# 4. Y-DNA Testing and Methodology Used

## 4.1 What Y-DNA Testing can show

The Y-chromosome is possessed uniquely by the male and is passed down largely unchanged from father to son, from one generation to the next. Thus Y-DNA tracks the male, name-bearing, family line. The basic Y-DNA test[5] used in this study provides a way of assessing the degree of relatedness between men living today who may or may not belong to the same genetic family. This can be done by comparing an individual's set of Y-STR marker results (e.g. a 37 digit haplotype) with those of other men, who have been tested in the same way, and whose haplotype results are available within public databases.

Thus expert analysis of haplotype data can:-

- Identify with a high level of confidence whether two men are related in a recent timeframe (i.e. whether they share a common ancestor some time in the recent past)
- Predict an approximate timescale for when their most recent common ancestor would have lived
- Predict approximately where that individual fits within the overall human male genetic family tree (haplogroup) – and hence form some view as to the possible route by whence the patriarch arrived on the Isle of Man.
- It should be noted that no other form of DNA testing (MtDNA or autosomal DNA) can provide such insights over the span of the last 1000-2000 years and thus the principal focus of the DNA testing in this particular study has been directed at men only.

A range of further, more sophisticated, Y-DNA tests (Y-STR 111, Y-SNP[6] and Next Generation Sequencing[7]) are also being used to try and pinpoint where an individual fits on the human genetic family tree and these are helpful in identifying connections between families and tribes before family names were adopted in a much more precise way. Such tests are more expensive however and are not supported from within the scope of the project's direct budget capability, although many participants have chosen to order such tests on their own behalf.

Over the course of time, increasingly more sophisticated testing and analysis tools are being developed, as, at the same time, our knowledge of the human male genetic tree is still very much incomplete, albeit our knowledge is expanding at a rapid rate. The branches of this genetic tree, and the early population movements associated with each position, or unique genetic marker, on the tree, can only be identified by the Y-DNA testing of men who possess such genetic markers. So, our knowledge only can be expanded by deeper and deeper testing of more and more men. This takes time and money and there is still a long way to go before the picture is sufficiently complete**. This means that long after the active phase of recruitment and testing within the Manx Y-DNA project is complete, then new knowledge of relevance to the project, will continue to be gained as a result of all the other research going on elsewhere and additional incremental testing on participants.**

## 4.2 Manx Y-DNA Study Methodology

### 4.2.1 Candidate Selection and Recruitment

Men bearing one of the ca 130 Manx family names were recruited to be tested and their results included in the study database. Evidence of their Manx ancestry was always sought before acceptance into the study to ensure confirmation of their Manx origins. In some cases such historical evidence was not available and the results of these candidates, whilst accepted into the study initially, were

[5] STR – Standard Tandem Repeats – the basic type of Y-DNA analysis. The greater the number of STR markers, the more definitive and useful the test. A minimum standard of a Y-37 marker test has been applied wherever possible within the project

[6] SNP – Single Nucleotide Polymorphism – a unique genetic marker

[7] Next Generation Sequencing tests such as the FTDNA Big Y test and the Full Genome test from FGC

periodically reviewed to evaluate whether they were genuinely of Manx origin or not, and if found not to be so, then their data was subsequently excluded.

Additionally, the Y-DNA results of other Manx men who had already been Y-DNA tested with other providers than FTDNA and whose haplotype results were already in the public domain were included in the study database.

A minimum of two men from each family were required for testing to eliminate the possibility of one man representing a false paternity line (NPE), thus allowing us to establish the male genetic fingerprint for that family. The genealogy information provided by each participant was used to ensure that the second test candidate for each same family name was not closely or knowingly related to the first candidate. Testing two men who were known to be closely related would not be cost effective.

If two men of Manx origin bearing the same family name were tested and did not match each other, then additional men with the same name, but non-close genealogy, would be recruited until such time their results matched with the earlier candidates' data. In this way the main Y-DNA signature for that family name could be validated. In such situations the non-matching results were usually considered to be as a result of a non-paternal event (NPE)[8] and in many cases the identity of the "intruding" genetic family could ultimately be determined.

Most Manx family names are considered in genealogy terms as being low-frequency names, i.e. the number of name-bearers worldwide is comparatively very low. For this reason, we would expect that all these Manx families would each be descended from one just male patriarch per family name, i.e. of single genetic origin. This is not the majority picture for example in larger geographical areas. In England for example, for family names where the number of name bearers per family is high, the root family name is one that might be based on the name of a place, or a profession (e.g. Smith) or of some physical attribute (e.g. Brown) – and so the family name has been adopted by unrelated men in different parts of the country at different times and in parallel. The result being that all these large families show multiple genetic origins on their male line and no one unique Y-DNA profile is possessed by all the men with that popular family name.

Surprisingly several Manx families appeared to be of multiple genetic origins. In such cases recruitment and testing continued until a sufficient number of men with that name had been tested and different Y-DNA signature could be attributed to different genealogical family lines or the difference could be clearly attributed to an early NPE.

### 4.2.2 Analysis Process

A systematic approach was used to analyse and interpret the Y-STR data for each participant, to detect which genetic Manx family he belonged to, to identify any early connections with other family groups and predict approximate timings for their common ancestors. In addition a prediction of the lowest identifiable Y-SNP would be made to establish their position on the human male genetic tree, which might also help identify where the patriarch for that family came from before they arrived on the Isle of Man. As more Y-STR data has been collected it has become possible to use additional analytical tools (namely phylogenetic trees and statistical analysis) to perform additional micro and macro analysis of the male population being tested.

[8] Where the male family genetic line has been broken in the past, i.e. through illegitimacy, adultery, adoption or name change and this has not been recorded.