We have been conducting DNA testing on the Y chromosome (males only) since December 2018, and as of May 2023 we have testers representing all but one of the Ayrshire branches we know exist today. (DNA results are not yet back from two further branches we consider likely part of the Ayrshire tree.)

From approximately the middle of 2019 we started considering the fast developing approach of SNP (Single Nucleotide Polymorphism) testing – which looks at mutations in single DNA component molecules. The results of this testing are that most of the branches of BICKETs, BICKETTs, BECKETs, and BECKETTs we have tested are all descended from a common ancestor, perhaps born around 1400.

SNP testing has given us astonishingly good results, and was a major improvement over the STR testing we had been doing previously. (See further description of STR testing in the paragraphs below.) SNP testing is more expensive than STR testing (i.e. requiring the Big Y 700 test). We started by experimenting with just a few testers. The initial results were very good, so we have now added detailed SNP testing for every single branch for which we have testers.

To explain further, there is one critical characteristic of SNP mutations, namely that they ‘rarely if ever’ back-mutate. The result is that SNP mutations give you a clear view of lineages because of the cumulative number of unique mutations as the branches diverge. [Note that individual molecule mutations can happen to any individual, so the same molecule mutation may therefore occur in totally unrelated trees. One of the many SNP mutations the Bicket(t)s show was previously named by a Chinese DNA organization, so it implies that some people tested by that organization have that same single molecule mutation. But they will not have the unique collection of shared SNP mutations that all tested Bicket(t)s and Becket(t)s have.]

SNP testing to determine the evolution of family trees (haplotrees) is literally quite new, with an ‘explosion’ of results since 2021. One term that has been used for it is ‘the SNP tsunami’. We are incredibly fortunate to have our work coincide with this research breakthrough.

Initially we used the 'traditional' (largely since about 2000) approach of testing for repeat sequences in the DNA called STRs (Simple Tandem Repeats). This test provides fairly strong evidence that people are related, but it does not show how they are related. The problem is in the nature of STR testing. Determining relationships using STR results is a case of educated (but not conclusive) analysis of how the earliest ancestor in a particular branch was likely related to the earliest ancestors in other branches, based on which branches show more common STR results for a limited number of STR locations (typically 37). This is a bit ‘iffy’ in any case because of the small number which can lead to 'false positives'. However, it becomes even more challenging because changes in the number of repeats is a reversible mutation, so you cannot be sure that what a current tester shows will accurately reflect what STR mutations his earlier ancestors had. To deal with that, STR testing relies on ‘triangulation’, i.e. getting multiple testers from a single branch, as distantly related as possible, to have a better estimate/assessment of what the STR results would have been for the earliest ancestor of that branch. This is a problem because we cannot find more testers who are not extremely closely related for many of our small branches. So the STR approach was not giving us much useful information, except the simple fact that our testers all appeared to be fairly closely related, but again we didn’t know what that relationship was.