)

The four male lines all show a distinctive Y-DNA signature which indicates they belong to a genetic group called the Little Scottish Cluster⁴. All men showing this particular genetic pattern share a common male ancestor who lived in Scotland (perhaps near Stirling or Perth) about 800AD. It is possible that the common ancestor of the 4 Manx families however lived on the Isle of Man more recently than that time.

[Duggan, Faragher, Kennaugh and Quirk](#)

These four families show another distinctive Y-DNA signature known as “ROX2”⁵ again indicating that they all show one early common male ancestor. This common ancestor had 9 distinct descendant male genetic lines who are distributed around the British Isles and Northern Europe today, and so the place of origin of the common ancestor remains uncertain. The four Manx male lines all descend from different descendant branches who subsequently must have arrived separately on the Island.

[Callister, Costain, Crellin, Crennell, Cringle, Garrett, Keig \(S\), Kinnish, Radcliffe and Teare](#)

These male lines all show the Y-SNP R-M222 which is the most frequently occurring haplotype in Ireland (28% of the male population). In view of the proximity of the Isle of Man to Ireland and the known historical migration routes, it is assumed that these Manx R-M222 families all originally came from Ireland.

The Irish R-M222 common ancestor lived around 1500AD and so the Manx M222 patriarchs must have arrived on the Island after then. There is little evidence to show that these 10 Manx R-M222 male lines shared any common ancestors on the Isle of Man suggesting that their patriarchs all arrived separately from Ireland and probably at different times.

[Callister and Kissack](#)

We would expect from the genealogy that Callister/Collister and Kissack were two separate families. However, the Y-DNA analysis shows that the present-day members of these two male lines are very closely related. Based on the sample of Callister and Kissack men tested in the study so far, the Kissack men all appear to descend from a Callister man living around 1600AD. The genetic analysis indicates that the Callister male line goes back earlier in time than the Kissack men tested and so is the older line.

The only conclusion to draw from this analysis is that there must have been a non-

⁴ See <http://www.littlescottishcluster.com/>

⁵ See <https://sites.google.com/site/rox2cluster/>

paternal event, or a family name change for another reason which resulted in the present-day Kissack descendants possessing the same Y-DNA haplotype as the Callister male line. Hopefully in time another Kissack man may present himself to be tested and who is not directly related in the same way from the Callister line, to provide evidence of the earlier separate male line of the Kissacks.

[Christian, Cowell, Creer, Moore \(N\) and possibly Quark](#)

These families all possess the Y-SNP R-L21>DF41. This mutation is at least 4000 years old and so this group of male lines are not all closely related. Cowell, Moore (northside line) and possibly Quark share a common ancestor who most likely lived on the Island before hereditary names were adopted. Christian and Creer are older separate lines and possibly arrived on the Island from Scotland.

[Corrin, Kewin, Killey, Kinvig and Watterson](#)

These five families all show the Y-SNP R-L21>DF13>FGC5496 and it seems likely that they share a common ancestor who lived on the Isle of Man some time before 1200AD. Additionally within that group, the Kewin and Kinvig lines both share a common ancestor some 500 years ago, after the time during which new hereditary family names were adopted. The phylogenetic tree suggests that neither of the two families descended from the other as it would do in the case of a non-paternal event, but more that they were equal. The etymology of the two names Kinvig and Kewin (Mac John, Mac John beg) is similar enough for them perhaps to have been interchangeable in those early days and we know that nicknames were widely used in those times, before literacy was widespread and names could be written down. More research is needed.

[Clague and the Arderry Quine family](#)

These two families appear to share a common male ancestor around 1100-1200AD. Deeper testing for these men would provide more clarity on this picture. On balance it seems more likely that their common ancestor lived before family names became hereditary, than there being a more recent non-paternal event to change the picture.