Clan Donnachaidh DNA report – extracts from newsletters in 2008

There have been a number of significant developments recently, including the fact the project now has over 400 participants.

A particular welcome to all those who have returned their kits and received their results recently. Do consider uploading your results to Y search, which you can do via your personal page. This means that other researchers will be able to make use of them. This does not involve revealing any personal information but it will add to the general pool of genetic information that has benefited scientific researchers.

In particular would you note the next item.

EARLIEST ANCESTOR DISPLAYED IN THE RESULTS
We have taken advantage of a facility offered by Family Tree DNA to display the earliest ancestor on the website. This will help those who have been seeking information on the families behind the names. We would still like to have some brief family trees and family information but we will deal with this separately.

In some cases we have taken the liberty of adding information provided by participants.

We should be very grateful if other participants would insert the information. which will help both the project administrators and other researchers.

You can do this under User Preferences on your personal page. If you prefer, we can do it for you. In either case, would you give the **name of your earliest known ancestor with a date and place name**.

All results are much more meaningful when associated with a particular location. Some of the more recent participants are able to locate their ancestors in Scotland and this information would be extremely useful for the project administrators and very interesting for other participants.

MORE FAMILY GROUPS
Suddenly, cheeringly, family groups have started to blossom among names other than Duncan. The Duncans got off to a very good start because of systematic research carried out by Duncan families in the USA. Suddenly the Robertson close matches have expanded and there are more matches among the Reids and Roberts, and the McConnachie variants.

RENAMED FAMILY GROUPS
It has always been obvious that there were going to be a lot of family groups. The Robertsons are now up to Q, and we will probably get to the end of the alphabet fairly soon. Because of this, it has been decided to distinguish the family groups by two letters. So A has become AA, B has become AB and so on.

OXFORD GENETIC ATLAS PROJECT AND R1B RESULTS
A second consideration has been keeping similar sets of results together. We have now listed the groups by surname and haplogroup. Stephanie has also embarked on a system for the R1bs (for everyone other than the Duncans) that makes use of the classifications identified by Kevin Campbell's analysis of the R1b results in the Oxford Genetic Atlas Project (OGAP) [1]. The Oxford Genetic Atlas Project provided the basis of Professor Bryan Sykes' book *Blood of the Isles*[2] which analyses the genetic history of the British Isles. The Project data can be seen online[3].

Kevin Campbell assigned OGAP designations sequentially, in decreasing frequency of occurrence. These provide convenient subdivisions pending the establishment of family groups. OGAP designations have been added to some R1b classifications, indicated by O and a number indicating the frequency of the haplotype (thus O01 indicates the haplotype most frequently found in the Oxford Genetic Atlas survey, O02, the second most frequent, and so on).

The closely-matched family groups have been further distinguished by the addition of colour. The general R1b OGAP groups have no colour.

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[1] *Geographic Patterns of Haplogroup R1b in the British Isles*, Kevin D. Campbell, *Journal of Genetic Genealogy, Spring 2007*; http://www.jogg.info/31/campbell.pdf.
[2] *Blood of the Isles: exploring the genetic roots of our tribal history*, Bryan Sykes, 2006.
[3] http://www.bloodoftheisles.net/results.html.

Advantages

- The OGAP categorization gives an indication of the profile of the Clan Donnachaidh results. They cover a number of different categories but a regional bias becomes apparent.
- It is possible to compare participants' results with the geographic location of samples taken throughout Britain.
- Categories of results are kept together. The nine markers in the OGAP groups represent nine markers of the first 12 tested by Family Tree DNA – eight of these are markers that Family Tree DNA assesses as being less likely to mutate (DYS439 is evaluated as 'faster moving').
- It starts to give an indication of the potential number of different family groups.
- It helps in the assessment of the results: it is possible to assume with more confidence that a 12-marker match between results that are not recorded in the OGAP survey and thus fairly rare is a family match. (In the case of fairly common haplotypes and 11/12 matches we are currently taking a fairly cautious approach as to how participants might be related.)
- It shows the probability that participants will have high-resolution matches with a number of different surnames. Those in the first OGAP categories are much more likely to have high resolution matches with people with different surnames.

Disadvantage

- Results are listed by frequency rather than numerical sequence. However, exact OGAP matches (including family groups) are kept together.
- This may conceal inter-relationships between groups. However, in any case, this is not easy to assess without more information about family and geographical relationships.

As more data become available it may be possible and indeed necessary to regroup some results. Subclades will probably become much more important.

FREQUENCIES AND REGIONAL AFFINITIES OF SOME R1B HAPLOTYPES, AS ANALYSED IN THE JOURNAL OF GENETIC GENEALOGY, SPRING 2007, BASED ON THE OXFORD GENETIC ATLAS PROJECT

The list below is not exhaustive but is given here to explain one of the current classifications of Clan Donnachaidh results. If you have a reference such as O01 in your R1b group heading in the list of results, you will find some indication of what this means below. (O01 is an abbreviation of OGAP1, because it is not possible to use more characters in the headings in the results table.)

It will be noted that the Clan Donnachaidh results do not follow the order in which results are found in Britain. In particular the North-West Irish haplotype, OGAP8 (which includes the haplotype associated with Niall of the Nine Hostages) has occurred more frequently among Clan Donnachaidh members than in the British population sampled for the Oxford Genetic Atlas Project.

In some other ways the results reflect the general population pattern: the two most frequent results are the most common in the population at large and in the Clan Donnachaidh results. Variations are revealed when these haplotypes are expanded – a number of participants in particular groupings are apparently not closely related in the recent historical period.

The participants in the most frequently occurring groupings tend to have a number of high resolution matches with participants with different surnames.

- **The regional affinities have been calculated on the basis of sampling and do not constitute proof of individual family origins.**
- **Many of these results are found throughout Britain; only certain concentrations are mentioned below.**
- **The conclusions below may change in the light of further testing.**
- **It has also become apparent that some haplotypes are found in more than one subclade.**

Order of frequency of haplotype in Clan Donnachaidh	Frequency of haplotype in OGAP survey (OGAP1 = most frequent)	Regional affinities	393	390	19	391	388	439	389i	392	389ii
1	**OGAP1**	Widespread core haplotype (Atlantic Modal Haplotype)	13	24	14	11	12	12	13	13	16
2	**OGAP2**	Widespread core haplotype	13	24	14	10	12	12	13	13	16
3	**OGAP8**	North-West Irish haplotype	13	25	14	11	12	12	13	14	16
4	**OGAP4**	Ubiquitous across all areas of Scotland and exceptionally strong in Grampian, Tayside and Strathclyde. Also among the strongest haplotypes present in Argyll and the Hebrides.	13	24	14	10	12	12	13	13	17
5	**OGAP3**	Widespread core haplotype.	13	23	14	11	12	12	13	13	16
6	**OGAP5**	Very prevalent haplotype that shows up predominantly in Ireland.	13	24	14	11	12	12	14	13	16
7	**OGAP7**	Found in Tayside and Fife in particular.	13	23	14	10	12	12	13	13	16
7	**OGAP6**	Prominent in Argyll and the Hebrides.	13	24	14	11	12	12	13	13	17
8	**OGAP14**	In Scotland shows an affinity for Tayside and Fife.	13	24	14	11	12	12	12	13	16
9	**OGAP17**	Particularly strong in Northern England.	13	24	15	10	12	12	13	13	16
9	**OGAP19**	Strong correlation with Ireland and the Scottish Highlands.	13	25	14	11	12	12	13	13	17
10	**OGAP9**	Shows an affinity for the Northern Isles and the Borders.	13	24	15	11	12	12	13	13	16
10	**OGAP10**	Associations with Ireland and the Hebrides; supports the conclusion of a Mesolithic northern migration along the coast of Ireland.	13	25	14	11	12	12	13	13	16
10	**OGAP11**	Shows an affinity for the Northern Isles (Orkney and Shetland) and the Borders.	14	24	14	11	12	12	13	13	16
10	**OGAP12**	In Scotland shows an affinity for the Borders.	13	24	14	10	12	12	14	13	16
10	**OGAP20**	In Scotland shows an affinity for Tayside and Fife.	12	24	14	11	12	12	13	13	16

OTHER HAPLOGROUPS
The Haplogroup I results represent a smaller percentage so it is fairly easy to keep track of them at present. We have a very few results in Haplogroups E, G, J and R1a.

HAPLOGROUPS
(Tim explains the background to haplogroups)
Our interest in the use of genetics for genealogical purposes is driving this field of science with a lot of research and thus a lot of new information is being gained almost weekly. As I have said many times "we are active participants in a very exciting and dynamic field of science but the final book has not been written yet. There is no cookie-cutter chart to plug ourselves into and get an immediate answer". By providing our DNA sample, continuing our research, corresponding with our matches, and taking new tests we all are helping in the understanding of our joint human history and our own personal family story.

When we first take our DNA test we are within the first field of DNA research which is Genetic Genealogy but let's talk about the second part of using genetics for genealogical purposes. This second part is called anthro-genealogy. This is the name given to the study of our ancient genetic history (i.e., tens of thousands of years). It is population genetics working to unravel the genetic migration of man through time.

This field of study is very involved but highly interesting to a number of project participants. The connection between genetic genealogy and anthro-genealogy is the inferred Haplogroup that each man fits into when tested. This Haplogroup is the branch of the Y-Chromosome Phylogenetic Tree that each man fits into. In the simplest of terms you can only match men who are within your Haplogroup.

BUT…….HAPLOGROUPS ……How do I understand all of this?

This is not an uncommon question so do not feel alone in trying to understand this new field of science.

As with our family history research we present our family in a tree format i.e. with a root, trunk, major limbs, smaller and smaller branches, twigs and right on down to the leaves on the tree. Your Haplogroup is presented this same way. As stated above the Haplogroup designation represents the branch of the human tree that we each sit on. The convention for writing a Haplogroup designation is with alternating letters and numbers i.e., R1b1b2h. Each one of these levels represents the branching of our specific male line through time on our ancestral family tree. Each level of the Haplogroup designation represents a Single Nucleotide Polymorphism (SNP) mutation that happen to a specific male who then passes that mutation on down his male line i.e. the nucleotide "G" changes to a "T" or the nucleotide "C" changes to an "A" or vice versa.

It is important to remember that this Haplogroup designation is being updated over time as new data (new SNPs) are learned from the genetic research. The important aspect of this is that each level (called a clade) of the Haplogroup is bringing us closer to our genetic genealogy time period; i.e. the man that had the R1b1c10 (R1b1b2h) SNP is closer to us in time than the man with the R1b1 or R1b mutation. Last month the Hammer et al. 2008 Y-Chromosome Phylogenetic Tree was released showing many updates and adjustments to the previous Phylogenetic Tree. Family Tree DNA has updated each participant's Haplogroup designation, both inferred and confirmed, to bring everybody into line with the new designations.

In the world of Haplogroups there are additional tests that can be taken. The first test is called the 'Backbone SNP' test which will confirm the inferred Haplogroup made from your STR haplotype when you first tested.

The next test is the 'Deep Clade SNP' test which will look for the additional known SNPs that you may have within your Haplogroup. This is the level that is changing rapidly as new SNPs are being discovered.

My feeling is that with all the progress being made in locating new SNPs we will one day bring them into our current time period. We will one day have regional SNPs and family specific SNPs. This will be the definitive data that connects family lines together.

RENAMING OF THE R1B SUBCLADES – FAMILY TREE DNA OFFERS TESTS FOR NEWLY IDENTIFIED R1B SUBCLADE SNP MARKERS

We shall have to get used to the new names for the R1b subclades, which have come into effect following publication in April of a paper by Dr Hammer of the University of Arizona and other researchers.

R1b subclades identified in the Clan Donnachaidh DNA project	
R1b1c	R1b1b2*
R1b1c6	R1b1b2d
R1b1c7	R1b1b2e
R1b1c9	R1b1b2g
R1b1c10	R1b1b2h

We not only have new names: new subclades have been identified (R1b1b2g and R1b1b2h) and tests have been offered for them. Family Tree DNA has entered messages on the home pages of participants who have taken an SNP test but who have not as yet been identified as belonging to a known subclade and are thus currently classified as R1b1b2 (formerly R1b1c), offering tests for the two newly identified SNP markers. The result R1b1b2* (meaning no subclade markers have been found) is most frequent in the Iberian peninsula and Ireland. Further east, there is an increasing frequency of various subclades. Family Tree DNA has estimated that in general 40% of participants are likely to be R1b1b2g or R1b1b2h. Many Clan Donnachaidh participants may well remain in the as yet undifferentiated R1b1b2 category common among those with Celtic origins.

However, there are some distinguishing subclades found among the Clan Donnachaidh results. Up to now we have had R1b1b2d (which is quite rare outside the Basque country) and R1b1b2e, which is associated with north-west Ireland and is also found in Scotland. These results are identifiers of the families in question. One Donnachie, one Duncan and one Robertson have now been identified as belonging to subclade R1b1b2h. One Stark and one Robertson have now been identified as belonging to subclade R1b1b2g. All the people concerned are in family groups. This indicates that their matches also belong to these subclades. A slight question mark hangs over the Donnachies, where one person has been tested for only 12 markers. As the surname is not one of the most numerous, the assumption at present is that the Donnachies who have been tested are related. There is also a slight question over the Robertson who is R1b1b2h. He is in the sixth R1b Oxford Genetic Atlas Project category (OGAP6). The question is whether the other four Robertson participants who are OGAP 6 – his close matches and two others – are also R1b1b2h. It is hoped that more information on this question will be coming shortly.

It has recently been reported that a new SNP marker has been discovered, which appears to divide the R1b group. R1b1b2e and R1b1b2h are apparently in one subgroup of R1b while R1b1b2g is in another. Ethnoancestry is offering testing for the new marker. Family Tree DNA has not as yet done so.

Before very long other SNPs will probably be identified that will further distinguish particular groups.

The interest of a subclade test is that it distinguishes the genetic profile of a family group. Members of one subclade cannot be closely related to members of another, even if their haplotypes look similar.

We are grateful to everyone who took a subclade test as the result provides additional information for the project, whether it reveals a subclade or not.

UNUSUAL MUTATIONS

Any marker can mutate at any time, though some much less frequently than others. The DYS references in red indicate those markers that been observed to mutate more often. However, we have at least two cases of known relatives (one Stark family and one Robertson family) where there has been an unusual mutation on DYS 390. There is nothing untoward about this – it is the law of averages.

We have the advantage in these families of knowing when the mutation occurred. When mutations such as these have occurred in the past it can be much more difficult to work out how families may be related. It may be that some of the participants grouped separately are related within a meaningful timeframe – but we need the missing pieces of the jigsaw.

THE GENERAL FUND
As Tim has already announced, the general fund has been set up using the facility provided by Family Tree DNA. Donations may be made to contribute towards further testing and support the project.

Very many thanks to those who have already generously contributed. The next objective should be to expand testing in Scotland or among men with known ancestry in Scotland.

HAVING TEST SAMPLES IN RESERVE
The last issue of *Facts and Genes* (published by Family Tree DNA) recommended that for the last living males in a direct male line additional tests should be selected conservatively or you should consider a second test kit of 12 markers only, to store an additional three vials of the sample. Samples are stored for 25 years. However, some other participants may be interested to know that a recent request for a third test resulted in Family Tree DNA asking for a new sample.

THE GENEALOGY OF THE CHIEFS OF CLAN DONNACHAIDH AND THE CADET BRANCHES
Gordon MacGregor's research has been published on the Clan Donnachaidh International site in the DNA section. Not only has Gordon revised the history of the early chiefs and found the documentary link to the Celtic Earls of Atholl, he has brought the lineages of the junior branches down to the 18th and 19th centuries, within reach of standard genealogical research.

This is of interest to a small number of current Robertson DNA participants. At present they all know who they are (apart from one case where there has been some difficulty with e-mail contact).

Most of these descendants left Perthshire and may now be found in other parts of Britain. Several families went to North America. This family has the somewhat unusual situation that almost all the senior lines have died out, leaving only junior branches. Gordon MacGregor would be interested in hearing from anyone who has a documented line of descent from identified descendants of the Robertson cadet lines. You may know Robertsons who have been researching their ancestry who might be interested.

It should be noted that there are very many Robertsons, perhaps the majority, who are not descended from the chiefs in the male line. This new research appears to confirm the chiefs' descent from Crinan of Dunkeld and thus Niall of the Nine Hostages. The haplotype is not identical to Family Tree DNA's Niall haplotype but it is close. This suggests a male-line relationship with participants who have a Niall match – various surnames – but this almost certainly goes back many hundreds of years, well before the adoption of surnames.

WHY ARE PARTICIPANTS GENERALLY NOT CLOSELY RELATED IN THE MALE LINE?
Studies of the clan system have long recognized that the great majority of clansmen in most clans cannot possibly have had a blood tie with their chief in the male line and thus probably not with each other. Cadets of chiefly families had ties of kinship that bound them to him. Other kindreds and individuals attached themselves and adopted the clan name. Many clans comprised several different surnames.

There were other kinds of kinship than blood kinship. Kinship created through marriage, fictive kinship, the relationship formed through fosterage (very important in Highland society), local association, feudalism, bonding or military and political cooperation. These relationships could at times be as close as a blood relationship.

On an individual level, clan members would be known by their patronymic, a name that identified people through their ancestors, usually the father and grandfather (e.g. Iain mac Dhomhnaill mhic Aonghuis – John son of Donald son of Angus), or by the place in which they lived or place of origin. This individual identification was used within the community of which they were a part; the collective name was used to identify members of the clan outside the Gaelic community.

WARLORDS IN THE FAMILY
Professor Sykes comments in Blood of the Isles on the similarity between many of the Y chromosome haplotypes in the Oxford Genetic Atlas Project Survey (these are 10-marker haplotypes).

'There are very large clusters of very similar chromosomes in one location, and not in others. For instance, the Ui Neill chromosome reaches a very high frequency in north-west Ireland but is rare elsewhere, and the Somerled chromosome is common in the Highlands and the Hebrides, but virtually unknown elsewhere – unless carried by a member of Clan Donald or Clan Dugall.

'This is the 'Genghis effect' and it is not confined to the Mongol Empire. In the Isles very large numbers of men, perhaps all of them in [Haplogroup R1b] are descended from only a few genetically successful ancestors. … One of the genetic consequences of the rise of powerful men is that they monopolize the women and have more children.'

Although most participants are not descended in the male line from Stout Duncan, accounted the first chief of Clan Donnachaidh, many come into various broad general genetic groupings, identified by the OGAP numbers mentioned above.

Those in the first OGAP groups have high-resolution matches with a number of other people. High-resolution matches are also found in some of the Haplogroup I categories. Those with a Niall of the Nine Hostages match can identify the name of the patriarch. A number of other participants will also have a shared descent from some patriarch in antiquity. The name may not be known, but lurking in many participants' ancestry is a domineering warlord.

Because of the very large number of people with a Niall of the Nine Hostages match or who belong to the associated North-West Irish group, it is not possible to assume that participants in this category (we have participants in this category from several of the clan surnames) are related to the chief through a recent ancestor associated with Clan Donnachaidh, though they share a more remote ancestor.

MITOCHONDRIAL DNA

We have said very little on the subject of mitochondrial DNA though we have mitochondrial DNA results from about 50 participants. One reason is that the participants are spread all over the world and their results do not represent the pattern in a particular region. With the worldwide spread of the Clan Donnachaidh project, we have participants whose mitochondrial DNA represents haplogroups not usually found in Britain. We would encourage participants who have taken mitochondrial DNA tests to join a project relating to their particular haplogroup as well as the Clan Donnachaidh project.

There is a great deal of interest in mitochondrial DNA results in identifying ancient settlement patterns – including differences in settlement history through male and female lines. The female settlement pattern in certain regions is sometimes older than that of the male settlement pattern, as groups of migrant men have arrived and established their domination over the existing population.

Mitochondrial DNA has been used in some high-profile cases of historical identification. The remains of the Russian Imperial family, discovered in 1991, were identified through mitochondrial DNA tests. New developments concerning the Russian imperial family are reported in 'DNA in the news' (see below).

Those who have taken a mitochondrial DNA test may be interested to know the Tsar was in Haplogroup T[4] (Tara's clan for those who have read Professor Sykes's book).

Several tests had to be carried out to confirm Tsar Nicholas II's identity because his DNA revealed a very rare state known as heteroplasmy, where a new mutation was part way to becoming established. His DNA was compared with that of a living cousin.

mtDNA Haplogroup of Tsar Nicholas II: **T**	**mtDNA Haplogroup of Count Trubetskoy:** **T**
mtDNA Sequence of Tsar Nicholas II: 16126C, 16169Y*, 16294T, 16296T	**mtDNA Sequence of Count Trubetskoy:** 16126C, 16169Y, 16294T, 16296T

The Tsarina was identified when her DNA was found to match that of her great-nephew, Prince Philip, Duke of Edinburgh. The Tsarina was in Haplogroup H, which is the most widespread in Western Europe (Helena for those interested in the seven daughters of Eve).

mtDNA Haplogroup of Tsarina Alexandra: **H**	**mtDNA Haplogroup of Prince Philip:** **H**
mtDNA Sequence of Tsarina Alexandra: 16111T, 16357G, 16263G, 16315.1C	**mtDNA Sequence of Prince Philip:** 16111T, 16357G, 16263G, 16315.1C

[4] These results were obtained from:
http://www.dnaancestryproject.com/ydna_intro_famous.php?id=tzarnicholas&typ=m

None of our participants matches the Tsar or Tsarina – some of the Haplogroup T participants come closest.

Haplogroup H participants will be pleased to know that Marie-Antoinette was also in this group. Her DNA came into the news when the heart of a child, identified as that of her son Louis XVII, was tested and the result compared with DNA extracted from locks of Marie Antoinette's hair and results from two living relatives. During the 19th century a number of men appeared claiming to be Louis XVII. These claimants said Louis had not died in prison in 1795 at the age of 10; he had escaped and another boy had been put in his place. However, during the autopsy on the child who had died in 1795, the heart had been removed. In the 20th century, DNA testing on this heart identified it as matching the DNA in his mother's hair. It was finally proved that Louis XVII did not survive to adulthood.

One advantage for royalty is that it is often possible to trace direct female-line ancestry back many centuries, whereas most people have traced theirs back only a few generations. A number of people can probably trace their direct female line back to their great-great-great-grandmother and may not get much further.

Even though it may not be possible to travel any further back to antiquity, it may be possible to work out something about the female lineage concerned. The relatively uncommon (in Britain) mtDNA haplogroup U4 has associations with Scandinavia. The present writer's great-great-great-grandmother died in Cambridgeshire but had a surname associated with nearby Norfolk, which was strongly affected by the Viking incursions of the 9th and 10th centuries. There is thus some likelihood that she represents one of the infrequent traces in Britain of Viking women settlers.

DNA IN THE NEWS

The Tsarevich and his sister

In 1991 the remains of nine bodies were found in a shallow grave just outside Ekaterinburg in the Russian Urals by Russian researchers who had been conducting a private investigation on the basis of accounts left by members of the execution squad that had killed Nicholas II, the last Tsar of Russia, his wife, five children and four servants around 2 a.m. on 17 July 1918. The bodies were of four men and five women, three of them young.

Official investigations then began. By means of mitochondrial DNA tests comparing the DNA of the remains with that of living relatives, one of the men was identified as Nicholas II and one of the older women as his wife, the Tsarina Alexandra.

The three younger women whose DNA matched that of the Tsarina were identified as three of her daughters. There was no controversy about the identity of one of them: the eldest daughter, the Grand Duchess Olga (22). There was a difference of opinion between Russian researchers and some American experts about the identity of the other two, which according to particular theories were variously identified as the Grand Duchess Tatiana (21), the Grand Duchess Maria (19) or the Grand Duchess Anastasia (17), with most controversy over whether the body of Maria or Anastasia was missing. The DNA result was of course identical. The Russians eventually identified the three bodies as Olga, Tatiana and Anastasia and these names were placed on the respective coffins, but American experts have questioned this.

The fact that the bodies of one daughter and the youngest child, the Tsarevich Alexei (who was not quite 14 at the time of the killings), were missing gave some comfort to those who believed that one of the Grand Duchesses and the Tsarevich had escaped, particularly supporters of Anna Anderson, whose claim to be the Grand Duchess Anastasia had over the years inspired much publicity and several books and films. The convictions of some of her supporters were so strong that their loyalty even survived reports of tests on a hospital tissue sample taken from Anna Anderson (who had died in 1984), which revealed that her DNA did not match that of the Duke of Edinburgh but did match that of a great-nephew of Franziska Schanzkowska, a disturbed young woman who had disappeared in Berlin in 1920 shortly before Anna Anderson appeared in Berlin. A detective investigating Anna Anderson's case in the 1920s had identified her as Franziska. DNA testing proved him right, though some of Anna's supporters continued to argue in her favour, especially as two Romanov bodies were missing from the grave found in 1991. Some Russian Orthodox Church leaders were also suspicious and would not officially recognize the 1991 remains as those of the imperial family, although President Yeltsin attended the funeral in St Petersburg in 1998.

In the meantime, investigations have been quietly continuing in Russia. The accounts left by the execution squad stated that they had first tried to dispose of the bodies by burning them. They had started with the smallest body, the Tsarevich, and that of one of his sisters. When they found that that the fire did not consume everything they had buried the remaining bodies. In June 2007 the Deputy Director of the Regional Centre for the Preservation of Monuments, a local historian and a member of the Mountain Shield military historical club decided to resume the search for the missing bodies, using more detailed information that had

been discovered. The SEARCH Foundation – the Scientific Expedition to Account for the Romanov Children – was set up.

They began with reconnaissance methods in areas that had not been searched and on 29 July located a pit containing coals, bone remains, nails and fragments from a ceramic vessel. An official team of scientific, archaeological and historical experts moved in. An archaeological dig was carried out and two pits were uncovered containing burned bone remains, nails, fragments of ceramic vessels and bullets.

The SEARCH press release of 24 August 2007 states: 'Initial anthropological analysis determined that the bone remains were human, subjected to varying forms of destruction – including burning. The bones belong to two young individuals – a young man between the ages of 10-13 years, and a young woman about 18-23.' It was also reported that the ceramic vessel fragments were identical to those found in the burial site found in 1991, which had contained sulphuric acid.

DNA tests will be carried out on the remains (again with the participation of the Duke of Edinburgh). The boy's DNA will also be tested for haemophilia. The Tsarevich's sufferings from this incurable hereditary malady led to his mother's over-dependence on Rasputin, whose hypnotic, calming powers were able to stop the child's bleeding. Rasputin's fatal influence was one of the factors that brought down the Romanov dynasty.

The SEARCH press release concludes: 'The location, area, bone remains, bullets, ceramics, iron fasteners, as well as the result from the anthropological analysis, allows one to come to the conclusion that the place [with] remains of members of the Romanov Imperial Family, Tsarevich Alexei and his sister, Grand Duchess Maria, concealed by revolutionaries in 1918, has been found.'

The SEARCH website in English (http://www.searchfoundationinc.org/index.html)
contains not only the press release but some interesting background information on the earlier investigation, including explanations of the DNA and forensic evidence and conclusions.

There are some fairly detailed accounts of the earlier investigation. The website also takes on some of the issues raised by sceptics and reviews the DNA tests. There is a full section headed 'Anastasia'. This is not about Anna Anderson but the controversy concerning the identification of the third daughter found in 1991. Perhaps now the fourth daughter has apparently been found, it will be possible to reach a generally satisfactory conclusion as to which girl is which.

Blue eyes originated with one person

More than 99.5% of blue-eyed people who volunteered to have their DNA analysed for this survey have the same tiny mutation in the gene that determines the colour of the iris. This shows that the mutation originated with just one person who became the ancestor of all subsequent people in the world with blue eyes.

These are the findings of Professor Hans Eiberg and colleagues at the University of Copenhagen. They are not sure when the mutation occurred but think from other evidence that it probably arose about 10 000 years ago when there was a rapid expansion of the human population in Europe as a result of the spread of agriculture from the Middle East. The mutations responsible for eye colour probably originated from the north-west part of the Black Sea region where the great agricultural migration of the northern part of Europe took place in the Neolithic periods about 6000 to 10 000 years ago. This is the best estimate – the area of origin could be further east in the northern part of Afghanistan.

Professor Eiberg has analysed the DNA of about 800 people with blue eyes in a range of countries including Jordan, India, Denmark and Turkey.

Originally everyone had brown eyes but a genetic mutation affecting the OCA2 gene in the chromosome resulted in a 'switch' that turned off the ability to produce brown eyes. Variations in eye colour can be explained by the amount of melanin in the iris but blue-eyed individuals have only a small degree of variation in the amount of melanin in their eyes. This indicates that all blue-eyed individuals are linked to the same ancestor as they all (with possibly one exception) have almost exactly the same genetic sequence in the part of the DNA responsible for eye colour. Brown-eyed people have a considerable amount of individual variation in that area of DNA.

It is not known why blue eyes spread in northern Europe and southern Russia. There may have been some advantage in long hours of daylight in summer or perhaps the trait was found attractive and thus encouraged sexual selection.

Animal and plant DNA provides a clue to human migration

Mice in Madeira

The history books state that Madeira was discovered by Portuguese mariners in 1419. Madeira's mice are not native and must have arrived in ships. Genetically they most closely resemble the mice of Portugal. However, some of their DNA has strong similarities to that of Scandinavian mice, which strongly suggests that Viking ships found Madeira long before the Portuguese.

Lice and clothes

The human head louse lives only in scalp hair. The body louse, a closely related subspecies, lives only in clothing and so must have evolved from the head louse sometime after early humans started wearing clothing regularly. Assuming this did not take long, dating the divergence of the two subspecies should give an approximate idea of when clothing became commonplace. Scientists at the Max Planck Institute for Evolutionary Anthropology in Leipzig (Germany) sequenced DNA fragments from head and body lice and counted the genetic differences. They compared this with the number of genetic differences between human and chimpanzee lice, which are assumed to have diverged about 6 million years ago. Based on this comparison, they estimate that human head and body lice diverged about 72 000 years ago.

Voles on Orkney

The voles of the Orkney Islands are most akin to those on the Atlantic coasts of France and Spain. However, Orkney voles are more diverse than anywhere else in Western Europe. This suggests that Orkney must have had a thriving sea trade with mainland Europe in Neolithic times and the island voles retain diversity that has been lost elsewhere.

Wheat

Wheat genotypes show two migrations of wheat-farming people into Europe from the Near East: an earlier migration along the northern shore of the Mediterranean and a later one along the Rhine and Danube rivers, according to studies by researchers at the University of Warwick (UK).

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