SWEDISH DNA PROJECT NEWS

Nº 4, May 2015

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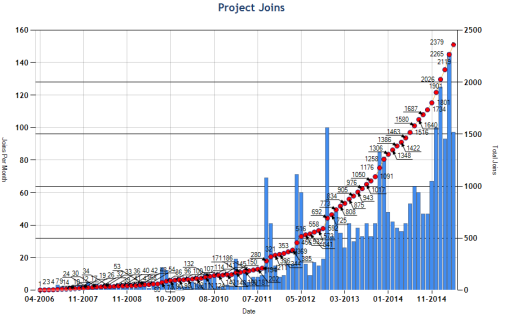


Our project is growing

As of May 5, 2015, the project has 2,373 members (+31% compared to November 30, 2014, when the last issue was published). The number of Family Finder-tests has increased with 34% to 1,489 tested members. The number of Y-DNA testtakers has increased with 25% to 1,432 and the number of mtDNA-tested persons has increased with 22% to 1,340 persons.

The Swedish DNA Project will likely pass the Norwegian DNA Project in numbers, since it has 2,430 members, if this trend continues. But our project is far from catching up the leading DNA nation of Scandinavia, Finland, which has 5,165 members.

Rolf Berlin

Presentations of two administrators

Peter Sjölund

I live in Härnösand – in the very middle of Sweden – and have my roots in mid Sweden, Dalarna, Germany and Latvia. I have been active within genetic genealogy in Sweden since 2010 and I give talks all over the country to inspire genealogists to use DNA in their research. The thing with genetic genealogy that thrills me the most is the ability to investigate relationships in the time before written sources. I run a couple of project where we research Swedish family trees in medieval times (see buredna.sjolunds.se) and my special areas of expertise are deeper investigations of Y-DNA and mtDNA. Apart from being an administrator of the Swedish DNA Project, I also admin the I1-L1302 Project and the I1-L1301+ L1302- Project. Right now the thing that keeps me most busy is writing a handbook on genetic genealogy that will be published in August.

Magnus Bäckmark

Photo: Crister Lindström.

I live in Österåker a little north of Stockholm and make my living as a family researcher, editor of Svenska Släktkalendern (The Swedish Family Register) and heraldic artist since 1998. The possibilites with DNA concerning genealogic research within the historic time frame stood clear to me first during a lecture which I listened to at the XXVII International Congress for Genealogy and Heraldry in St Andrews in 2006. I have published a handboook (in Swedish) on the subject DNA Genealogy, *Genvägar – praktisk handledning till DNA-jämförelse i släktforskning* (2nd edition 2013). On my webpage gronastubben.se/wordpress/ I also write (in Swedish) on the subject.

Looking for books on DNA genealogy?

Here's a selection:
http://www.isogg.org/wiki/Genetic_genealogy_books

Facebook group for DNA genealogy in Swedish

If you are a Facebook user, feel welcome to join if you don't mind that the discussions are in Swedish.

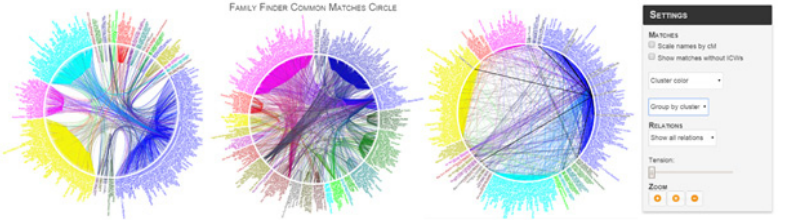
DNA Genealogy Experiment

The Swedish project DNA Genealogy Experiment, with the purpose to simplify family tree comparison of Family Finder matches, has been closed for new registrations for some time, because of discussions with Family Tree DNA about data security and the appropriateness of copying user data to third party servers.

Meanwhile, Göran Runfeldt in cooperation with Staffan Betnér have been developing new tools for analysis of Family Finder matches. As opposed to the tree matching functions on Dnagen (http://dnagen.net), these tools run in the web browser as bookmarklets on top of familytreedna.com, without any data being sent to third parties. These new functions focus on visualization of In Common With-relations in new ways, to give a better visual overview of how matches are connected to each other.

Family Finder Common Matches Circle

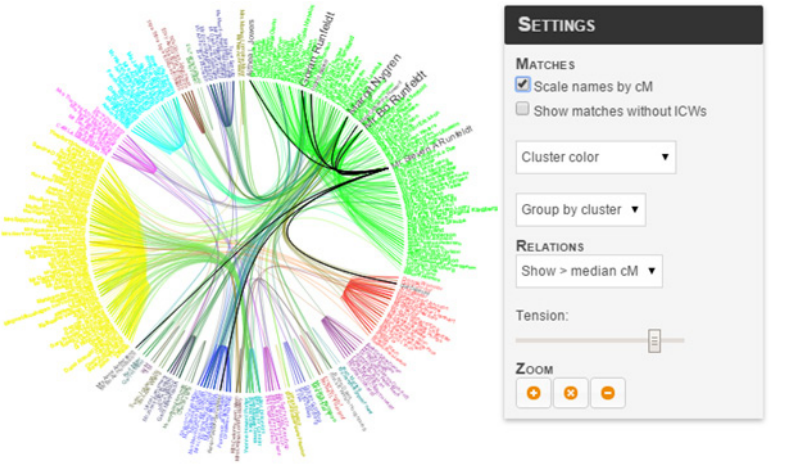
The **Common Matches Circle** arranges your Family Finder matches in a wheel structure and draws lines between those who have In Common With-matches. Your matches are arranged in clusters based on how they are connected and are grouped and colour coded accordingly, to give a clearer overview.



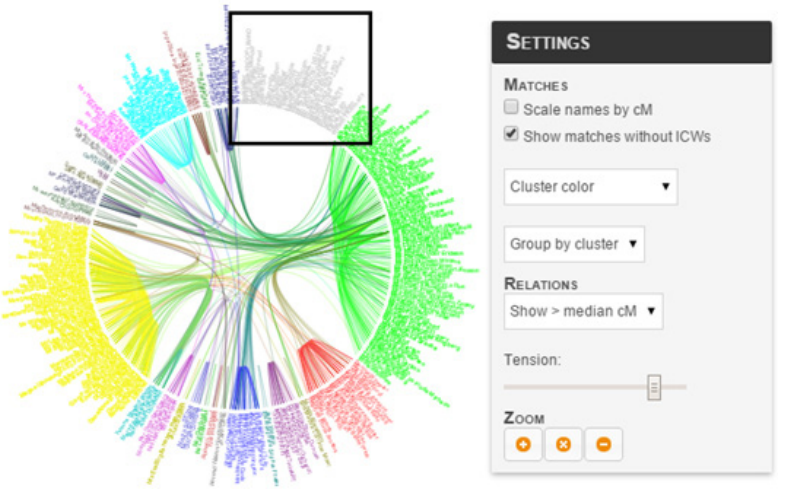
The wheel can be zoomed and panned using the mouse pointer and a person can be highlighted to see which matches you have in common with that specific person. (Zoom with the scroll wheel, left-click and drag to pan around, and hover over a person's name to highlight)

The **settings panel** on the right of the page controls the look of the wheel:

- **Scale names by cM** – The text size is adjusted based on the number of shared centimorgans between you and the person, so that closer relatives are shown in larger text.

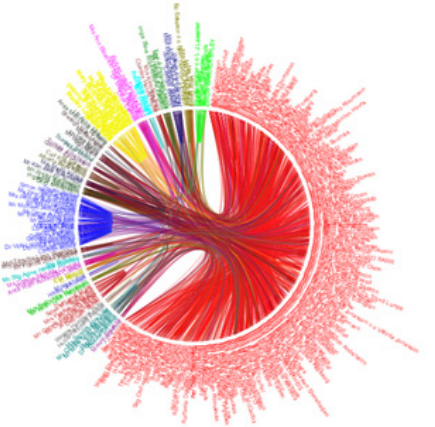


- **Show matches without ICWs** – Show matches that do not have any In Common With-matches according to the current relation filter (see below).

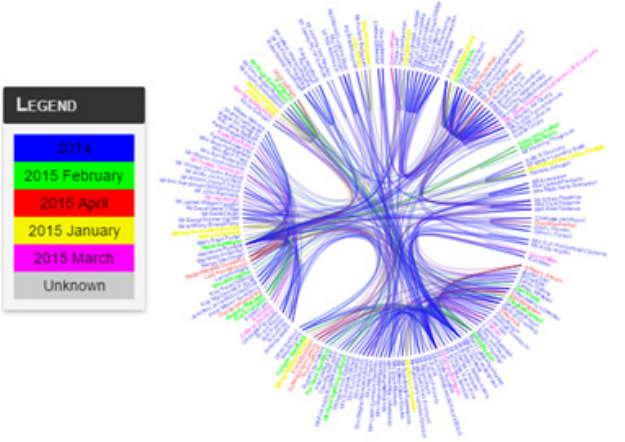


- **Colour** – Colour code people's names based on different criteria. Colour descriptions are shown in the Legend box on the left of the page.

- Monochrome – No colour coding.
- Cluster colour – The default setting where matches are colour coded based on which clusters they have been grouped in.

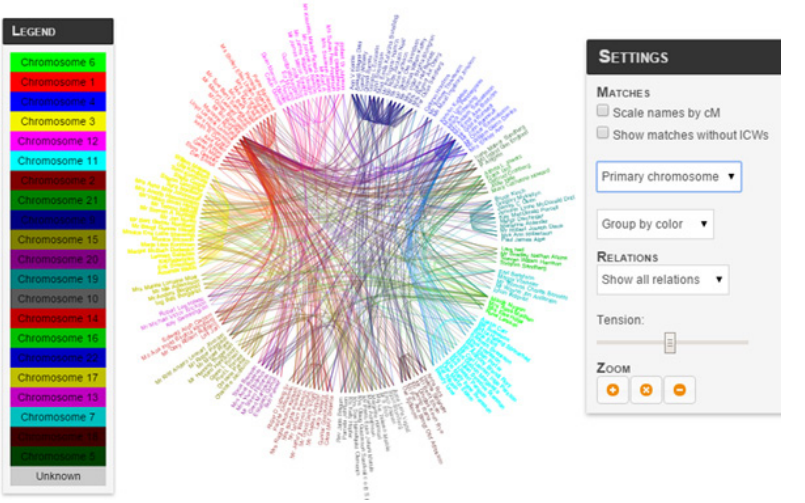


- Email country colour – Tries to guess people's country based on email address top level domain (.com/.net/.org domains are shown in grey).
- Y-Haplogroup colour – Matches are colour coded based on the first letter of the Y-DNA Haplogroup.
- mt-Haplogroup colour – Matches are colour coded based on the first letter of the mtDNA haplogroup.
- Match date colour – Colour code based on the year or month when the match appeared. Useful to see in which clusters that new matches appears in, over time!



- Primary chromosome – Colour code based on which chromosome that contains most shared DNA (total cM) with the person.
- Predicted range – Colour code based on estimated relationship distance.

- **Group by** – The default setting groups matches based on cluster, but by changing to Group by colour the matches are instead grouped by the criteria used for colour coding, which enables you to for example group by email country, haplogroup or primary chromosome and visualize the relations between those groups.



- **Relations** – ICW relations are filtered to give a better overview of the strongest relationships, based on the amount of shared DNA (total cM) between the matches.

The default setting "Show > median cM" will filter around half of the ICW relations. Try lowering the threshold to see more ICW relations (lines) between the matches. Most users should not have any problems using "Show all relations".

However, if you have many Family Finder matches, the wheel can take a long time to load and slow down the computer. If that happens, try changing this setting to "Show > 200% cM" and then lower the threshold gradually until you have a manageable amount of relations to investigate.

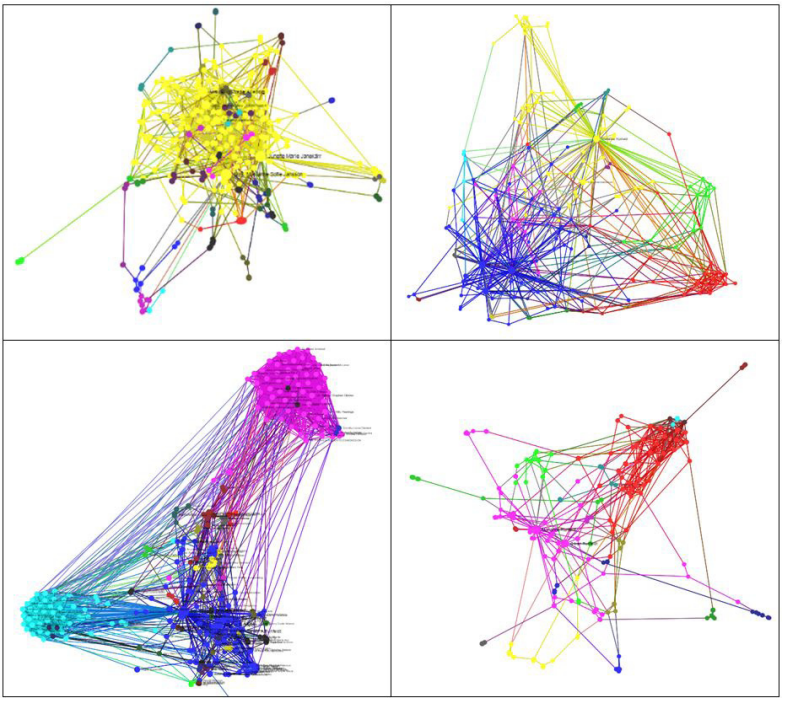
- **Tension** – Try changing the line tension by moving the slider and see what you like best.

Would you like to tell your story in Swedish DNA Project News?
Do you have an article, hints or tips,
or related news item to publish?

Please contact one of the project administrators.
This issue was edited by
Magnus Bäckmark (magnus.baeckmark@swipnet.se).

Family Finder Common Matches Graph

The **Matches Graph** gives a slightly more advanced and interactive visualization of the relationships between Family Finder matches. By using a visualization algorithm called Forced Atlas 2 the matches are arranged in a graph structure which is sometimes reminiscent of a spider web and sometimes a ball of twine.

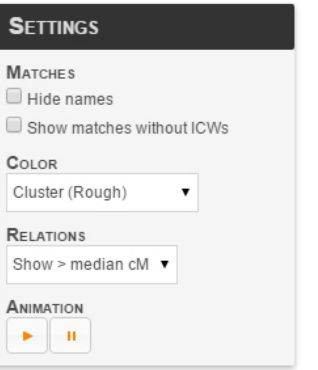


Each circle represents a DNA match and the circle size says how close the match is to the main person (total shared cM). Each line represents an In Common With-match between two people.

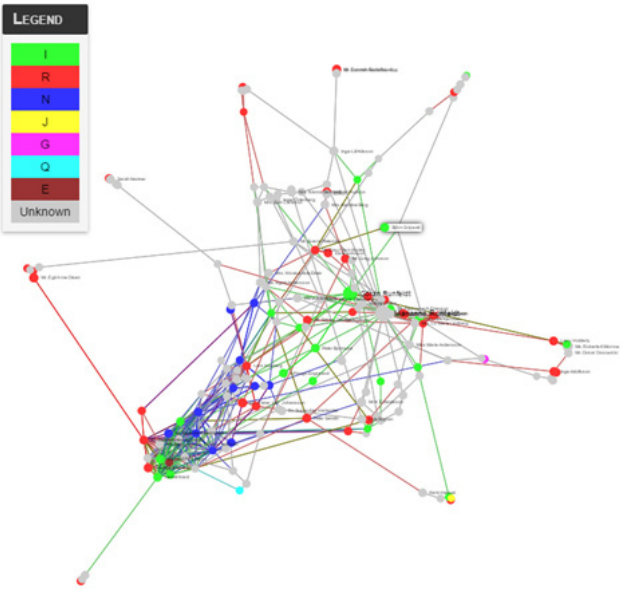
When zooming in with the mouse wheel the names of the people will display. Click on a circle to highlight the ICW-matches with a specific person.

The look and loading time of the graph will vary greatly between different match results. For some people the graph will stop moving around after some time and for others it will keep moving indefinitely. You can always click the pause button to stop the animation and the start button to restart the animation.

The **settings panel** on the right of the page controls the look of the graph:

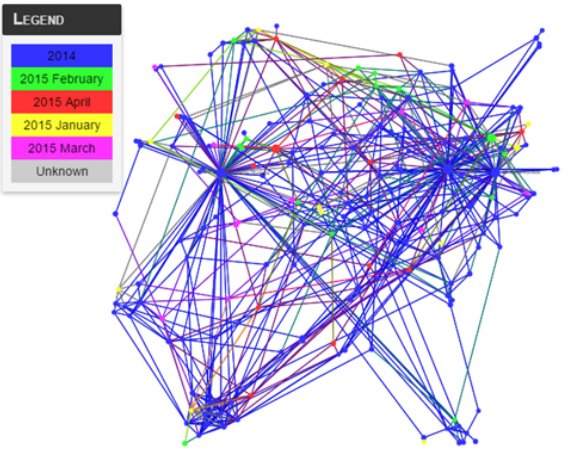


- **Hide names** – Hiding the names can make the graph look cleaner and is also useful if you want to share a screenshot while protecting the privacy of your matches. You can still see the names of your matches by hovering over a circle with the mouse pointer.
- **Colour** – Colour code persons' names based on different criteria. Colour descriptions are shown in the Legend box on the left of the page.
    - o Cluster (Rough) – The default setting where matches are colour coded based on which clusters they have been grouped in
    - o Cluster (Fine-grained) - Identifies more detailed clusters (Smaller groups with more colours)
    - o Email country – Tries to guess people's country based on email address top level domain (.com/.net/.org domains are shown in grey)
    - o Y-Haplogroup – Matches are colour coded based on the first letter of the Y-DNA Haplogroup.

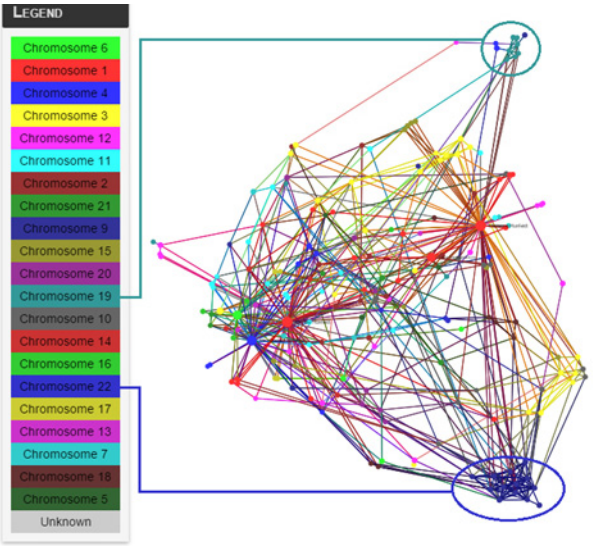


    - o mt-Haplogroup – Matches are colour coded based on the first letter of the mtDNA haplogroup.

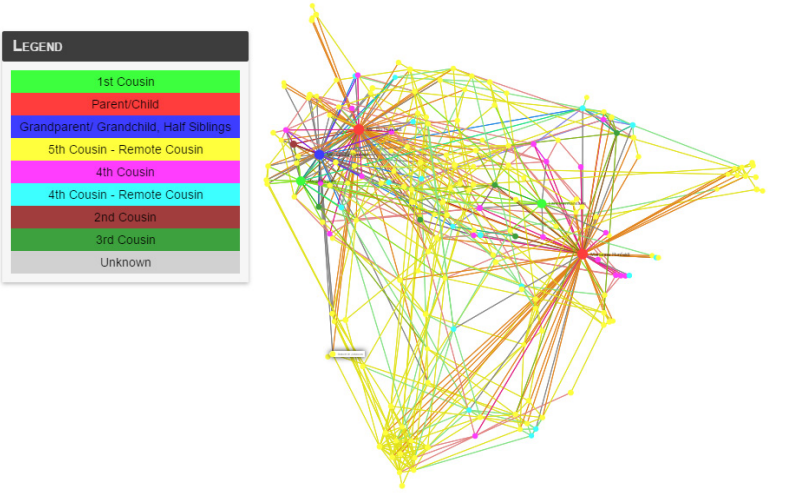
- Match date – Colour code based on the year or month when the match appeared. Useful to see in which clusters new matches appear in, over time!



- Primary chromosome – Colour code based on which chromosome contains the most shared DNA (total cM) with the person. Can give interesting results when whole clusters are shown to belong to the same chromosome segment!



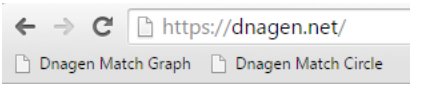
- Predicted range – Colour code based on estimated relationship distance. Gives a hint about which clusters originate further back in time.



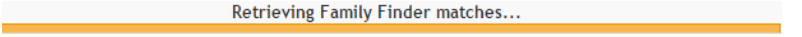
- **Relations** – The relationship filter makes a big difference for the Matches Graph. "Show all relations" will use all information and is therefore the most truthful graph, but with many matches it can quickly become convoluted. All match results work differently, so experiment with the settings here!

Getting Started

- First you need to create two bookmarks in your web browser. Go to http://dnagen.net and drag-and-drop the two links Dnagen Match Graph and Dnagen Match Circle to your bookmarks or favourites bar. (With Firefox and Internet Explorer you can also right-click the links and choose Bookmark/Add to favourites)
- Example result:



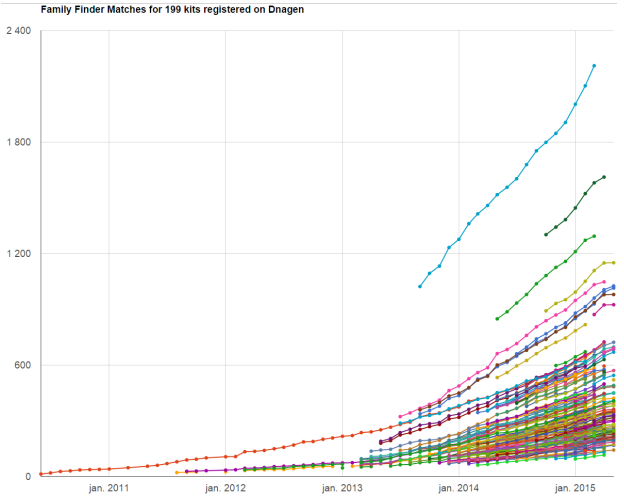
- Login to Family Tree DNA and go to Family Finder – Matches
- Click on one of the bookmarks
- Your matches will now be loaded into the web browser



- When the result has been loaded you can browse it and try the different visualization settings in the panel to the right
- When you are done checking the results you can simply navigate to another web page or close the web browser
- Feedback and discussions about the functionality are welcome in the Facebook group DNA Tools or the Swedish speaking group DNA-anor.

Göran Runfeldt

Increase in number of Family Finder matches



The lines represent the number of matches over time for persons registered at Dnagen (http://dnagen.net). Most of them are Swedish speaking, so the graph indicates the common number of matches and the growing popularity of Family Finder among people who have many of their roots in Sweden.

Ed.

The Swedish Society for Genetic Genealogy (SSGG)

SSGG is a network for DNA Genealogy in Sweden, formed in 2014. In our webpage ssgg.se you find answers to many questions concerning how to use DNA for family research. You also find links to many of the tools available for analyzing DNA results deeper than whan the testing companies do.

(from SSGG's site)

A maternal lineage from Nordingrå, Sweden, within mtDNA-haplogrupp T2e1 > T16296C! > T16126C > G8152A

At the end of January, the mtDNA test results for my dad Sven were completed. The results provide clues to the research of the maternal line of which he belongs. With this writing I want to share what we discovered and provide an example of what a full sequence mtDNA test can provide.

What is analyzed here is the mitochondrial DNA (mtDNA), which every individual (man or woman) has inherited from his or her mother. By comparing the mtDNA you can see how closely or distantly related you are to other test takers on the direct maternal line. The oldest direct maternal ancestor of Sven that I knew of lived nine generations before him. The ancestor in question was Elisabet Johansdotter, born ca. 1653 in Valmsta and died 1698 in Omne. Both villages are situated within Nordingrå parish in Ångermanland in northern Sweden.

The oldest maternal ancestor of Sven Nyberg who has been photographed, as far as I know, is Margareta Westerlund (b. 1849). She was at this time a worker's wife, living in Kubikenborg, Skön parish. She was photographed by the photographer (Finn) Erik Larsson (b. 1855), who had his atelier at Skönvik, Skön parish.[1] The picture is taken between 1892, when he moved there from Rättvik, and 1898, when he died.[2]

1 http://digitaltmuseum.se/011014697428.
2 Skön AI:9a, p. 479, and AIIa:2, p. 814.

One part of the test results is the information about the mtDNA haplogroup Sven belongs to – T2e1. Like any other branch on the human maternal family tree, it can be distinguished thanks to mutations that have occurred. This group is estimated to have branched off 9,100 ± 2,400 years ago from the older and larger maternal branch T2e, which is thought to have spread from the Near East into Europe, first into the Southeastern part, from 11,000 years ago and onwards. One element of T2e exists today in the populations spanning all the way from the Arab world to Iceland.[1] The frequency is considerable for example in Egypt, Saudi Arabia, and Italy, but falls gradually northwards to 0.2% of the population of England "and some other Northern European locales".[2] The indication is that the frequency of T2e is about 0.3% among people whose oldest known maternal ancestor lived within present-day Sweden.[3]

The subclade T2e1 is interesting, because within it, two branches are found (-a and -b) that many of Jewish maternal descent belong to. It is possible that both branches emerged directly from the Near East, but also that they could have emerged in Southern Europe or the Mediterranean area, after which a back-migration to the Near East would have taken place.[4] Members of subbranches on which no or only one mutation has occurred – individuals with maternal lineages from both the Sephardic (Arabic-Spanish) and Ashkenazi (Eastern European) Jewish populations – show up as matches in Sven's matches list, thanks to the fact that his own maternal line only has been subjected to a single mutation during the last millennia.

T2e1 has also been identified in several individuals buried during pre-Christian times in Iceland.[5]

As a test taker, you receive a list of matches. That is, those among the company's now over 51,500 full sequence mtDNA tested individuals who have few enough differences (mutations) compared to your full sequence, so that the connection on the maternal line could be within the last one thousand years. I quickly opened the matches list. In it were 47 matches. Surprisingly to me, not a single one of them had a Swedish name. Of the 47, there were two who had one difference (mutation) compared to Sven, 17 who had two, and 28 with three. (Since January, one more match with a Genetic Distance of 2 has appeared.) In conclusion, not a single match appeared to be close in time to Sven. The oldest recorded ancestors on the maternal lines of the tested individuals lived anywhere from Ireland to Israel. See the map below.

Where should I start to find out more? Many of the test takers had provided information about their oldest known maternal ancestor, but no one seemed familiar to me. But then I spotted "Ulrika Sjoberg". It sounds Swedish… The test taker had a Genetic Distance = 2 to Sven, but still.

Luckily, the owner of the kit, Jeanne Ann Oas of Wetmore, Michigan, USA, also had a family tree (GEDCOM file) attached to her account. It showed that her grandmother was born in Nordingrå in 1885! Now that I had found her I

[3] Maria Pala et al., Mitochondrial DNA Signals of Late Glacial Recolonization of Europe from Near Eastern Refugia, in The American Journal of Human Genetics, 90, 2012.
[4] Felice L. Bedford et al., Clarifying Mitochondrial DNA Subclades of T2e from Mideast to Mexico, in Journal of Phylogenetics & Evolutionary Biology, 2013.
[5] 3 of 863 fullsequence mtDNA tested members of the Swedish DNA Project – except from Sven Nyberg and Jeanne Ann Oas a person belonging to T2e2.
[6] Bedford et al., see above.
[7] Agnar Helgason et al., Sequences From First Settlers Reveal Rapid Evolution in Icelandic mtDNA Pool, in PLoS Genetics, 5(1), 2009. The Coding Region wasn't analyzed, so from this study can't be found how close to Sven Nyberg they are within T2e1 (or if any of them belonged to the subclades -a or -b), only that they belong to T2e1 like he does.

Where the oldest known ancestors on the maternal lines of Sven Nyberg's close matches lived. Each testtaker is represented by a number which stands for the number of mutations (Genetic Distance) that the testtaker has compare to Sven's mtDNA fullsequence. (Where within the countries the numbers have been placed has no significance; they are placed randomly within the country borders only.)

was compelled to continue my research. I found that the grandmother's 5th great grandmother was Karin Johansdotter, b. ca. 1666, and according to Teo Sundin, "Släkter och Gårdar i Nordingrå 1535–1890" (1975), she was also born in Valmsta.

According to the book mentioned, Elisabet and Karin were sisters. At the death of their mother, it was recorded how long her marriage had lasted, which tells us that she got married ca. 1652. Now that Elisabet, b. ca. 1653, and her younger sister Karin, by way of DNA through their now living descendants, turns out to belong to the same maternal line, provides supporting evidence to Elisabet being born in that marriage (and not in her father's previous marriage), so the recorded time and age may be correct.

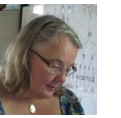
The book indicates that the sisters' maternal grandmother's name was Elin. With her, we are now as far back in time as year 1600. One cannot help fantasizing about where this maternal line came from before that and when it arrived in Nordingrå...

But why are there two differences between Sven and Jeanne Ann when they are so closely related? This can be studied in more detail. You also get information about your specific mutations, below mtDNA > Results. It turns out that one of the mutations present in Jeanne Ann is a so called heteroplasmy. That means, in this case, that she has the same constitution on the position in question (16,189) as Sven in some cells, but another constitution in other cells. A heteroplasmy occurs during a temporary phase when a mutation is established. It may take a number of generations before the new type has been fully established or it may disappear.

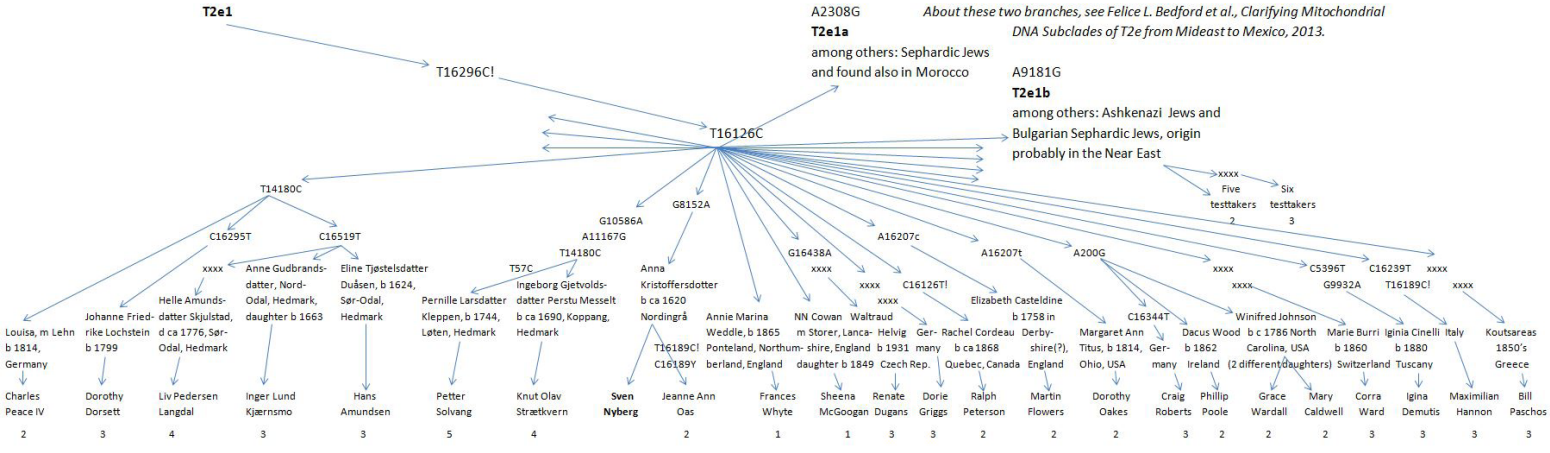
In other words, of the two differences between Sven and Jeanne Ann, only one of them is fully established. Also worth noting is that all mutations occur randomly (although, on average, very seldom). This means that you can never directly eliminate a match, who has several differences compared to you, as they may still be related to you on the maternal line within the relatively recent past. Individuals with more differences may be more closely related to you than individuals with fewer… It is when you sort out the family tree structure that the picture becomes clearer. With guidance of the dividing mutations, different individuals can be attributed to different branches. Mutations in the HVR1 and HVR2 areas are found in the project tables. If your matches are not members of any projects, or if the relevant mutations are within the Coding Region, you have to personally contact the matches through email to exchange the information.

In conclusion, Sven and Jeanne Ann turned out to be 9th cousins. I and Jeanne Ann are now keeping in touch via email and she is delighted with her newfound Swedish relatives.

Annika Lindqvist
Sundsvall (annika@lindqvists.net)
(Magnus Bäckmark has assisted with information and the reconstruction of the family tree below T2e1.)



The maternal relationship between Sven Nyberg and 34 of his 48 mtDNA matches



(Numbers 1–5 below names show differences in number of mutations compared to Sven Nyberg. xxxx = a Coding Region mutation of the testtaker's private knowledge only.)

Elin NN, lived still in 1640
m Kristoffer Staffansson
farmer in Nyland, Nordingrå
known from 1589, died 1622/23

Anna Kristoffersdotter
b. around 1620 in Nyland, Nordingrå

Elisabet Johansdotter b. c:a 1653 in Valmsta, Nordingrå	Karin Johansdotter b. c:a 1666 in Valmsta, Nordingrå
Margeta Kristoffersdotter b. 1690 in Omne, Nordingrå	Anna Persdotter b. 1693 in Ulvvik, Nordingrå
Karin Månsdotter b. 1724 in Mädan, Nordingrå	Brita Jonsdotter b. 1719 in Mädan, Nordingrå
Greta Persdotter b. 1759 in Sund, Nordingrå	Brita Johansdotter b. 1749 in Mädan, Nordingrå
Katarina (Kajsa) Johansdotter b. 1793 in Allsta, Nora	Brita Göransdotter b. 1789 in Mädan, Nordingrå
Greta Stina Jonsdotter b. 1822 in Allsta, Nora	Eva Sofia Mårtensdotter Norlin b. 1823 in Edsätter, Nordingrå
Margareta Westerlund b. 1849 in Allsta, Nora	Brita Sofia Matsdotter b. 1848 in Näs, Nordingrå
Emma Wilhelmina Näslund b. 1879 in Dingersjö, Njurunda	Ulrika Sjöberg b. 1885 in Näs, Nordingrå
Magda Eleonora Engelmark b. 1902 in Römsta, Skönsmon	(Private)
Sven Axel Nyberg b. 1936 in Kubikenborg, Skönsmon	*Jeanne Ann* Oas

The fourth most common 12-marker haplotype in Sweden, within Y-DNA-haplogroup R-L151 (R1b1a2a1a)

It is time to have a closer look at the fourth most common 12-marker haplotype in our project. Statistics show us that it is also the fourth most common among individuals who state that their oldest known paternal ancestor lived within present-day Sweden. Below, Ht 4 stands for Haplotype 4, this haplotype, which has the allele values 13-24-14-11-11-14-12-12-11-13-13-29 (the markers are given in the order listed by FTDNA).

The members of our project who have Ht 4 are the following (kit numbers):

101688	213979	271791	318763	N31836
134820	235632	288492	365891	N35424
174347	247419	29135	B7101	N37019
201661	26326	303280	N113653	N44206
203184	266699	305827	N114052	N85413

Aslo discussed: 150831, 243831, N23795 and N31725.

The three previously examined haplotypes are all within Y-DNA haplogroup I1 (I-M253). Ht 4 is the first one that belongs to another mega-group, R1b (R-M343). It is one of the four that FTDNA refer to with the collective name the Western Atlantic Modal Haplotype (WAMH). The WAMH group represents a larger share of the Western European population than it "should". FTDNA estimate that its share of the whole population there is somewhat over 1%. The group has expanded faster than others within Western Europe. If you belong to this group, you get an unusually large lot of matches at low comparison levels (12, 25, 37 markers), because quite a few matches happen to have allele values that, by coincidence, correspond to your own. There are so many lineages within this cluster that there are always a few, through occurred mutations, whose haplotypes appear close to others'.

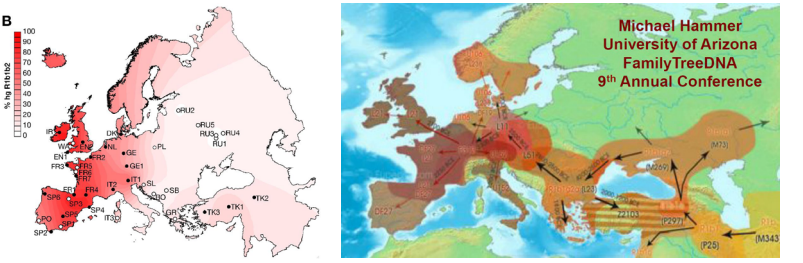
WAMH
Western Atlantic Modal Haplotype

DYS	393	390	19	391	385a	385b	426	388	439	389-1	392	389-2	
Allell	13	23	14	11	11	14	12	12	12	13	13	29	
Allell	13	24	14	10	11	14	12	12	12	13	13	29	
Allell	13	24	14	11	11	14	12	12	11	13	13	29	← Ht 4
Allell	13	24	14	11	11	14	12	12	12	13	13	29	

WAMH refers to a set of four 12-marker haplotypes, close to each other, within R-M269.

As with all haplotypes, one must understand that a certain haplotype does not only appear on a single branch. Random mutations have made it so that some lineages from related branches end up with the same allele values. Also, a lineage which has had Ht 4 for several thousand years may have been struck by a recent mutation, resulting in the lineage ending up in a neighboring haplotype instead.

Ht 4 is, like the other three within WAMH, a branch within the larger haplogroup R-M269 (R1b1a2). That haplogroup branched off around 13,200 (14,800–11,600) years ago. The most recent common ancestor (MRCA) for the now living members lived considerably later than that, around 6,400 (7,200–5,600) years before present (YFull). He probably lived somewhere in Southwestern Asia, but his descendants initiated a powerful expansion in Europe starting around 5,000 years ago (the R1b-M269 Project). Western Europe has become the core area in terms of the high frequency of individuals having this paternal origin.



The latest frequency map for R-M269 is found in Balaresque et al., A Predominantly Neolithic Origin for European Paternal Lineages (2010). In the picture it says "R1b1b2", which was the long name of R-M269 five years ago; branches have moved around a bit in the family tree since then. Michael Hammer's map from 2013 (to the right) shows the main routes of migration of this haplogroup. The spread to the north is considered to have happened especially with the branch R-L51 (R1b1a2a1) from Eastern Central Europe from the Bronze Age and forward in time, and also via the younger subclade R-P312 (R1b1a2a1a2) from the area just north of the Alps (https://gap.familytreedna.com/media/docs/2013/Hammer_M269_Diversity_in_Europe.pdf).

Ht 4, specifically, has to date only been found on branches below R-L151 (R1b1a2a1a) among people who have done SNP testing (how it is done, see Swedish DNA Project News Nº 1, p. 2). R-L151 branched off around 5,600 (6,300–5,000) years ago and the MRCA of the now living members is considered to have lived around 5,000 (5,500–4,500) years ago (YFull), in other words during the beginning of the expansion period mentioned above.

984 test takers – 0.19% of FTDNA's 525,827 Y-DNA clients – have Ht 4, of whom 25 are members of the Swedish DNA Project. Paternal lineages appear, as far as we know, in the following countries (in proportion to the total number of test takers with a paternal lineage from the country in question):

(Australia 2.2%)
Spain 2.0%
Ireland 1.9%
France 1.5%
(Algeria 1.4%)
Mexico 1.4%
Portugal 1.4%
Scotland 1.4%
UK 1.4%
Sweden 41 of 2,876 test takers or 1.4%
USA 1.4%
England 1.3%
Wales 1.3%
Northern Ireland 1.2%
Norway 1.0%
(Puerto Rico 1.0%)
Belgium 0.9%
USA (Native Americans) 0.9%*
(Brazil 0.8%)
Canada 0.8%
Switzerland 0.7%
Netherlands 0.6%
Germany 0.6%
Denmark 0.5%
(Czech Republic 0.5%)
Italy 0.4%
(Bulgaria 0.3%)
Romania 0.3%
(Latvia 0.3%)
Austria 0.3 %
Greece 0.2%
Poland 0.2%
Ukraine 0.2%
Lithuania 0.1%
Russian Federation 0.1%

The use of parentheses above indicates test numbers below 500, which may lead to skewed statistics. There are too little data from the following countries to provide meaningful statistics: Barbados (1 of 36), Belize (1 of 2), Colombia (1 of 65), Costa Rica (1 of 8), Ecuador (3 of 20), El Salvador (1 of 28), Jamaica (1 of 62), and Nicaragua (1 of 11). *) Their paternal lineages probably came from Europe, even though it can have been before the time which they can trace them in written records.

A cluster within R-Z372

Among our project members with Ht 4 there are two clusters that are close to each other, see the extract from the project table on the next page. Four members who have other 12-marker haplotypes are included as well, since a larger number of markers indicate that they are relatively closely related. The altogether twelve test takers have their roots, according to written records, in the provinces of Värmland, Dalsland, Bohuslän, Västergötland, and Småland in the western, southwestern, and southern parts of Sweden. The individuals in the first group of the project table above see each other, in many cases, in their respective matches list at the 67-marker level. The second group is united, and at the same time differentiated from the others, by having four specific markers in common. All three have each other in their respective 67-marker matches list. Several of these twelve have confirmed their place in R-Z372 (R1b1a2a1a1b1a). R-Z372 is not a young branch (see the image on p. 22 and associated text), so it is relatively certain that all twelve belong to it.

1		
DYS-393		
N=1418		
Repeats	Count	Freq.
12	30	2%
13	1352	95%
14	36	3%

2		
DYS-390		
N=1427		
Repeats	Count	Freq.
21	1	.1%
22	14	1%
23	405	28%
24	787	55%
25	209	15%
26	10	1%
27	1	.1%

3		
DYS-019		
N=1417		
Repeats	Count	Freq.
13	7	.5%
14	1320	93%
15	82	6%
16	6	.4%
17	2	.1%

4		
DYS-391		
N=1425		
Repeats	Count	Freq.
9	5	.3%
10	454	32%
11	896	63%
12	69	5%
13	1	.1%

5		
DYS-385a		
N=1421		
Repeats	Count	Freq.
9	2	.1%
10	40	3%
11	1275	90%
12	83	6%
13	7	.5%
14	9	.6%
15	4	.3%

6		
DYS-385b		
N=1434		
Repeats	Count	Freq.
11	23	
12	24	2%
13	125	8%
14	992	52%
15	236	20%
16	32	1%
17	2	.1%

Only on the ninth marker (in the order listed by FTDNA) does Ht 4 have an allele value that is not the most common within the whole of R1b. The other three WAMH haplotypes are in a similar way very close to the 12-marker haplotype (with allele values highlighted in yellow) which is the most common within R1b. Whit Athey, Resource Data for Haplogroup R1b (www.hprg.com/R1b). The tables are continued on the following page.

In addition to each other, the members of the selection above also see individuals in their 67-marker matches lists whom according to written records have their origins in Norway, Scotland and Denmark, besides Sweden. One member's match has an ancestor who lived in Mexico. A not too bold presumption is that the common origin of all these individuals was somewhere in Scandinavia, perhaps during the Iron Age.

Those of you who descend from John Johnson, Charles Anderson and Erik Larsson, consider specifying more specifically where they were born or where they lived – perhaps the genealogies can be taken further back in time? You make adjustments to that information under Settings (in the top right corner, when logged in) > Genealogy.

The descendants of Håkan Andersson, Frykman and Blomdahl (the name changed to Blomquist the next generation) have done the Big Y test and have, by FTDNA, no known SNPs to separate them. Anders Bengtsson's descendant, who also has done that test, has one FTDNA-SNP difference to the other three, in that he is positive for L484. One individual in the cluster, Blomdahl's descendant, has also tested positive for S7015 (warburtontrees.net/DNA/KingsClusterTree.pdf, s. 3). Frykman's descendat has just received his YFull analysis, which has revealed several SNPs on his branch.

Kit Number	Paternal Ancestor Name	DYS393	DYS390	DYS19	DYS391	DYS385	DYS426	DYS388	DYS439	DYS389i	DYS392	DYS389ii	DYS458	DYS459	DYS455	DYS454	DYS447	DYS437	DYS448	DYS449	DYS464
N23795	John Johnson, b: 4/13/1851; d: 7/11/1929	13	23	14	10	11-14	12	12	12	13	13	29	18	9-10	11	11	26	15	19	30	15-15-17-
243831	Håkan Andersson b 17660922 Nordmark Värmland	13	23	14	11	11-14	12	12	11	13	13	29	18	9-10	11	11	27	15	19	30	15-15-17-
150831	Anders BENGTSSON b. 1640 Sweden	13	24	14	11	11-13	12	12	11	13	13	29	18	9-10	11	11	25	15	19	30	15-15-17-
271791	Nils Andersson b1773 Säbyn, Ånimskog, Sweden	13	24	14	11	11-14	12	12	11	13	13	29	17	9-10	11	11	26	15	19	30	15-15-17-
N114052	Jon Larsson, b. 1733, Askum parish, Sweden	13	24	14	11	11-14	12	12	11	13	13	29	18	9-10	11	11	26	15	18	30	14-15-15-
N37019	Magnus Frykman, b 1775, Rudskoga, Varmland	13	24	14	11	11-14	12	12	11	13	13	29	18	9-10	11	11	26	15	19	30	15-15-17-
174347	Isak Persson Hörsberg, b. 1730, Berga, Sweden	13	24	14	11	11-14	12	12	11	13	13	29	18	9-10	11	11	26	15	19	30	15-15-17-
N113853	Måns Blomdahl, b. 1764, Skäggalösa, Sweden	13	24	14	11	11-14	12	12	11	13	13	29	18	9-10	11	11	26	15	19	31	15-15-17-
26326	Charles Anderson, Gothenberg, Sweden	13	24	14	11	11-14	12	12	11	13	13	29	18	9-10	11	11	26	15	19	31	15-15-17-
134820	Johan Ström, b. 1776, Småland, Sweden	13	24	14	11	11-14	12	12	11	13	13	29	18	9-10	11	11	26	15	19	31	15-15-17-
365891	Lars Jönsson 1626-1697 Stackerud, Ekshärad; S SWE	13	24	14	11	11-14	12	12	11	13	13	29	18	9-10	11	11	26	15	20	31	15-15-17+
N31725	Erik Larsson, b. 1650 and d. 1717	13	24	14	11	12-14	12	12	11	13	13	29	17	9-10	11	11	26	15	18	31	15-15-17-

Project members with a relatively high resemblance on 67 markers and all except four of them have Ht 4.

7	
DYS-426	
N=1416	
Repeats	Count	Freq.
10	2	.1%
11	7	.5%
12	1388	98%
13	14	1%
14	5	.3%

8		
DYS-388		
N=1416		
Repeats	Count	Freq.
11	4	.3%
12	1393	98%
13	16	1%
14	3	.2%

9		
DYS-439		
N=1428		
Repeats	Count	Freq.
10	5	.3%
11	208	15%
12	1058	74%
13	136	10%
14	18	1%
15	1	.1%
16	1	.1%

10		
DYS-389a*		
N=1426		
Repeats	Count	Freq.
10	1	.1%
11	6	.4%
12	52	4%
13	1223	86%
14	140	10%
15	4	.3%

11		
DYS-392		
N=1416		
Repeats	Count	Freq.
12	8	.6%
13	1277	90%
14	125	9%
15	6	.4%

12		
DYS-389b*		
N=1431		
Repeats	Count	Freq.
13	2	.1%
14	0	0%
15	72	5%
16	1134	79%
17	197	14%
18	23	2%
19	13	1%

* DYS-389a = DYS-389i; DYS-389b = (DYS-389ii – DYS-389i)

Explanation to the tables: see the previous page.

An individual close to Group 2 in the selection above has tested positive for S3207 (warburtontrees.net/DNA/KingsClusterTree.pdf, s. 3). He lists his paternal ancestor as Andreas Nicolai (died 1579). However, according to his tree at Geni he descends from Lars Mörling, born 4/26/1859 in Väse, so something is not right. Some kind of connection has evidently been presumed to exist to the noble family Mörling, but Andreas Nicolai, vicar of Burseryd, whose father's stepfather's father to the ennobled Mörling – and mother's father's stepfather's father to Olof, born ca. 1657/58, who took the name in the form Meurling (the articles in Elgenstierna's genealogies on Mörling and Gyldenbring with the corrections in the supplementet from 2008, the article Meurling in Svenska Släktkalendern 1989). Researchers at DISBYT have a different opinion about the paternal line of the man born in Väse, i.e. back to his great grandfather Gustav Hansson (ca 1730–1818), who died in Gräs in Lundsund parish in Värmland. Hopefully the test taker will consider joining our project in the future (at present, he has declined to do so). Without project cooperation, it remains unclear for example which values he has on the much relevant four markers, within his matches group, that unite the individuals in Group 2.

DYS460	Y-GATA-H4	YCAII	DYS456	DYS607	DYS576	DYS570	CDY	DYS442	DYS438	DYS531	DYS578	DYF395S1	DYS590	DYS537	DYS641	DYS472	DYF406S1	DYS511	DYS425	DYS413	DYS557	DYS594	DYS436	DYS490	DYS534	DYS450	DYS444	DYS481	DYS520	DYS446	DYS617	DYS568	DYS487	DYS572	DYS640	DYS492	DYS565
17	10	11	19-23	16	15	19	16	34-37	13	12	11	9	15-16	8	10	10	8	10	10	12	23-23	16	10	12	12	16	8	11	22	20	13	12	12	13	11	11	13	12
17	11	11	19-23	16	15	20	16	36-37	13	12	11	9	15-16	8	10	10	8	10	10	12	23-23	14	10	12	12	16	8	11	22	20	13	12	12	13	11	11	13	12
17	10	11	19-23	16	15	20	16	36-37	13	12	11	9	15-16	8	10	10	8	11	10	12	23-23	16	10	12	12	16	8	11	22	20	13	12	12	13	11	11	13	12
17	10	11	19-23	16	16	20	16	36-37	13	12																													
17	11	11	19-23	16	15	19	16	36-37	13	12	11	9	15-16	8	10	10	8	10	10	12	23-23	14	10	12	12	16	8	11	22	20	13	12	12	13	11	11	13	12
17	10	11	19-23	16	15	19	16	34-37	12	12	11	9	15-16	8	10	10	8	10	10	12	23-23	16	10	12	12	16	8	11	22	20	13	12	12	13	11	11	13	12
17	11	11	19-24	16	15	19	16	36-37	12	12	11	9	15-16	8	10	10	8	10	10	12	23-23	16	10	12	12	16	8	11	22	20	13	12	12	13	11	11	13	12
17	10	11	19-23	16	15	19	16	35-36	13	12	11	9	15-16	8	10	10	8	10	10	12	22-23	16	10	12	12	16	8	12	22	20	13	12	12	13	11	11	13	12
17	10	11	19-23	16	15	20	16	36-37	13	12	11	9	15-16	8	10	10	8	10	10	12	23-23	14	10	12	12	16	8	11	22	20	13	12	12	13	11	11	13	12
17	11	11	19-23	16	15	20	17	37-37	13	12	11	9	15-16	8	10	10	8	10	10	12	23-23	16	10	12	12	17	8	11	21	20	13	12	12	13	11	11	13	12
18	11	11	19-23	16	15	20	17	37-37	13	12	11	9	15-16	8	10	10	8	10	10	12	23-23	16	10	12	12	16	8	11	21	20	13	12	12	13	11	11	13	12
17	10	11	19-23	16	15	20	17	37-37	13	12	11	9	15-16	8	10	10	8	10	10	12	23-23	16	10	12	12	16	8	11	21	20	13	12	12	13	11	11	13	12

Explanation to the table above: see the previous page.

R-Z372 with the presently known subclades through Big Y-test takers' participation at YFull. The branch formed around 4,200 (5,000–3,500) years ago, and the MRCA lived around 3,500 (4,400–2,700) years before present. – The confidence intervals are displayed on the webpage when you hover over the text line with years for "formed" and "TMRCA". – The lineages appear in Great Britain (GBR) and USA. CEU means 'resident of Utah with Northern or Western European descent'. When around three or more individuals are on the same branch it can generally be divided into subbranches, that way the tree gets new branches closer and closer to present time. At least twelve of our project members (those in the selection above) probably belong somewhere in this cluster. The bottom one ("new) is Frykman's descendant.

The above mentioned SNPs S7015 and S3207 and others are not yet available for testing at FTDNA. Contact your haplogroup project administrator or Rolf Berlin or Peter Sjölund (responsible for R1b within our project) if you want to test any of them, so that they may notify FTDNA that there is interest in testing these SNPs. If you do not want to test SNPs systematically one by one, another option is to do the Big Y test, which, however, is more expensive. Those who already have done the Big Y test may analyze it at YFull at a cost of $49 USD. It would help shed a light on who belongs to which branch closer to modern times – and reveal young SNPs that the others within the cluster then may test. Jakob Norstedt-Moberg describes how you can participate at YFull in Swedish DNA Project News Nº 3, pp. 6–9.

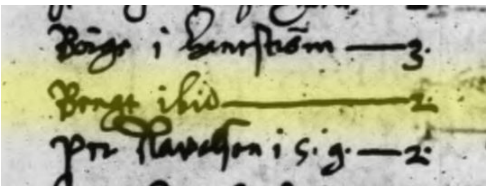
About S3207 can be added that the R1b-U106 Project presumes that it, as well as S5704, presumably is shared by many within R-Z372 with paternal lines appearing in West Sweden and Norway.

Banks(t)on

Anders Bengtsson, b. ca. 1640 (calculated from his age at his death), has his Y-DNA-profile secured thanks to matching tests by no less than 16 Bankson and Bankston descendants originating from two of his sons (the Bankston Project). Through them it is revealed that Anders' 12-marker haplotype was the same as that of his descendant on row 3 in the selection on p. 21. In other words, a mutation has happened on the sixth marker. Since Anders is close to the others in the selection, the mutation has probably occurred on the branch leading up to Anders. In other words, the Banks(t)on family does not have Ht 4, but they can still be mentioned here since they belong to the cluster mentioned above.

Anders was one of the emigrant pioneers to New Sweden in 1656, and it is stated at his death in 1705 that he was born in Hanström, Fuxerna parish, Västergötland. For more information about him and his family, see my book *Genvägar* (2013, in Swedish), pp. 74–75. In the book I mentioned that no Bengt, which must have been the name of Anders' father, lived in Hanström in 1630 or 1642. But I did not know at that time that Fuxerna parish was listed in cattle records from that province for the years 1631 and 1635. In Hanström 1631 lived: Börje ("Börie") (1 taxpaying person), a widow (1) and Anders Larsson (2), in 1635: Börje ("Börge") (3), Bengt (2) *ibid(em)* (latin, 'at the same place') and Per Ravalsson i s(amma) g(ård) ('on the same farm') (2). In other words, Bengt took over a farm in Hanström at some point between the years 1631 and 1635. The fact that there were two taxpaying persons in his household in the latter year probably means that by then he had a wife. This Bengt, who like his neighbors, was a frälsebonde (peasant on a farm owned by a nobleman), is therefore probably the father of Anders Bengtsson.

More tested individuals within Scandinavia are needed in order to better pinpoint the origin of the Hanström family. Today there are matches who have 6–7 differences at the 67-marker level compared to the Bankstons (the Bankstons themselves match each other with 0–5 differences). Those matches, who the Bankstons have today at their 67-marker level, excluding themselves, are individuals whose paternal lines come from the Oppland, Hordaland, and Vestfold counties in southern Norway, excluding several of the project members in Group 1 above.



The only known record of the ancestor of the American Banks(t)on family in Sweden (judging by his name, residence, and time period). Boskaps- m fl längder, Västergötland och Dalsland, Volume 43 (1635), p. 33, Swedish National Archives. DNA clues might in the future reveal close branches of the same paternal family, which could potentially take the genealogy further back in time.

Nisbet(t)

Worth mentioning is that six Nisbet(t) men are Big Y-matches to the mentioned group above, with only one FTDNA SNP difference between them; the six men have SNP CTS5860. They are also differentiated from other R-Z372 lineages by the SNP S4037 (warburtontrees.net/DNA/KingsClusterTree.pdf, s. 3).

They are referred to as "Group 3" in the Nesbitt Project and several of them descend from Alexander Nisbet, born 1731 at sea on his parents' journey to America. The family settled in North Carolina and his descendants are found today in USA, Canada, Australia, the UK, and Norway. It is clear that the American branch has a connection to still prospering Nisbet families on the British Isles. The Nisbet of Greenholm branch includes Murdoch Nisbet (died 1559), one of the first translators of the Bible to Scots, and John Nisbet "the martyr" (1627–1685), a forceful member of the covenants, who was executed in Edinburgh. The Nisbet of Carphin branch is known through the physician Josiah, whose widow married Lord Nelson. This family can be traced back to the county Ayrshire in southwestern Scotland in the 15th century.

It has been shown that there is no connection (which was earlier presumed) between these Nisbet(t)s and the clan Nisbet/Nesbitt from Nisbet in Berwickshire in southeastern Scotland. The clan has been proven to belong to another haplogroup, through 22 tested individuals, R-P312 (R1b1a2a1a2). The Swedish noble family Nisbeth is said to belong to this same clan. However, its paternal line can only be traced through written records to Wilhelm Nisbeth, reputedly born 1596 in Scotland, who came to Sweden in 1627. Y-DNA-testing could shed light on which family he belonged to.

A royal family with this haplotype

Sachsen-Coburg-Gotha is one of the ducal branches within the house of Wettin, whose members have been electoral princes (until 1806) and kings (1806–1918) of Saxony. Their genealogy can be traced back to the castle Hassegau in Saxony in the 10th century. One branch, Windsor, is the royal dynasty of Great Britain since 1901. In addition to the different Saxon ducal families, the royal house of Belgium, the latest royal house of Bulgaria and king Carl XVI Gustaf's mother's family are branches of this family. Brad Little, who lives in USA, has convinced one individual within the Sachsen-Coburg-Gotha branch to do a Y-DNA test (and also the Family Finder test) and also one from the Belgian branch, to compare with tested individuals from his own family. In his family there was a rumor that King George V of Great Britain had fathered his grandfather. Matching DNA supports this rumor. Brad Little wrote a book about this (new edition 2012), see www.the-kings-son.com.

The results of the first mentioned test is published at YSearch (ysearch.org), with the number P93DY. It shows that the 12-marker haplotype is Ht 4. Those who share the same haplotype also see the tested individual's name in their 12-marker matches list – as well as the name "Van Eppinhoven", which indicates that the testing efforts also have led to proving a biological connection between the royals and the family von Eppinhoven. (This name was given by King Leopold I of Belgian to two of his illegitimate sons born 1849 and 1852.)

fraenkische-wappenrolle.kleeberg.biz/s/s030.html.

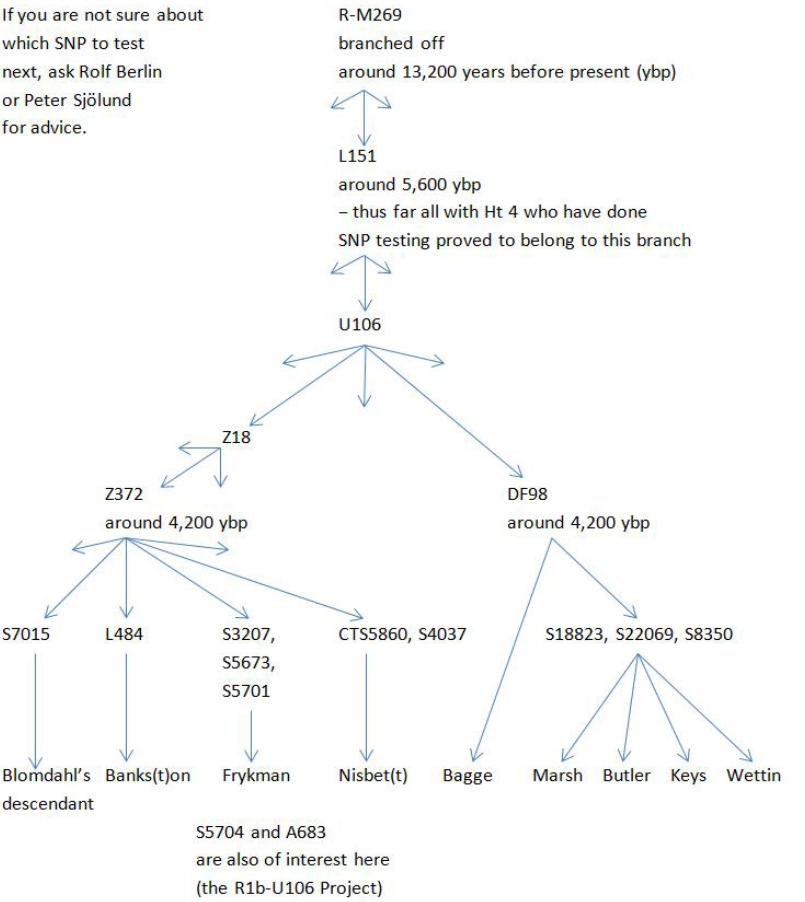
Wikimedia Commons.

Duke Francis of Sachsen-Coburg-Saalfeld (1750–1806). His Y-DNA profile is determined through Y-DNA tests of now living descendants. Pictured is a rendering of his coat of arms from 1790, at the time of his father's reign.

Brad Little has continued the research on this large family, which has raised interest for closer testing of particularly those who prove to having a connection traceable through Y-DNA, although distant, with the royals. The cluster is, thanks to that, more carefully studied than many others at this time. An overview of the research can be studied here: warburtontrees.net/DNA/KingsClusterTree.pdf.

The different branches mentioned have Duke Francis of Sachsen-Coburg-Saalfeld (1750–1806) as their MRCA. His descendants are positive for S18823 and S22069 within R-DF98 (R1b1a2a1a1c1a1). The latter SNP, S22069, is estimated to have occurred around 1200 BC (2100–600 BC). Downstream of that SNP is S8350. In addition to the royals, as far as we currently know, it is also shared by individuals with the surnames **Marsh** (five individuals, MCRA born 1748), **Butler** (four individuals, presumed MCRA around 1500), **Keys** (four individuals, MRCA born 1647) and several others, so far all with paternal lines originating in England and Scotland within historical time; they are estimated to having a common origin with the royal line at some point between the 7th and 13th centuries. Historically speaking, the connection appears plausible: Saxons (Anglo-Saxons) were the dominant tribe in regards to holding power in Britain from the late 8th century up to the Norman invasion in 1066.

Overview



At present, the closest individual to this branch having a Swedish connection is Erki Vaino (not a project member), who is not closely related to it, rather only via the root DF98. This means that the MRCA with the royals lived around 3,600 (4,700–2,600) years ago (YFull). Earlier, his paternal line carried the surname **Bagge**. The paternal line has migrated from Norway via Sweden to the Baltic countries (beta.groups.yahoo.com/neo/groups/R1b1c_U106-S21/conversations/messages/29871).

Magnus Bäckmark