SWEDISH DNA PROJECT NEWS

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Presentations of three administrators

Rolf Berlin

I currently live in Järfälla, but my ancestors are for the most part from Morlanda parish on the west coast of Sweden. I spend a lot of time updating my web site www.morlanda.se which is dedicated to the people of Morlanda, most of whom were fishermen and skippers. With the help of DNA testing, I hope to show that many fishermen immigrated from Germany, Holland, and Scotland during the 1500s. I became the administrator of the Swedish project at FTDNA in August 2011 and shortly thereafter founded the Facebook group DNA-anor.

Anders Berg

My name is Anders Berg and I live in Stockholm, Sweden. I have been doing genealogical research since the late 1980s. My ancestors on my father's side are from Skåne (Scania) and on my mother's side from Ångermanland (and a small slice of Värmland). My interest in DNA genealogy started in 2011, and I have tested with both Family Tree DNA and 23andMe. I am especially interested in deep ancestry, from the dawn of humanity, that can be traced through the haplogroups on the direct paternal and maternal lines. My Y-DNA haplogroup is I1-Y5473, a new branch under L22, which was discovered through BigY. My mtDNA haplogroup is U5a1a1b.

As co-admin of our project I am the contact person for southern Sweden (primarily Skåne) and responsible for the project statistics of haplogroups presented in the Swedish Haplogroup Database (SHD).

Donald Ekberg

I currently live in Clearwater, Florida, USA. All four of my grandparents immigrated to the USA about 125 years ago. My Mormor was from Östergötland. The other three were from Skåne. They settled in the town of La Grange, Illinois, a suburb of Chicago. The Sweden Project was started in 2006 when I was asked by FTDNA to start a surname project. After telling them that Swedish surnames were established patronymically, they suggested a Swedish geographic project. I agreed and we started out with eight people. Ann Berge, one of the Norwegian FTDNA administrators, offered to help and suggested Rolf Berlin as a co-administrator. As the only administrator in the United States, I would like to add one or two USA co-administrators. Since I do not speak Swedish, it would be helpful if they spoke Swedish.

When I complete my family tree using Arkivdigital and Heritage, I intend to compare Swedish-American DNA with DNA from Swedish nationals. I also would like to compare ancient Scandinavian DNA with modern Swedes and Americans with Swedish heritage.

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.

Branches of mtDNA haplogrupp T1a1 present among the members of our project

The mtDNA haplogroup T1a emerged with a mutation that happened in a woman 17,200 ± 2,900 years ago, probably in the Near East. T1a is the largest branch within T1, accounting for about 90% of its now living members. T1a is today widely distributed and reaches its highest frequency in Romania (about 9%), Tunisia (about 8%) and Northeastern Iran (about 8%). The calculated age of the subclade T1a1 is 15,500 ± 2,800 years and is presumed to have spread over Europe during the late glacial period, about 12,000–16,000 years ago (Maria Pala et al., Mitochondrial DNA Signals of Late Glacial Recolonization of Europe from Near Eastern Refugia, in American Journal of Human Genetics, vol. 90(5), 2012).

Among people whose maternal line emerges in Sweden, as far as is known, at least 1.4–1.5% belong to T1a1 (Swedish Haplogroup Database and Swedish DNA Project). The actual share is larger (within the total share of T1 which is 2.6–2.7%) because assignment to Ta1a is only possible with a mtFull Sequence test at Family Tree DNA. Many have yet only taken mtDNA tests with less resolution.

In the overview on the next page you will see the relationships between the T1a1 members of our project. Most of them see each other in their match lists. In other words, they have only three differences or less in their full mtDNA sequence. There is one exception: the lineage know from Tofta in Skåne (Scania) in the 18th century (to the right in the overview); it has recently received a name of its own at phylotree.org, T1a1e (not yet implemented at FTDNA).

Within the group who see each other there is, remarkably, a cluster of no less than *73 test takers who have the exact same full sequence*. That means 0.16% of all the 45,689 full sequence clients at Family Tree DNA. According to their oldest known country on the maternal line they are distributed geographically as shown in this table:

Country	tests	total	=	share
Belgium	1	113		(0.9%)
Ukraine	4	521		(0.8%)
Romania	1	152		(0.7%)
Slovakia	1	157		(0.6%)
Norway	5	917		0.5%
UK	7	1,684		0.4%
Sweden	4	1,097		0.4%
Switzerland	1	299		(0.3%)
USA	3	1,178		0.3%
England	9	3,870		0.2%
Poland	2	1,181		0.2%
Germany	8	3,290		0.2%
Finland	1	1,263		0.1%
France	1	1,001		0.1%
Ireland	2	2,784		0.1%
Scotland	1	1,483		0.1%

Parentheses indicate low test numbers, which lead to skewed statistics.

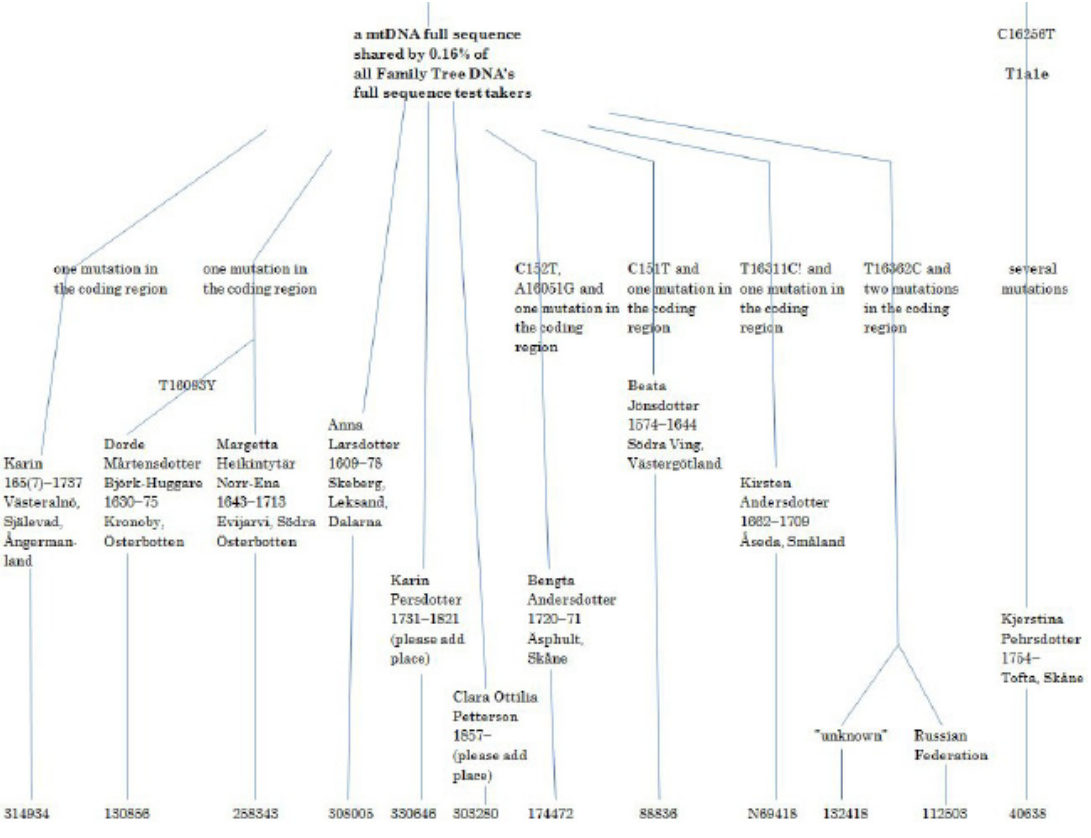
→

Since so many individuals are each other's perfect matches, this means their mtDNA has been unchanged for a very long time. A contributing factor may be that this maternal clan might be larger than others.

When the match list looks like this, one must bear in mind that close relatives can hide not only among the perfect matches, but also among the GD=1 (2 etc) matches. Even if a mutation has not happened on the line up to you, it may very well have happened within the past few generations on another branch of your maternal family tree.

Those of you who belong to T1a1, please let any of us administrators know if you in pairs or groups succeed in identifying common foremothers within historical time or if you find anything else of interest, so that we can follow up on it here in the newsletter.

Magnus Bäckmark



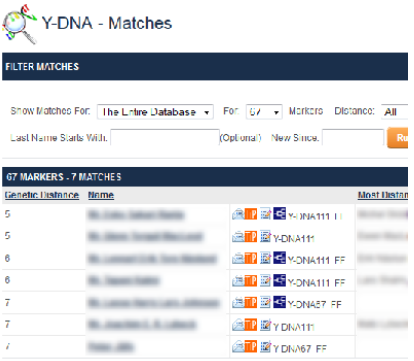
Y-DNA, BigY and then Yfull

By testing the male Y chromosome one can get a good view of the paternal line, i.e. the origin of one's father's father's father's father's... The Y chromosome remains more or less unchanged from generation to generation but small changes appear and they may be used to trace the origin. All men having a certain change also have a common paternal ancestor.

There are a few different Y tests. Some give clues and hints while others are more exact.

STR tests

Most men (only men have the Y chromosome) start the discovery of their paternal line with an STR test like the ones FamilyTreeDNA calls Y-DNA37 or Y-DNA67. These basic tests can give an idea of the haplogroup and the origin going back one or a few thousand years. You will also get a list of matches of people who have also taken the test, and these matches may give you clues to closer relationships.



List of matches for Y-DNA67 STR test.

The problem with these tests are their randomness. Two individuals may end up with the same deviation without being as closely related as one might think. The similarity may simply be a function of chance. Therefore, watch out and take the results with a grain of salt.

BigY

The matches you get from an STR test like Y-DNA67 can be doubtful and the haplogroup information can be rather inaccurat. This makes the BIG Y the natural next step. BIG Y is based on a different technology. Where STR tests show markers that can act unpredictably, BIG Y delivers SNPs that are very stable.

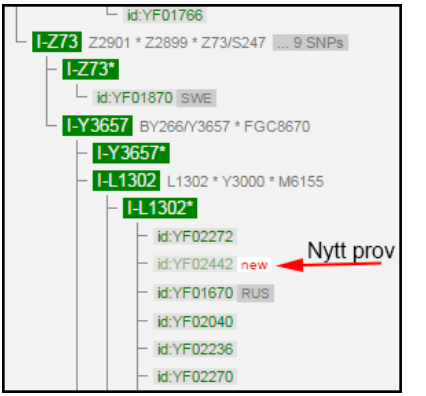
An SNP is a mutation which could be thought of as a spelling error in the genetic code. A mutation will be carried on from generation to generation and never disappear. The men who have a certain SNP also have the same common ancestor, and by matching individuals with similar sets of SNPs one can build a kind of family tree of the paternal line.

BIG Y is an analysis of a large part of the Y chromosome and it results in a list of previously discovered SNPs. These SNPs have been named and cataloged and placed in the official haplogroup trees, e.g. the ISOGG tree. But there is more. You also get a list of novel SNPs, i.e. SNPs that have not been previously discovered. These SNPs can be matched with SNPs from other new BIG Y tests. If two individuals share a novel SNP, it can be concluded that they are related and the SNP will be named and will not be considerer novel anymore.

Thus, BIG Y defines the exact location in the haplotree and it contributes to the research and growth of the tree. Your BIG Y can be matched with the tests

of others so new branches and twigs can be found.

However, this matching is not done by Family Tree DNA. They trust the haplogroup projects to compile the common results, and it is here that Yfull is needed.



Yfull Experimental Tree.

Yfull

Yfull is an independent service for analyzing BIG Y data.

With Yfull you get a much deeper analysis of the data produced by the BIG Y test. Yfull finds valuable details that were screened out by Family Tree DNA, and in addition to SNPs provide some bonus information:

- In addition to SNPs, you will receive many more STR markers than you would ever get from a standard STR test at Family Tree DNA. There may be voids, but normally you would get around 400 markers which would assure a much more reliable STR matching and relationship evaluation than if you only had 37, 67, or a maximum of 111.

- You will receive your mtDNA haplogroup (your maternal line). The information is almost the same with BIG Y and Yfull as the information a dedicated mtDNA test would provide. The result is not quite as accurate and your will not get a list of matches, but the mtDNA haplogroup is in fact there without any additional cost to you.

- Your kit will be inserted into the Yfull's experimental tree which you can browse here: http://yfull.com/tree/.

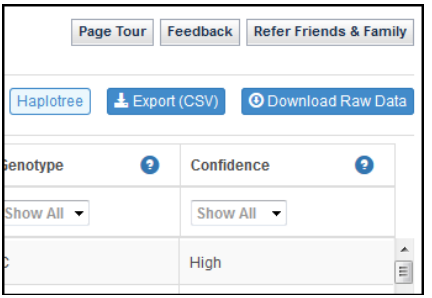
The tree is revised and changed quite often. Go back and check the tree now and then to see if there are any changes surrounding your kit. All of a sudden, you may have a new cousin.

The Yfull analysis costs $49 but is in fact necessary for getting the full value out of the BIG Y test. The project administrators need Yfull to evaluate your BIG Y test.

How do you send your BIG Y to Yfull?

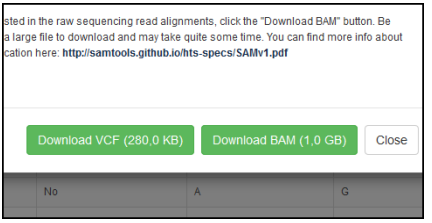
When your BIG Y results are ready you send an email to helpdesk@familytreedna.com with the message: "I request the BAM file for my kit number xxxxxx". FTDNA will prepare the data file, the BAM file, for you. It is huge, about 1 GigaByte, and it takes a couple of days until it is ready.

When you believe it is ready, you log in to your Family Tree DNA account and go to the BIG Y Results page which has a button on the right hand side called "Download Raw Data".



Download Raw Data – You find it on the BIG Y Results page.

Click the button. If the BAM file is ready you wil see the option "Download BAM". If it is not ready after a week or so, you should contact helpdesk again.



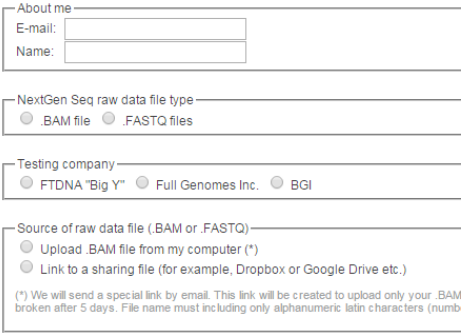
Download BAM.

Download the BAM file to your computer. It may take hours if your have a slow Internet connection. When you have the file stored on your computer, go to yfull.com and click "Order now" at the bottom of the page:

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).

Fill in the form



A new account at Yfull.

- **E-mail** and **Name**, the e-mail address is used for login.
- **NextGen Seq raw data file type** – select .BAM file
- **Testing company** – select FTDNA (FamilyTreeDNA).
- **Source of raw data file** – you have two options:
  1) *Upload .BAM file from my computer* – you get a link from Yfull that you will use for uploading your BAM file.
  2) *Link to a sharing file* – you upload the file yourself to a service like Google Docs or Dropbox, share it and send the link to Yfull. They fetch the file.

If this does not work, please ask your project administrator for advice.

What happens next?

When you have sent the file or a link to it, you will soon get a confirmation from Yfull together with your Yfull kit number and a password to the account. After just a few days, the kit will appear in the experimental tree, but the analysis will not be ready for another month. It is only then you are requested to pay the fee of $49.

Log in with your email address and the password you received to pay the fee.

When you have payed and received access to your data at Yfull, you should join a group. You find the groups under the menu option "Groups" when logged in. The groups are usually managed by the same people who manage the projects at FTDNA, and you should choose the group that your administrators recommend. With a Yfull group they get a good view of all the details in your BIG Y and can use it to build as accurate of a haplogroup tree as possible.

BIG Y is rather new. It has only been around since the late 2013. The means that if you are unlucky you might have a long genetic distance to you closest cousin. But do not despair. The number of tested individuals is growing fast and sooner or later you will have several around you.

Good luck!

Jakob Norstedt-Moberg

New findings about the time when farmers and foragers met

Photo: Inger Österholm.

Site of excavation at Ajvide.

Around 6 000 years ago farming started reaching Scandinavia. The new way of living had spread gradually over Europe via Balkan and the Mediterranian from the Near East, where it had been invented at least 10 000 years ago.

The landscape which saw the first grazing cattle and the first primitive tillages was of course quite different to that of today. The conquests of agriculture was helped by a climate warmer than nowadays. Oak, linden and elm grew far up in Norrland. The Baltic Sea had received its connection to the Western Sea, but the provinces around Stockholm, Södermanland and Uppland, were part of the archipelago and a broad strip of the northern coast lay under water.

How did agriculture spread? Did it happen by exchange of ideas or by farmers gradually moving to new areas? Internationally, DNA-analysis has given important clues. In April, a study was published that gives some information concerning present-day Sweden: Pontus Skoglund et al., Genomic Diversity and Admixture Differs for Stone-Age Scandinavian Foragers and Farmers, in Science, vol. 344, nr 6185.

The study includes, on the one hand, remains of sex individuals on Gotland belonging to the Pitted Ware culture which is associated with foragers, and on the other hand, four individuals found in Gökhem in Västergötland (in western Sweden) belonging to the Funnel Beaker culture whose members were farmers. In the DNA from the remains you cannot see if they were foragers or farmers. However, the archaeological context gives indications with varying certainty.

Findings are that the presumed foragers had a significantly lower genetic diversity (DNA variation between them) than the representatives of probable farmers. It points to foragers being relatively few in numbers. The geographic isolating of the site Gotland, being an island, may be part of the explanation. In any case, the foragers were quite different from the farmers. One measure of genetic differentiation is Wright's Fixation Index. That index came to 0.057 ± 0.017 between the groups studied, which can be compared to 0.013 ± 0.00059 for the now living reference groups in Italy and Finland (from the 1000 Genomes project). A farmer during the Neolithic within present-day Sweden seems to have been significantly more different, DNA-wise, compared to a contemporary forager in the same area than Finns today are to Italians, according to some sort of average. (The comparison cannot be anything other than crude. Nonetheless, it does give us some indication.)

Compared to present-day reference groups, a representative of the forager group (Ajvide58) comes closest to now living people in Lithuania, while a representative of the farmers (Gökhem2) seems closets to now living Sardinians and have significant similarities to people now living in Southern Europe and the Near East. (That DNA from only those two individuals has been compared is explained by the fact that those two samples were the two with the lowest estimated degree of contamination.)

Photos: Göran Burenhult.

The man from grave 58 at Ajvide (Ajvide58).

In grave 52 at Ajvide two children lie. At the right lays the boy, around 7 years old, whose DNA has been analyzed. His feet are placed on the shoulders of the other child, who was about 2 years old at the time of death.

The two ways of living coexisted in Scandinavia for more than a thousand years, more than 40 generations. There are no DNA signals in the foragers that suggest any substantial gene flow to them from the farmers. On the other hand, there is evidence of gene flow going the other direction, pointing to foragers having been successively assimilated into the farming society.

There is also an 11th individual in the study, much older than the others. He has been found at Stora Förvar, Gotland, and is between 7,250 and 7,500 years old. This individual is relatively close, DNA-wise, to the over 2,000 years younger foragers from the same island but also to the about 7,000 years old forager excavated in 2006 in La Braña in northern Spain (Iñigo Olalde et al., Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European, in Nature 507, 2014). This study caused a wave of interest in the media earlier this year, since it turned out that the La Braña man had the ancestral allele of the gene SLC24A5 which is involved in skin pigmentation. The same goes for Ajvide58. Gökhem2 — like virtually anyone with roots in Europe and many in South Asia (for example India) — has the younger derived allele, causing lighter skin. Consequently, old schoolbook illustrations presenting Stone age foragers in Scandinavia and Europe as having a light complexion could be wrong.

CSIC.

A reconstruction of how the man from La Braña could have looked like.

Furthermore, it can be mentioned that the man from Stora Förvar belongs to Y-DNA haplogroup I2a1 (I-P37.2). That is a branch on the human paternal family tree which at present accounts for 0.7% of the project members with the paternal line from Sweden (six individuals). (There are more individuals within I2 who have not yet done SNP testing, so the share may in fact larger. It is unknown how much larger the share is of the total I2 share, which is 3.5%.) The mtDNA haplogroup has been established for all individuals in the study:

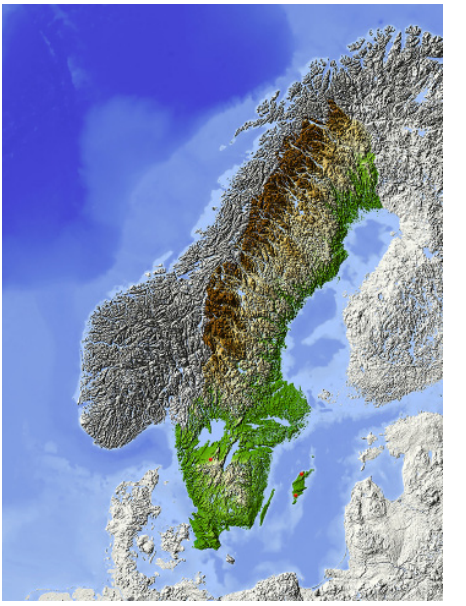
	Age (years before present)	Sex (M/F)	Age at time of death	mtDNA haplogroup
Foragers				
StoraFörvar11	7,500–7,250	M	adult	U5a1
Ajvide52	4,900–4,600	M	7	V
Ajvide53	4,900–4,600	F	ca 60	U4d
Ajvide58	4,900–4,600	M	50–60	U4d
Ajvide59	4,900–4,600	M	25–35	U
Ajvide70	4,900–4,600	M	20–25	U4d
Ire8	5,100–4,150	M	40–50	U4d
Farmers				
Gökhem2	5,050–4,750	F	20–30	H1c
Gökhem4	5,280–4,890	M	20	H
Gökhem5	5,050–4,750	F	20–40	K1e
Gökhem7	5 050–4 750	F	20–40	H24

Previous analyzes of Stoneage remains from all over Europe indicate that U with subclades has dominated among foragers and that K was more common among farmers. However, both mtDNA haplogroups are found in Stoneage Europe within both types of societies. Thus far, H is only known in farmers within Europe (Qiaomei Fu et al , Complete Mitochondrial Genomes Reveal Neolithic Expantion into Europe, in PLOS ONE 3/13/2013). V does not seem to have been found in a forager context before — and among other mtDNA haplogroups HV, N, U3, and W also belong to those associated with the expansion of farming, while J, T, and U5a are found within both types of societies, and U4 and U5b among foragers (Oleg Balanovsky et al., Ancient DNA from European Early Neolithic Farmers Reveals Their Near Eastern Affinities, in PLoS Biology 8(11), 2010).

The Atlas Project

Sweden will be at the forefront of archeogenetic studies in the coming years. Extensive funding grants have been assigned to a research project called "The Atlas of Ancient Human Genomes in Sweden", involving Mattias Jakobsson, Department of Ecology and Genetics, Uppsala University, Anders Götherström, the Archeological Research Laboratory, Stockholm University, and Jan Storå the Osteoarcheological Research Laboratory, Stockholm University.

In the next six years, they aim to have genetic information for about 400 ancient individuals in Sweden from the time after the glacial ice melted and forward with complete genomes for 25 of them. They will compile genetic information in combination with archaeological and osteological information, dating, and isotope information.

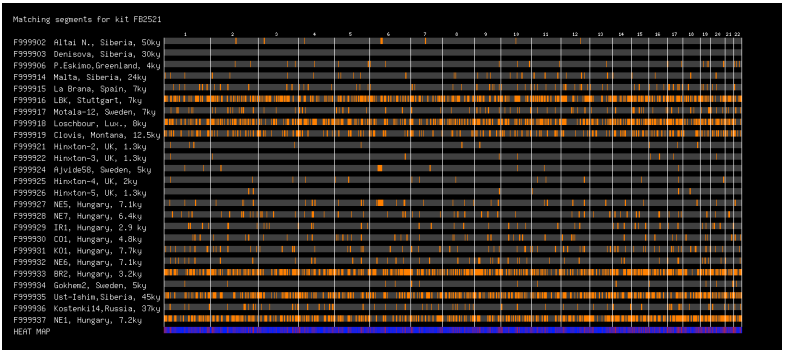


Research results from the Atlas Project will be publicly accessible at www.theatlas.se. It is already possible to click on the red pins and read about findings from Gökhem, Ire and Ajvide.

— With the help of this data and new population-genetic tools we will be able to describe the demographic prehistory of Sweden in a completely revolutionary way, Mattias Jakobsson is quoted saying on the Uppsala University website.

Magnus Bäckmark

Who of the prehistoric humans do you share matching segments with?



Segments colored orange are present in my autosomal DNA as well as 25 different prehistoric individuals. The threshold is is set to 1 cM<. When I change to 4 cM<, only three segments remain, one segment per Stone age individual found in Hungary and Germany. The age of the individuals is given in thousands of years (kilo years, ky).

25 different genomes of prehistoric humans were recently made available for individual comparison at GEDmatch with help of the computer programmer Felix Chandrakumar in Adelaide, Australia.

After having logged in, chose Archaic DNA matches. Your own raw data and the 25 prehistoric genomes will be compared simultaneously. The threshold of displayed segments in common may be altered from 0.5 cM to 10 cM. The GEDmatch kit numbers of the prehistoric samples are displayed in the resulting image. You may use those for one-to-one comparison in order to find out the locations of the common segments. A known bug is that the result image often does not change after changing the threshold value. If that happens, refresh the page (either by clicking on the circular-shaped arrow next to the URL window in your browser, or hitting F5 on your keyboard).

You can up-load your raw data to GEDmatch (www.gedmatch.com) for more types of comparison than are available at Family Tree DNA. It is free, but a possible downside from a privacy point of view is that the site is completely open: your matches see your GEDmatch kit number and can use it for different comparisons just as easily as you can do. Your submitted email address is also shown in the match list. It is the only clue to which individual the raw data belongs to. This is good to know. If you do not want to give a clue to whom the data belongs to, the best approach is to use an anonymized email address.

The autosomal DNA comparison between prehistoric humans and now living individuals shows that chance, which governs how DNA is inherited, sometimes has the effect that both samples happen to have an unexpectedly large segment in common. Lucky has in those cases been so favorable that a sign of the mutual relationship is still present despite the distance of time. Common segments of over 5 cM are not entirely uncommon among now living individuals and some of the prehistoric samples. In a few extreme cases, segments just above 10 cM have been observed. Generally, in those cases, only that segment is in common (and no other smaller segments). This can be studied because Chandrakumar has transferred the raw data of the prehistoric samples to GEDmatch and to Family Finder.

www.lagranepoca.com.

In 2008 this femur was found at the shores of the river Irtysh at Use-Ishim, Sibiria. Carbon dating determined it to be about 45,000 years old. A research team lead by Svante Paabo at the Max Planck Institute in Leipzig has sequenced the genome, which is at the present time the oldest genome of a modern human outside of Africa and the Middle East. The man from Ust'-Ishim proved to have some Neanderthal ancestry. Those traits are calculated to be the result of a mix with the Neanderthal 7,000–13,000 years before his lifetime. This indicates that the contacts with Neanderthals probably happened relatively soon after the expansion of the modern man out of Africa and the Middle East.

The website of Max Planck Institute (http://www.mpg.de/8710423/genome-earliest-modern-human), 10/22/2014.

A segment that has traveled down unchanged through several generations, in addition to a few smaller segments, will cause the match to be visible in Family Finder (the predicted relationship to now living individuals are in those cases "5th Cousin — Remote Cousin"). GEDmatch predicts "5.1" generations or more to the most recent common ancestor. Even the Ust'-Ishim man (see above right) has different segments on just over 10 cM shared by a handful of now living people. The exceptional record of the longest segment in common to a now living person has "NE1" from a 7,200 year old archaeological site at Polgar-Ferenci-hat in Hungary: 29.2 cM (if the data is correct!).

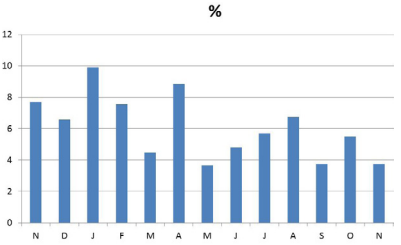
Family Finder users know that matches predicted to be distant relatives ("4th/5th Cousins — Remote Cousins") can be exactly that; distant — while also realizing that the matches could be 4th or 5th cousins. The comparison to prehistoric humans opens one's eyes to the fact that "distant", in the most extreme cases, does not just mean relationships spanning the Middle Ages, but may mean relationships spanning several thousand years.

Magnus Bäckmark

Felix Chandrakumar: Felix Thought Logs, http://www.fc.id.au/2014/11/ust-ishim-ancient-dna-has-matches-with.html (11/20/2014), http://www.fc.id.au/2014/11/ancient-hungarian-neolithic-ne1-dna.html (11/25/2014).

How many Family Finder matches is it common to have?

The answer here is based on what people have replied on surveys in the Facebook group DNA-anor. So, the statistics is based on Swedish speaking test takers, who of course have varying backgrounds. Nevertheless, the numbers will at least give you and indication of the number of matches one can expect to get if one has many roots in Sweden.



The average increase of matches per month.

By the end of June 2014, the number of total matches varied between 107 and 862, and on average 261. By the end of November 2014, **between 120 and 1,079 matches, and on average 331**. (The number of replies to the survey has varied between 26 and 168, and has on average been 97 replies per month.)

Magnus Bäckmark

Genetic genealogy and traditional genealogy in harmony

When I started doing family research five years ago I had the luck of having inherited extensive research made by my great uncle during several decades. In this comprehensive research I found plenty of interesting things, for example hints about relatives in the USA. My mother's father's father Herman had five siblings, one of whom was his brother, Sven Fredrik. That brother emigrated to America in 1893, when he was 20 years old. Younger generations in the family have completed the research findings. On our family's web site you can read about this man marrying a woman in the USA who came from the same parish as he did in Skaraborg's län. This couple had five children.

Svante Brolin (b.1847) and Anna-Stina Svensdotter (b. 1849). The parents of the two brothers Herman and Sven Fredrik.

In beginning of October I received notice about a new match in Family Finder. The calculated relationship was 2nd to 4th cousin. This match, by the name of Marsha, did not have a family tree uploaded to her account. However, I sent her an email and received the reply that her father's surname was Brolin! Thanks to that name we quickly found our common link. With the help of the information I have, I was able to complete her records of her roots. Our actual relationship is 3rd cousins, so the Family Finder calculation was right on the spot.

As a result of DNA testing I easily found my American relatives. If I had only done research in books and archives it would not have been as easy. Now I have a new branch on my family tree — and soon there will be a card with Christmas greetings from Sweden making its way over the Atlantic.

Maria Brolin

How I found my father's 2nd cousin in USA

John Jacobsson and his two daughters.

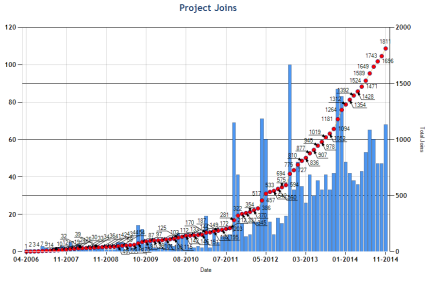
In the end of the 1990's I found this photo in my grandma's (father's mother) box with old photos. I learned that it showed her uncle (mother's brother) John Jacobsson, who had emigrated from Ås parish in Jämtland to America in the early 1900's. I got curious and started looking for him, but it was impossible to find him in America. Eventually his younger sister had travelled to him, and I found her in the immigrant records of Ellis Island. There her destination was noted as her brother, Duluth, Minnesota – then I could start following him and his life in the new country. I found his family, wife, four children and some grandchildren. Of some reason I stopped there.

The other day when I checked my match list at FTDNA I saw a name that seemed familiar – Sharon Cooper, she was predicted to be my "2nd–3rd cousin" and she has 235 cM in common with me. When I checked my research database I found a woman with that name; she is a 2nd cousin of my dad. Sharon hadn't uploaded a family tree, so I could get any help that way, but I e-mailed her. After only a couple of hours I received a reply from her confirming my guess was correct – her mother's father's name was John Jacobsson and he came from Sweden.

It was a tremendous feeling to get a confirmation that my research results were correct to 100% and that FTDNA had made a correct prediction of the distance between us. That makes me feel more confident in the results in the match list.

Eva Eklund

Our project grows



As of 11/30/2014 we have 1,811 members, after an increase of 20% over five months. Of these individuals around the world with some connection to Sweden, 1,111 have done Family Finder (+25%), 1,146 Y-DNA (+19%), and 1,096 mtDNA (+18%) at one of the levels available for these two tests.

In one year and two weeks, since 11/17/2013, the increase of project members has been +59%, test taker of Family Finder +87%, Y-DNA +56%, and mtDNA +61%..

Magnus Bäckmark

The third most common 12-marker haplotype in Sweden

In Swedish DNA Project News N° 1 and N° 2 the two most common 12-marker haplotypes in our project were examined. Now it is time for the third most common. Statistics show it is also the third most common among people tracing their paternal line from present-day Sweden, as far as they know. Below "Ht 3" means haplotype 3, this haplotype, which has the values 3-**22**-**15**-10-**13**-**14**-11-14-11-12-11-28 (in the order FTDNA lists them).

The first four markers (in bold) that are different compared to Ht 1 and Ht 2 are DYS390, which has the value 22 instead of 23, DYS319, which has the value 15 instead of 14, and the double marker DYS385. The latter is represented by two values, 13-14, where Ht 1 has the values 14-15 and Ht 2 13-14. This marker is more instable than the two first mentioned. Note, there was only one difference between Ht 1 and Ht 2 — to Ht 3 there are four and three differences respectively.

As with all haplotypes, one must understand that a certain haplotype does not only appear on a single branch. Random mutations make it so that some lineages from related branches get the same allele values. Also, a lineage which has had Ht 2 for several thousand years may have been hit by a recent mutation, resulting in the lineage ending up in a neighboring haplotype instead.

640 test takers — 0.12% of the 516,767 Y-DNA clients at Family Tree DNA — have Ht 3, 24 of whom are members of the Swedish DNA Project. The paternal lines of the test takers emerge as far as we know in the following countries:

Norway 2%
Sweden (49 of 2,702 test takers or **1,8%** of men with stated paternal lineage from Sweden)
Wales 0.7%
Finland 0.6%
Canada (0.5%)
Belgium (0.4%)
England 0.4%
Nederlands 0.4%
UK 0.3%
Germany 0.3%
Russian Federation 0.2%
Switzerland 0.2%
Denmark 0.1%
France 0.1%
Ireland 0.1%
Lithuania 0.1%
Poland 0.1%
Scotland 0.1%
Czech Republic (0.1%)
Hungary 0.1%
USA (0.1%)

Parentheses indicate test numbers below 1,000, which may lead to skewed statistics. There is too little data from the following countries to provide meaningful statistics: Jamaica (1 of 60 test takers) and Kuba (1 of 79).

Families within I-Z60 (I1a2a1) with this haplotype

61 tested men belonging to the **Hull** family carry Ht 3. The name is quite common, so there are clusters of Hulls with completely different Y chromosomes as well. However, among the test takers with this surname, this family is the largest in numbers. The name may be derived from various place names (Hull) in England with the meaning hill. Alternatively, it may be derived from the male name Hulle, a pet name of the Norman name Hugh/Hugo. In Normandy it was common with names of Germanic roots but pronounced with a French accent, as this one. The name consists of one word, in old Saxon *hugi*, in old High German *hugu*, related to Swedish *håg* with the meaning 'mind, joy, courage, inclination'. About half of the 61 test takers descend according to written records from early immigrants to Massachusetts (in the 1620s and 1630s) from two different sons

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of Richard Hull of Crewkerne in Somerset in Southeastern England. His will was written in 1599. DNA tests have shown that nine branches of the Hull family in the USA, who cannot trace their paternal lineage longer than the 18th or 19th century, belong to this family.

Relatively closely related to the Hulls are eight individuals called **Seamans**, **Seamands**, **Simmons**, of whom several have known descent from either William Seamans († 1820) or Joseph Seaman(d)s/Seamons (1683–1730), Richmond county, Virginia (DNA testing has proved that this is one and the same family, within which different spelling of the name occurs), and also three men called **Gibson**. These three can follow their paternal lines back to David Gibson (ca 1842–1910) of Clay county, Kentucky, John Gibson (1795–1879) and Henry Gibson (1563–) respectively. The test taker who is a descendant of Henry Gibson has tested positive for the SNP CTS1679. Consequently, we can also presume that the Hull and Seamans families are located within haplogroup I-Z60 (I1a2a1), which is the larger group within which this SNP has emerged.

The town Crewkerne, where Richard Hull lived in the late 1500s, grew up in the late Medieval period around the textile industry. The picture of the present day town square is from the town's official web site.

Within I-L1302 (I1a2a1b1)

The family name **Norstedt** was assumed by Christoffer Larsson Norstedt (1672–1755), who was a fourth generation "bergsman" (a shareholder of a mine) on the farmstead Höjen outside Falun, Sweden. His Y-DNA profile is revealed on most markers through four descendants, from two of his sons, who have taken Y-DNA tests. The younger branch has the value 16 (instead of 15) on the third marker, and one of the two test takers on the older branch has the value 27 on the last marker of the twelve (the three others have the value 28). That means that only one (324479) of the four test takers carries Ht 3, and it is still unknown if this line originally had this haplotype or if it had a 12-marker haplotype close to it but with the value 16 on the third marker. Because of SNP tests on both branches, it has been proven that the Norstedt family belongs to haplogroup I-L1302 (I1a2a1b1).

Map from 1655 with Höjen ("Höge(n)") at the top center, from Jakob Norstedt-Moberg's webpage http://hoijen.se/category/dnaresultat/.

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gerbovnik.ru.

Coat of arms of the Vorontsov family.

One **Vorontsov** and one **Vorontsov-Veliaminov** have ht 3 (and one **Vorontsov-Velyaminov** a 12-marker haplotype with one difference compared to the other two). According to tradition, they descend from a noble Varangian in Kiev, where he took part in a battle in 1068. A 13th century chronicle mentions him as nephew to "Jakun" who participated in the battle of Listven in 1024 but was exiled by him after the death of his father. In Kiev he was called Šimon Afrikanovich. It has been suggested that his Nordic name was probably Sigmundr and that he may have been a son to an unsubstantiated brother (Afreki?) of Hakon Eriksson of the Earls of Lade. Earl Hakon was the regent of Norway under Danish reign until his death in 1029.

A few of our project members have one or more of these three test takers in their 37 marker match list, in that case with four differences; in other words, just barely showing up in the match lists at that level.

The SNP BY126 was found by our project member Erik Holmlund in his Big Y test and also in Vorontsov's. After having reported this to ISOGG, the SNP BY126 was included this year as a new subclade (11a2a1b1b) under L1302. To date, in addition to Vorontsov, three men with paternal lines from Västerbotten and two men from Ångermanland (both in northern Sweden) have tested positive for it, all through Big Y (it is also possible to test for this SNP with a single SNP test at FTDNA). Projects have started this year for both the group L1302 and 1301. They will probably reveal interesting information. More information, see www.familytreedna.com/groups/i1-11302 and -l1301 respectively.

Within I-M227 (I1a1a)

Ht 3 is also carried by nine out of eleven DNA-tested descendants of John **Littlechild** († 1551), Essex, England. The remaining two have close 12 marker haplotypes, each with a single difference compared to their relatives. One of the two mentioned descendants has with an SNP test confirmed that the family belongs to haplogroup I-M227 (I1a1a).

The distribution of Ht 3 in different haplogroups

It appears that Ht 3 mainly occurs in I-DF29/S438 (I1a) and its subclades. Its predecessor I-M253 (I1) is presumed to have been branched off 4,000—5,000 years ago in Europe, possibly in present-day Denmark (see the Wikipedia article about I-M253 and the references there). Presumably, I1a is not very much younger than that. There are individuals within the Ht 3 carrier group who belong to different subclades below I1a but are still visible in each other's match lists at the 37 marker level.

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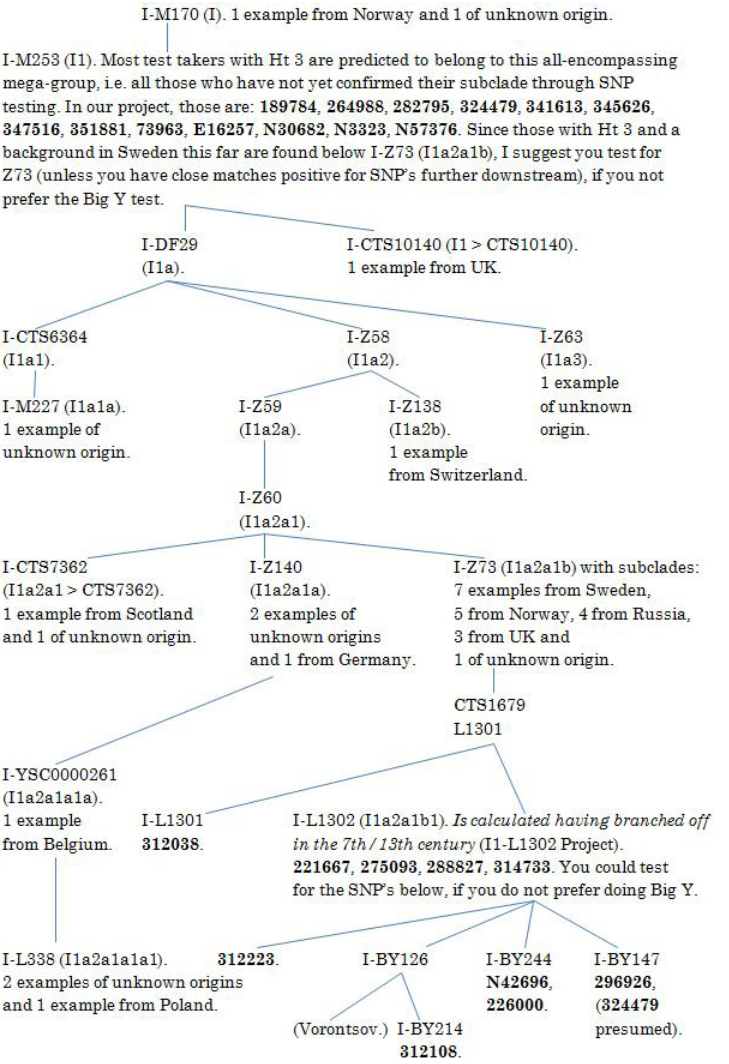
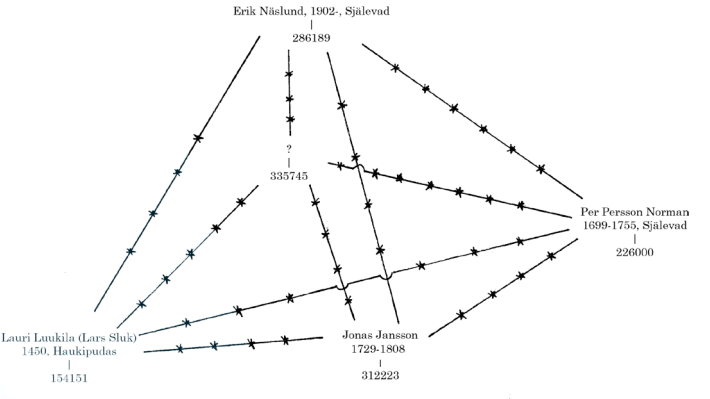
Thanks to those who have done more careful testing it is evident that haplogroup I-Z60 (I1a2a1) with subclades seems to have an extraordinary high frequence of Ht 3 carriers. See the overview below. The country listed is the country or origin of the test taker's oldest known ancestor on the paternal line. The overview also includes where the project members with Ht 3 currently are in their SNP testing.

Note that the knowledge of this part of the tree develops quickly. FTDNA makes use of the SNP CTS743, ISOGG and Yfull do not. CTS743 and CTS1679 are regarded phylogenetic equivalent to Z73. Those who at FTDNA at present have the label I-CTS743 are therefore found below I-Z73 in the overview here:





The diagram above displays an STR marker match cluster that is present among the carriers of Ht 3 and who are members of our project. The stars indicate the number of differences between the project members at the 67 marker level. The test takers 228000 and 312223 have four differences between themselves and are close to three project members who have another 12 marker haplotype, specifically one where the third marker has the value 16 instead of 15. One of the members in this cluster has a different haplogroup label at FTDNA than the others, I-CTS1679. However, as mentioned on p. 20, the SNP CTS1679 is placed on the wrong branch in the FTDNA tree; 154151 has tested positive for CTS743 like the other four members.

Among the remaining four, it is interesting that 286189 and 335745 have the same differences in relation to the others. I.e. the value 16 instead of 15 on the third marker and the value 15 instead of 16 on the marker named DYS576 (approximately in the middle of the row, see the chart to the right). (Columns marked green, like the column for the marker just mentioned, indicate markers that are more unstable than others.) The shared differences in relation to the others indicate that the two test takers may be more closely related to each other than to the others. The fact that they both have the lowest number of differences at the 67 marker comparison level, only 8, points to that as well. The TiP tool (TiP , next to the person's name in the match list) takes into account if differences are on more stable or more unstable markers. In the case of these two test takers, their differences lead to the prediction that their common ancestor, with 90% certainty, lived within the past 12 generations.

Two of the five project members in this cluster has indicated that their paternal lines, according to written records, appear in Själevad in Ångermanland in northern Sweden and Haukipudas in Northern Ostrobothnia in Finland. The remaining two of you, please consider specifying where Jonas Jansson (1729–1808) lived and what you know about your paternal line (it can be anything from "adopted, unknown father" to whatever you know about your father, grandfather etc.).

Magnus Bäckmark