

WhoDoYouThinkYouAre magazine – article for 27 August publication

DNA and the Declaration of Arbroath

The year was 1320, the place, Newbattle Abbey, a Cistercian Abbey a few miles from Edinburgh. Despite the overwhelming Scots victory over the English at the Battle of Bannockburn in 1314, the many years of conflict between the two countries continued. The Scots, led by King Robert the Bruce, sought peace and recognition of their place as an independent nation. Here, at Newbattle, a great council of the nobles and barons, deliberated on the content of a letter to be sent to Pope John XXII, asking him to encourage King Edward II of England to grant this recognition and reach a peace agreement. Some weeks later, as a result of the council's decisions, the letter, expertly drafted by the Scots Chancery at Arbroath Abbey, was dispatched from there, dated 6 April 1320, in the name of the nobles, barons freeholders and the 'community of the realm of Scotland'. It has become known as the Declaration of Arbroath.

The Declaration of Arbroath Family History Project, run by the Genealogical Studies Postgraduate Programme within the Centre for Lifelong Learning, University of Strathclyde, and funded by the Foundation for Medieval Genealogy, marks the 700th anniversary of the Declaration.

The Project's aim is to throw light on the 'signatories' of the Declaration from a genealogical point of view. (The term 'signatories' is used in this context to indicate individuals who were either named in the document or attached their seal to it).

There are two strands to the Project – the documentary strand, researching the 'signatories' and their families and the genetic genealogy strand. The first of these is based on the work of Postgraduate Diploma students and the second on work by staff with some input from students.

Each of the students was set the task of researching two of the 'signatories' and then creating a brief biography, a four generation genealogical chart and providing details and images of coats of arms. The result is the creation of a major resource, which forms a foundation for further research. This includes information on all 48 of the 'signatories', 39 of whom are named in the document and another 9 not named, but whose seals are attached.

Students were not expected to access original primary sources from the period, due to the challenges of reading such documents in unfamiliar scripts and in medieval Latin, however they were required to use authoritative secondary sources with the possibility of also accessing printed versions of some primary sources. The major secondary sources used included the Oxford Dictionary of National Biography, The Scots peerage, Cawley's Medieval lands, The People of Medieval Scotland (PoMS) website and histories of individual families. These all to some extent reference primary sources, the content of which can in some cases be accessed online. The PoMS website in particular is an excellent source of data from original primary sources, consisting of a database of people of Scotland between 1093 and 1371. One of the valuable primary sources are the relevant volumes of the Calendars of documents relating to Scotland, which in total number five volumes covering 1105 to 1516 and are available online on the Internet Archive.

The second strand of the research, genetic genealogy, involved the use of two types of DNA testing, Y chromosome testing and autosomal testing. This research was undertaken mainly by staff with

some input from students and collaboration with various DNA surname project administrators. For investigating surnames, the primary type of test is the Y-chromosome test. The Y-chromosome is only carried by men. A male inherits his Y-chromosome from his father, who in turn inherited it from his father and so forth back in time. Over time small copy errors occur in the Y-chromosome that can be measured by genealogical tests.

The methodology employed in the project involved identifying men documented as having an unbroken male line pedigree going back to one of the 'signatories'. Once identified they were invited to take a 37 marker Y-DNA test and their test results compared to others within the Family Tree DNA database. In the majority of cases they matched other test takers who bore the same surname. The 37 marker test is only an introductory test, so more refined testing was then undertaken to identify when the matching test takers shared a common ancestor with the documented test takers. This was achieved by testing for SNP markers (see explanation in boxout) using FTDNA's Big Y-700 test.

SNPs can be used to identify when surviving male lines diverged from each other as SNPs can be dated and placed in chronological order. This can be achieved by looking for SNP markers that are not carried by other surviving male line descents. For example, if only one descendant line carries a particular SNP marker and the others do not, the founder of the line is known as the SNP Progenitor. In other words, the copy-error must have occurred in him. All his male descendants carry the marker and so belong to his branch of the family or Clan.

A copy-error on the Y-chromosome within the portions sequenced by the Big Y-700 test are calculated to occur on average every 90 years (82-98 years). A positive outcome from identifying SNP Progenitors is that the statistically based model of SNP dating can be improved and refined. In the future, the discovery of SNPs that indicate branching, the more accurate dating of SNPs and the identification of SNP Progenitors will benefit those whose genealogy halts due to lack of documentary evidence. Therefore, opportunity now exists to connect a brick walled lineage to a medieval genealogy beyond reasonable doubt.

This is the methodology which has been used in the Project, resulting in a number of significant conclusions relating to a number of the families of the 'signatories', in particular the Boyd, Dunbar, Seton and Stewart families. Two examples can be seen in the Case studies included in this article.

A report on the Project will appear later in the year and further articles are also projected. It is hoped that the Project Exhibition, originally planned for this year, will be presented at several venues including Arbroath Abbey, at some point next year. The Exhibition will feature displays on sixteen of the 'signatories' and their families as well as information on the findings of the genetic genealogy strand relating to several of the families studied. Supplementary material on the rest of the 'signatories' will also be available.

Progressing with your research (step-by-step)

For those who have taken a test with Family Tree DNA and login to their account, here are a few pointers to help you progress with your research.

Y-DNA Matches – this link will display the test takers you match closely through STR testing. Have a look to see if there is a predominant surname amongst your matches, since this may be different from your own surname. If not, there could be a number of reasons for this. Verifying your genetic surname is helpful in suggesting which DNA surname project you should join.

Y-DNA Haplotree & SNPs – this shows the position in FTDNA’s haplotree of the current most recent (terminal) SNP, which will be either: a backbone SNP test undertaken by FTDNA as part of your STR test or tested positive as a result of any SNP testing you have done. A haplotree is a family tree based on known SNPs rather than on named ancestors.

Join a DNA surname project and relevant haplogroup project - compare results with members of the project who may not show up as close matches on your Matches page and most importantly seek advice from project administrators on upgrading to a 37 or 111 marker STR test and SNP testing. To avoid wasting money, do not order SNP packs without the advice of project administrators.

Proceed with further testing – following advice from project administrators and/or based on a prediction from a haplogroup predictor such as NEVGEN. This should progress to SNP testing via ordering a single SNP (if available); SNP packs or NGS testing. Since NGS testing can discover new SNPs, it is an investment for the future as over time, new test takers may match on your test result.

Big Y Block tree –only available to those who have taken a Big Y test, showing the position in FTDNA’s haplotree of their current most recent (terminal) SNP and also test takers who match them on this and other related SNPs. The Big Y-700 test identifies SNP markers that define your subgroup and private variants, which may become family SNPs when others test and are found to share them.

Big Y Private Variants – by clicking on the Big Y Matches link and then selecting the Private Variants tab, you can view the variants which you carry but no other current test taker carries. At some future date a new test taker may be found carrying one or more of these variants and it will become a named variant (SNP). This shows the advantage of NGS testing in having the potential to discover distinct branch markers.

STRs

STRs (short tandem repeats) measure the number of times a sequence of genetic code is repeated at a specific location on the Y-chromosome. Common tests available are on 37 or 111 markers. As the values for these markers change over time they are useful for establishing the time frame when two men shared a common paternal ancestor. This is the type of test recommended for establishing male line relatedness in the last 400 to 500 years.

Pros – can often be indicative of your genetic family surname; may be suggestive of what haplogroup and subgroup you belong to

Cons – not stable markers; cannot define precisely when your most recent common ancestor with your matches lived

SNPs

A single nucleotide polymorphism (SNP) – pronounced ‘snip’ – is a mutation in one of the nucleotide bases that are the building blocks of our DNA code. Unlike STRs, SNPs are very stable over many generations. When a mutation does occur, it is carried indefinitely by descendants of the individual

in whom the SNP was formed, who is known as the 'SNP progenitor'. This makes them particularly useful in distinguishing one genetic lineage from another.

Over centuries and millennia, individuals and families accumulate a hierarchy of SNPs, so for example the section of the hierarchical string leading to Sir John Stewart of Bonkyl is:
Oldest > DF41>S775>L745>FGC34909>S781 < youngest.

Further SNPs more recently formed than S781 have been discovered in descendants. These more recent SNPs are only carried by a few individuals and define distinct Stewart lines.

SNP tests are available as single SNP tests, SNP packs or NGS testing such as Big Y-700. SNP packs only test a limited number of SNPs and in most cases they will be SNPs that were not formed recently.

Pros – stable markers; can usually define more accurately than STRs when your most recent common ancestor with your matches lived

Cons – require additional expense beyond STR testing

Case study: Ann Stewart Burns

Ann lives in Massachusetts, USA and had been researching her family history for many years, with a particular interest in her paternal line, the Stewarts. Documentary evidence took the research back to James Stewart, born around 1800 in Donegal, Ireland, but beyond that the family could not be traced. At this point Ann considered whether DNA testing could help in her quest for the earlier origins of the family.

Her brother Thomas Philip Stewart was happy to take a basic Y-DNA test and at the 67 STR marker level this shows 204 matches, of which 151 were Stewarts. Such a preponderance of the one surname was clear evidence that Thomas was genetically a Stewart, but was this of the line of the Ancient High Stewards of Scotland? The next step was to do some SNP testing and the results of a Big Y test from FTDNA showed that he carried the SNP Y14197.

Fortunately for Ann, as part of our research at the University, we had enlisted the participation of documented male line descendants of three sons of King Robert II, who all took a DNA test. From their results, we knew that the SNP Y14197 indicated descent from one of his illegitimate sons, Sir John Stewart, Sheriff of Bute (b ca 1360). This information bridged a gap of over 400 years in Ann's research. She may not be able to discover the ancestors from every generation of this period but now knows the identity of one specific ancestor from medieval times.

Case study - Martin Dunbar

Martin Dunbar lives in Glasgow and was prompted to look into his genealogy after taking an autosomal test in 2016. He had always assumed that his family had adopted the surname because an ancestor had lived on the lands of a titled Dunbar at some point in the past. Through documentary research, his earliest Dunbar ancestor was identified as Alexander Dunbar, born in 1775, a farmer from Alves in Morayshire.

Martin discovered that Family Tree DNA (FTDNA) had a Dunbar surname project so he took the introductory Y-DNA 37 marker test in 2017. The result revealed his Dunbar line belongs to haplogroup R-M269 which was formed approximately 13,300 years ago. At this level of testing,

Martin had over 140 matches who carried a host of different surnames: Dunbar, Tait, Cockburn, Harlan, Lawson, Croxford, Lanley and Brown. The 37 marker test was not sufficient to predict his Y-DNA subgroup or weed out false-positive matches.

To help clarify which matches were most relevant Martin upgraded to 111 markers, which weeded out some false-positive matches. The administrators of the Dunbar project were also able to confirm that he belonged to the main Dunbar lineage that is descended from Crinan the Thane (b ca 975).

In 2019 Martin took a Next Generation Sequencing test (NGS), Big Y-700, with FTDNA. It sequences large portions of the Y-chromosome and identifies SNP markers shared with other test takers and private variants that might become family markers when other relations test.

The results from the Big Y-700 test confirmed that Martin shares a common Dunbar ancestor with a group of Americans. They reputedly descend from a Robert Dunbar who was captured at the Battle of Dunbar in 1650 fighting against Oliver Cromwell, and deported to Boston for seven years forced labour. American Dunbar family lore has it that Robert was a member of the Dunbar of Durn family in Banffshire. The results suggested that Martin shares a common ancestor with the Americans shortly before the birth of Robert (b ca 1634).

The test results also revealed that Martin and the Americans shared a marker called FT29439 with Craig Dunbar a documented descendant of the Dunbar of Durn line. The Durn family descend from David Dunbar of Durriss born ca 1460.

The marker FT29439 can be identified as indicating descent from David Dunbar of Durriss. This can be deduced as two present day baronets with documented descents from Alexander Dunbar of Conzie and Kilbuyack (1455-1498) the brother of David Dunbar of Durriss have tested and they do not carry this marker.

"I still find myself astonished to think that there is an unbroken line of men with the Dunbar name, whose Y-DNA was passed down from father to son across umpteen generations, for the past 1,000 years." Martin Dunbar

Resources sidebar

Principal Y-DNA STR testing company

<https://www.familytreedna.com>

This is the only company providing a relational database, which is important for matching purposes.

DNA projects

<https://www.familytreedna.com/group-project-search>

Search here amongst the over 10,000 surname and geographical projects.

<https://learn.familytreedna.com/group-projects/haplogroup-project/>

DNA haplogroup projects - Search here for haplogroup and subclade projects when you login to your FTDNA account.

Cleary, John and McDonald, Iain. (2019) Projects. In: Holton, Graham S., ed. *Tracing your ancestors*

using DNA. Barnsley: Pen & Sword. pp.163-190.

Useful reading on the benefits of projects and how they work.

Companies offering NGS and other SNP tests

Family Tree DNA <https://www.familytreedna.com>

YSEQ <http://yseq.net/>

These are the principal companies offering these type of tests.

Haplotree & haplogroup predictor

Y-DNA haplotree

<https://www.familytreedna.com/public/y-dna-haplotree/A>

The largest and most up to date haplotree, a family tree based on known SNPs rather than on named ancestors.

Nevgen

<https://www.nevgen.org/>

Y-DNA Haplogroup Predictor. This tool requires that you have taken 67 marker test to predict a haplogroup and subclade.