The Värmland-Hedmark Cluster

No. 6 (December 2021)

A newsletter with updates about the genetic genealogy project "The Värmland-Hedmark Cluster." The project is run by a group of hobbyists who try to learn about the early history of their patrilineal ancestors in southern Värmland (Sweden) and in Hedmark (Norway). What can be said about the ancestors' whereabouts before they start to appear in the written records, i.e., in the 1500s and earlier? Where did the ancestors live before they arrived in Värmland and Hedmark? In technical terms, the project concerns the study of the Y chromosome haplogroup R1b → M269 → U106 → Z18 → S11601 → Y112538 → Y130179 and surrounding clades.

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The Värmland-Hedmark Cluster and a Neighboring Branch (Dec. 2021)

Confidence intervals for age estimates

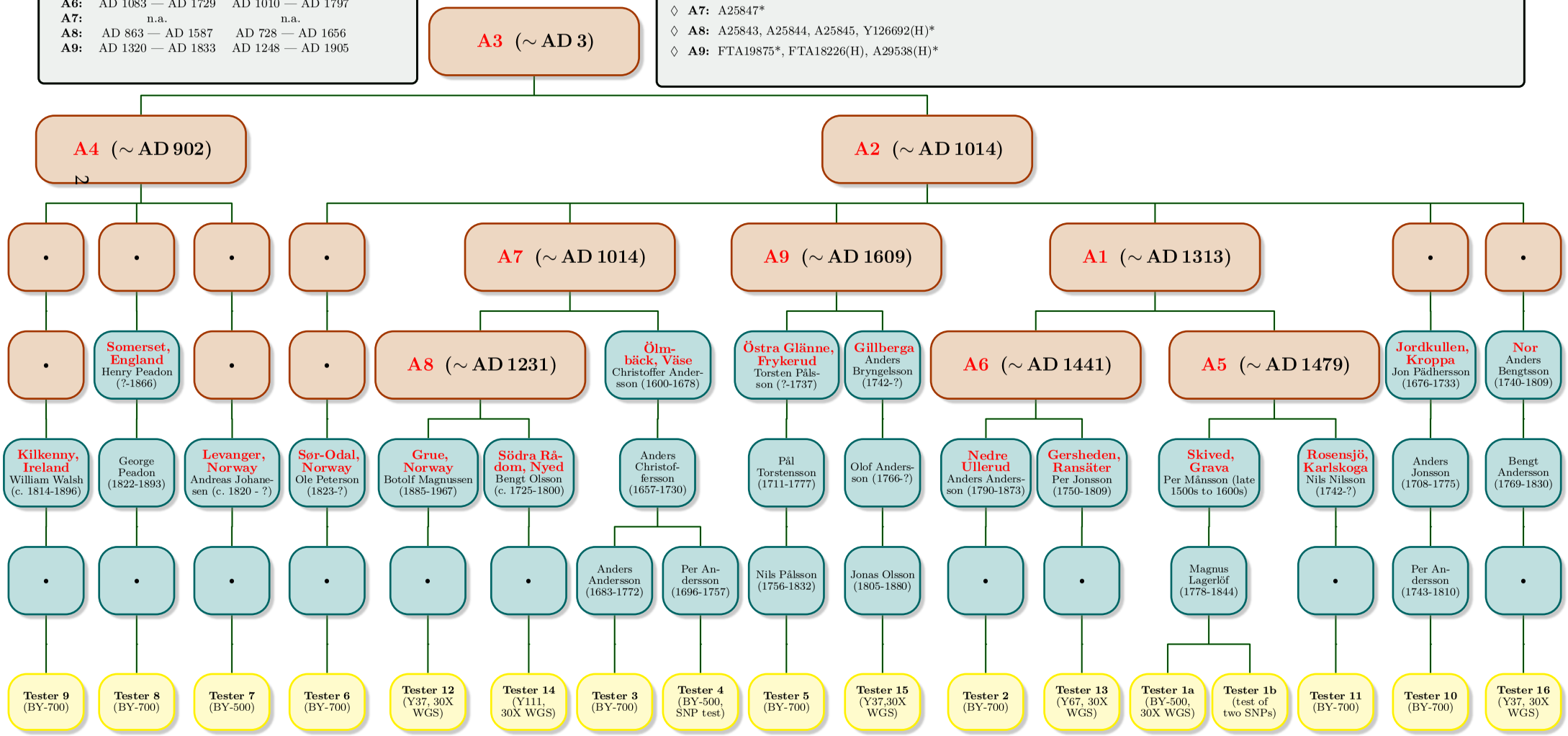
The age estimates in the tree are from my (Johan Lagerlöf's) own calculations—see No. 6 of the VHC newsletter for some discussion. The estimates are based on the number of SNPs in the combBED region, as reported by YFull (YTree v9.05.00). Below are confidence intervals at the 90% and 95% levels (some of them are not available this time due to technical problems):

	90% CI	95% CI
A1:	n.a.	n.a.
A2:	n.a.	n.a.
A3:	n.a.	n.a.
A4:	AD 517 — AD 1239	AD 421 — AD 1335
A5:	AD 1195 — AD 1738	AD 1134 — AD 1778
A6:	AD 1083 — AD 1729	AD 1010 — AD 1797
A7:	n.a.	n.a.
A8:	AD 863 — AD 1587	AD 728 — AD 1656
A9:	AD 1320 — AD 1833	AD 1248 — AD 1905

SNPs that define the branches

The Värmland-Hedmark cluster is a twig on the R1b branch of the human Y chromosome haplotree: R1b → M269 → U106 → Z18 → S11601 → Y112538 → Y130179. For more information, see www.johanlagerlof.com/gengen. The branches shown in the tree are defined by the SNPs listed below (an asterisk indicates that the SNP is located outside of the so-called combBED region of the Y chromosome, and it is therefore not used by YFull for age estimation; an "(H)" means that the SNP is located in a homologous region—i.e., one that is similar to other regions on the Y chromosome or on other chromosomes—and therefore is less reliable). The named ancestors for Tester 15 are still uncertain—we will do further DNA testing to try to have the names confirmed.

- ◊ **A1:** Y86344, Y107658*
- ◊ **A2:** Y100873*, Y128033, Y101814*, Y103246, Y130179, Y83455, Y125815*
- ◊ **A3:** Y112538, Y129064
- ◊ **A4:** BY71612, Y159325, BY116275, BY146620, BY78202, BY99722, BY100142, BY102070
- ◊ **A5:** FT146431
- ◊ **A6:** BY12164
- ◊ **A7:** A25847*
- ◊ **A8:** A25843, A25844, A25845, Y126692(H)*
- ◊ **A9:** FTA19875*, FTA18226(H), A29538(H)*



A WHILE AGO, I was looking through printed copies of the old issues of this newsletter, which I keep in a file. I was struck by how similar the covers are. They all look close to identical, except for the number of the issue and the date, which one can read in small font near the top of the page. I realized that it might be useful, and just nicer, if the different issues were more easily identifiable and distinguishable. For that reason I have now, in the present issue, put a photograph on the cover, and I let the main text begin only here on page 3 (as usual, it is convenient to put the latest version of our tree on page 2). I try this as an experiment, and if it seems to be a good idea I will continue in future issues. There are plenty of digitized photographs and other pictures available publicly and for free. The cover picture for this issue is a photograph from 1905, and it shows some people in a boat on a river in Gillberga parish, Värmland. Gillberga is the likely place of origin of Tester 15's patrilineal ancestors. One can find some further information about the photograph in the box at the bottom of this page.

This issue of the newsletter is slightly delayed (it looks as if I will be able to send it out and upload it to my website on January 1, although it is supposed to be a December issue). The reason is that I have spent a lot of time working on age estimations of the ancestors A1-A9 in our tree. Instead of sitting down around Christmas and New Year to write text for the newsletter, I used this time to produce code that is supposed to generate the age estimates and the associated confidence intervals. I have been partly successful (although unfortunately not fully...), and the new version of our tree includes age estimates and confidence intervals computed with an alternative approach, relative to YFull's. I will explain more of this later in this issue. This issue of the newsletter also discusses a new branch in our tree (this is the fifth time running that the tree has a new branch). The new branch connects Testers 5 and 15, with oldest known patrilineal ancestors in Frykerud and Gillberga parishes, respectively. Tester 15 is the one who used to have an unknown patrilineal great grandfather, with the grandfather being born in Stockholm in 1915. It appears as if we now have found the identity of the great grandfather, although it remains to carry out DNA tests to confirm this. This issue includes a short account of how we found the great grandfather and what we currently know about the tester's patrilineal ancestors. Furthermore, there is a new tester in the tree, namely Tester 16. This is the person whose WGS test at Dante Labs had a low number of reads on the Y chromosome, and one can in this issue read about how this story has developed. In the end of the issue, there is a brief account of a new technological development that has been dubbed "telomere-to-telomere," as well as some reading tips.

About the cover picture

The cover photograph is from 1905 and shows some people in a boat on river Lillälven in Gillberga parish, Värmland. The photographer is unknown. The photograph is part of the collections of Järnvägsmuseet (identifier: JvmKCAC12512; public domain mark 1.0; see also `https://digitaltmuseum.se/021018110983/batfard-pa-lillalven-vid-gillberga`).

The text written on the photograph is "Kohlsätersälfven med Bryggan", which can be translated as "the Kohlsäter river and the bridge". I presume Kohlsätersälfven is just another (perhaps older) name for Lillälven, but I am not sure and I have not looked into this.

A New Branch That Connects Frykerud and Gillberga

WE HAVE a new branch in our tree that was not present in the most recent issue of the newsletter. The new branch is represented by the ancestor A9, and it connects Testers 5 and 15. When that last issue was published in July 2021, Tester 15's BAM file had just been submitted to YFull. Also, Tester 5 had a little bit earlier (I believe in the spring of 2021) upgraded his test from a Big Y-500 to a Big Y-700. The latter test investigates a larger part of the Y-chromosome, and it therefore is better at discovering new SNPs that, if they are shared by other testers, can be used to identify new branches. I am not

sure whether the upgrade to the 700 test was critical for the formation of the new branch, but it is conceivable that it helped.

The new branch is defined by three SNPs: FTA19875, FTA18226, and A29538. The two last ones are in YFull's tree shown with the suffix (H), where H stands for homologous. This means that the SNP is located in a homologous region—i.e., one that is similar to other regions on the Y chromosome or on other chromosomes—and therefore is less reliable. The SNP FTA18226 is, however, located in the so-called combBED region of the Y chromosome, which by construction is meant to be reliable (see Adamov et al., 2015). I therefore suspect that the H added to FTA18226 is simply a typo on YFull's part (I have asked them about this but not yet received a reply). The other two SNPs, FTA19875 and A29538, are located outside the combBED region. Such SNPs are sometimes still used by YFull to build the tree, but they are not considred by YFull (nor by me in the calculations discussed in this issue) when doing age estimations of the branches. Since some time, YFull has started to show all the homologous SNPs in the tree, although with the added H.

The oldest known patrilineal ancestors of Testers 5 and 15 lived in Frykerud and Gillberga.[1] Although not sharing boarders, these parishes are located quite close to each other in southern Värmland. Moreover, Frykerud and Gillberga are the parishes that are located in the most westward direction among all the Värmland places of origin among our testers. It thus makes sense that they now have formed a branch. Still, it is true that for *all* the Värmland testers (so for all of Testers 1-5, 10-11, and 13-16), the oldest known patrilineal ancestors lived relatively close to each other. It was quite feasible for someone in the, say, 1600s to relocate from Gillberga to a place like Karlskoga or Kroppa. Yet the very close geographical proximity of Testers 5's and 15's oldest known ancestors is interesting to note. Possibly, with the help of more work and some luck, we could later in the church records find a common patrilineal ancestor to Testers 5 and 15, who indeed lived somewhere in the neighborhood of Gillberga and Frykerud.

Two Unknown Fathers Found—Probably

TESTER 15 in our project lives in Stockholm. On his own initiative, he first did a Y37 test with Family Tree DNA; later, on my initiative, he did a WGS test with Dante Labs. Tester 15's main reason for testing, as I understand it, was that he wanted to identify his unknown (patrilineal) great grandfather. His paternal grandfather was born in Stockholm in 1915 to a woman called Olga. At the time, Olga was 34 years old and unmarried. She was born in Småland in the south of Sweden, but in April 1900, at the age of 20, she moved to Norrköping (a relatively large city). In November 1901, she moved again, and this time to Stockholm. During the following years, she stayed at several different addresses in the capital. In one of the records, for the period November 1904 until 1905, it is stated that she "har kafé" (has a cafe). Later, in a record for the longer period 1912-25, it says that she is a cleaning woman. In the record for December 1909 to January 1912, she is listed together with a boy, Karl Georg, born in 1910. The family relation is indicated as child out-of-wedlock, and the boy has the same surname as Olga. In the record for 1912-25 she is listed with two boys, Karl Georg and Tester 15's grandfather, called Karl Evald.

After Tester 15 had done the Y-chromosome tests, we could conclude that he belongs to the Värmland-Hedmark cluster. This, in turn, strongly suggests that Karl Evald's unknown father had a patrilineal ancestry that goes back to Värmland or Hedmark. We realized that this information could prove useful when looking for the father, although in itself it would of course not be of much help. In the fall of 2021, I emailed a question to *Stadsarkivet* (the City Archive) in Stockholm about Karl Evald and whether their records said anything about the unknown father's identity. I received a reply that was very helpful. To understand what the reply said, we should first note that, by a Swedish law that was introduced in 1918 (see an account of this in Reuterswärd, 2016, pp. 54-56), every woman who was unmarried and had a child must have a *barnavårdsman* (literally: childcare man) appointed for this child; the woman

[1] The claim that also Tester's 15 oldest known ancestor is indeed *known* is subject to some caveats, which are discussed in the next section.

could not refuse. It was the task of the *barnavårdsman* to try to find out who the child's father was. Tester 15's grandfather, Karl Evald, was born before the law was introduced. However, the law also stated that if the child was not yet 16 years old, the mother had the right to, retroactively, receive support from the *barnavårdsman* (so, in this situation, involvement of the *barnavårdsman* was voluntary on the part of the mother).

The reply that I received from *Stadsarkivet* said that, indeed, a *barnavårdsman* for Karl Evald had been appointed, and there were documents associated to this case in the archive. The fact that such a case had been opened for a child born already in 1915 indicates that Olga herself wanted the authorities to be involved. The documents from the *barnavårdsman*'s investigation show that a man called Karl Edvard Jonasson had been named as the father (presumably by the mother, Olga). The alleged father had, however, not acknowledged paternity, and the case had been closed in 1923. The documents also showed Jonasson's address (Fridhemsgatan 5), which makes it possible to unambiguously identify him in the church records. Jonasson was born in 1863 (thus being Olga's senior with about 16 years); moreover, he was married and had a daughter born in 1998. Importantly, the church records also indicated that Jonasson was himself born in Tveta parish in Värmland.

We thus know a couple of things that, in my eyes, strongly suggest that Karl Edvard Jonasson is Karl Evald's father:

- It appears as if the mother, Olga, named Karl Edvard Jonasson as the father of the child. This is the likely reason why Karl Edvard Jonasson's name appears in the investigation of the *barnavårdsman*. Also the fact that the child was given a name (Karl Evald) that is very similar the alleged father's name (Karl Edvard) suggests that Olga believed, or knew, that Karl Edvard Jonasson was the father.[2]
- The named father, Karl Edvard Jonasson, turns out to have been born in Värmland, which we—now many years later, thanks to Y-DNA tests—know is the likely place of origin for the unknown father's paternal ancestry.

Based on the above, I consider it being very likely that Karl Edvard Jonasson is the father. However, I intend to carry out one or more DNA tests to have this confirmed (see below).

After having reached the conclusion summarized above, I followed Karl Edvard Jonasson's patriline back in time. Annoyingly and frustratingly, however, I soon bumped into another unknown father. The father of Karl Edvard Jonasson was born in Gillberga parish in 1833 to an unmarried woman (Stina Ersdotter), with the father apparently being unknown. Fortunately, though, in one place in the church records, the name of the father (Jonas Olsson, b. 1805) is indicated. It seems likely that this alleged father is the right one, but—just like with the name of Karl Evald's father, discussed above—it could be the wrong name. I will therefore try to confirm the two hypotheses about paternity along Tester 15's patriline with the help of DNA tests. I have managed to find a patrilineal descendant of Jonas Olsson's brother (Anders Olsson, b. 1802). By testing a small number of key SNPs on the Y chromosome of this descendant, we can—in a simple and cheap way—test both hypotheses in one go. If both our hypotheses are true, and if we choose the SNPs cleverly, the test will be very hard to pass for some arbitrary person on the street. Still, perhaps depending on the outcome of that test, I might choose to do some further tests, to be absolutely sure (e.g., there are now-living grandchildren of Karl Evald's half-sister—we would expect them to match with Tester 15 if we let them take autosomal tests).

A New Tester in Our Tree

IN THE NEW version of our tree, there is a new tester included, namely Tester 16, whose oldest known patrilineal ancestor came from Nor parish in Värmland. This is the tester who had a problematic 30X WGS test at the Italian company Dante Labs, which was resequenced after the first sequencing round gave us a very low number of reads on the Y chromosome. The case was problematic, because also the

[2]However, Olga's first son, born five years earlier, also was called Karl (as one of his names). I have not yet looked for the father of this boy.

resequencing gave us a very low number of reads on the Y chromosome. I wrote about this tester in the previous issue of the newsletter (see the July 2021 issue, pp. 7-8).

I thought for quite a while about what to do. In the end, I decided to try with one of the ideas that I mentioned in my discussion in the July 2021 issue. I asked the German company YSEQ to merge the two files that I had received from Dante Labs—the one from the original sequencing round, and the one from the resequencing. The combined BAM file that I received was very large (about 63 GB). Moreover, the number of reads on all of the chromosomes except for Y was exceptionally high. The number of reads on the Y chromosome was not great, but still better than for the two original files individually. I submitted this merged BAM file to YFull, hoping that the number of reads would be high enough for the company to be able to put the sample in YFull's tree. It seems to have worked at least reasonably well. The test is now there in the YFull tree (the YFull ID is YF93936). According to YFull, the average depth coverage on the Y chromosome is 7, and the median depth coverage is 5. The sample has not yet been included in YFull's age estimations—we will have to wait until the next one, which is likely to appear in early January 2022—but I have myself, manually with the help of YFull's information, counted to three private SNPs in the combBED region for Tester 16.

Overall, this tester appears to have unusually many private SNPs—also such SNPs of lower read quality and outside of the combBED region. I therefore wonder if there might be some issue with this tester's Y chromosome, either with the sample (contamination from a female sample, in spite of our checks to spot this?) or with the Y chromosome itself. If there is any such issue, I should maybe take back some of my harsh words directed at Dante Labs in the previous issue. I honestly still do not know what has happened and how we can understand the low number of Y chromosome reads for this tester. Perhaps we can learn more about that in the future. In any case, I am very happen that we now have the tester, representing the Nor lineage, in the tree.

At the moment there are no tests in the pipeline. However, I still have two 30X WGS test kits at home, which I would like to use to test likely members of the Värmland-Hedmark cluster. During the fall I made some attempts to recruit testers, although I have not yet been successful. I hope that I will be able to use the test kits in some good way and reasonably soon.

Age Estimations

FOR SEVERAL years, I have been talking about doing my own age estimations of the branches in our tree, and I had the intention of presenting estimates already in the previous issue. Indeed, I worked hard with my calculations in July last summer but then bumped into practical problems, which meant that I had to give up on that occasion. During the early part of the fall, and now again in the preceding week, I have tried to make progress with my age estimations. I am happy to say that I eventually have something to report. However, I had to compromise in two ways: (i) the estimator that I am using is not my preferred estimator, although it has some advantages, I believe, relative to the one that YFull is using; (ii) I failed to obtain confidence intervals for some of the branches (the problem I faced concerned the programming, not the statistics or the mathematics). Still, by being able to present these age estimates now, I think I have made at least some progress. I hope to get time in the future to take some further steps forward.

I will not here and now explain in detail what my methodology is. Instead, my message to the rest of the world (if it cares) is that I am working on the problem of finding good age estimates of the branches in a haplotree. At some point in the future, I will report more fully, as what I am doing now is just work in progress. Below I will briefly show my results and discuss them.

My estimations, as opposed to those at YFull, do not assume that the testers all are of the same age. For those members in the project for whom I know the age, I have used that age in the calculations, instead of the convention that any tester's age is 60. More important, though, is that the approach (since it permits different ages) has allowed my to treat two known ancestors in the tree—namely Anders Christoffersson, born in 1657, and Magnus Lagerlöf, born in 1778—as effective testers in the age estimations. (Thus, I have not had to use Testers 1a, 1b, 3, 4, or 11—at least not directly.) This means

	Point Est.	Median	90% CI	95% CI	99% CI
A1:	AD 1313	n.a.	n.a.	n.a.	n.a.
A2:	AD 1014	n.a.	n.a.	n.a.	n.a.
A3:	AD 3	n.a.	n.a.	n.a.	n.a.
A4:	AD 902	AD 902	AD 517 — AD 1239	AD 421 — AD 1335	AD 276 — AD 1431
A5:	AD 1479	AD 1502	AD 1195 — AD 1738	AD 1134 — AD 1778	AD 991 — AD 1778
A6:	AD 1441	AD 1438	AD 1083 — AD 1729	AD 1010 — AD 1797	AD 863 — AD 1858
A7:	AD 1014	n.a.	n.a.	n.a.	n.a.
A8:	AD 1231	AD 1231	AD 863 — AD 1587	AD 728 — AD 1656	AD 580 — AD 1738
A9:	AD 1609	AD 1609	AD 1320 — AD 1833	AD 1248 — AD 1905	AD 1106 — AD 1961

Table 1: Age estimates of the birth years of ancestors A1-A9 in the tree shown on page 2. The left-most column shows the point estimates. The next column shows the median value of the estimator's distribution. The three remaining columns show confidence intervals at different levels. The confidence intervals and the median are obtained with the help of simulations (100,000 runs). All estimations and simulations have been carried out with the software R.

that we can avoid estimating the time that has elapsed between the birth of, say, Anders Christoffersson and today. To do that is unnecessary as we already know how long time that is (from the church records, which we trust). Moreover, to estimate that time would be a waste of scarce information coming from the observed number of SNPs. Another difference between the age estimations presented here and those at YFull is that the confidence intervals here are obtained with the help of simulations, and thus they do not require any Normality assumption (which would be questionable, given the small samples).

The point estimates for the birth years of the ancestors A1-A9 are shown in the tree on page 2, as well as in the left-most column of Table 1. The next column shows the median of the estimator's distribution. In most cases, but not all, the median coincides with the point estimate, which is consistent with a symmetric distribution. The remaining columns show confidence intervals at different levels. One can note that they are fairly broad, and they do not shrink substantially by considering the confidence level at the 90%-level.

Telomere-To-Telomere

On June 26, 2000, at a White House event with Bill Clinton and Tony Blair, the sequencing of the DNA in human cells was famously announced. However, this was only a rough draft of the human genome, and the sequencing had many gaps. Only recently, a reasonably complete sequencing has been achieved by members of the so-called Telomere-To-Telomere (T2T) consortium[3] ("telomere" is the name of the end parts of a chromosome). A recent publication was given the title "The Complete Sequence of a Human Genome" (Nurk et al., 2021),[4] although the sequence actually did not include the Y chromosome (which we in the VHC project obviously care about). Even more recently, also the Y chromosome has been sequenced "telemore-to-telemore".[5]

These very recent technological developments have been quickly picked up by some people in the haplogroup research community. Since December 29, 2021, the German company YSEQ offers a service that remaps raw data files from a WGS test to the new T2T reference genome (to find it, search for "CP086569.1" on this page: `https://www.yseq.net/`). This is the same kind of service that I have been using a number of times to have WGS data realigned to the Hg38 reference genome, as Dante Labs supplies files aligned to Hg19, which is not as good as Hg38 for genetic genealogy purposes. Both the service that I have been using and the new T2T service have a quite modest fee of $25.

[3]See `https://sites.google.com/ucsc.edu/t2tworkinggroup`.

[4]See also the blog post here: `https://terra.bio/calling-variants-from-telomere-to-telomere-with-the-new-t2t-chm13-genome-refere?fbclid=IwAR0HDH2E2tpb5JJAgryuNRyCjkyH6zsP7pMwhzg7dW8lTQ5jfgKQMfkV-K0`.

[5]I cannot find a publication with this result, but here is the relevant NCBI data page: `https://www.ncbi.nlm.nih.gov/assembly/GCA_020881995.1/`.

The potential gain from having the files remapped to the T2T reference genome would be that it might help us discover new SNPs that can be used to create new branches in the haplotree and thereby facilitate inferences about migration paths and answer related questions. However, the service is unlikely to be useful for us in the VHC projekt, at this early stage, as we belong to the R1b branch of the haplotree. YSEQ recommends the new service primarily to people who belong to haplogroup J and especially J1. Even for such people, the service should be thought of as being on an experimental stage. Still, it is very exciting to observe these developments, and they give us a hint of what we might hope for in a not very distant future. Also people in the Y-DNA Warehouse project and at the International Society of Genetic Genealogy follow this development and have created designated T2T web pages (see here: `https://ydna-warehouse.org/t2t-experiments`; and here: `https://isogg.org/wiki/FTT_SNP_index`).

Some Reading Tips

LET ME finish this issue of the newsletter with a few reading tips—about a relaunched genetic genealogy journal, recovering DNA from century-old stamps, and reconstructing the migration routes of Polynesian boat travelers.

The Relaunched Journal of Genetic Genealogy

The Journal of Genetic Genealogy was founded in 2005, although it has been dormant in the last few years (the penultimate issue came out in 2016, and the one before that was published in 2011). Yet very recently, now in December 2021, the journal was relaunched and a brand new issue was published. All the articles are available online for free. The journal's home page can be found here: `https://jogg.info/`. From that home page, one can download the articles as pdf files (either each article individually or, by clicking the picture of the journal's cover, the whole issue).

The journal has a new editor—David Vance, who also is the author of a book on Y-DNA testing, Vance (2020), that I have discussed in a previous issue and which I strongly recommend (see the July 2020 issue, p. 9, of the newsletter). I think it is a very good news that the journal has been relaunched. I particularly welcome the fact that the articles will be freely available, which should help prospective authors to spread their results and ideas. I do not expect that the journal will be peer reviewed in the sense that good academic journals are peer reviewed. Still, however, the journal will hopefully prove useful both for authors who look four suitable outlets and for readers interested in learning about genetic genealogy.

Recovering DNA from Old Postcard Stamps and Solving a Family Mystery

I enjoyed reading a recent paper published in the journal Forensic Science International, titled "19th Century Family Saga Re-Told by DNA Recovered from Postcard Stamps " (Haas et al., 2021). Here is the abstract of the article:

> Old postcards with stamps might help unravelling historical family stories and relationships. By employing ancient DNA recovered from world war I postage stamps, we disprove a family saga of an illegitimate child born in 1887. We developed a protocol to collect DNA from saliva, trapped and protected on the backside of postage stamps glued on postcards. With replicate STR analyses we were able to assemble almost full autosomal and Y-STR profiles of three male, deceased family members. The illegitimate child turned out to be a legitimate child of a later married couple.

At least to some extent, the technology required to extract DNA from old human samples like hair, envelopes and stamps gradually start to become available also in the direct-to-consumer DNA testing market. However, it appears as if it is still difficult to get good and and useful results, and the costs are high. There are at least two companies in the world that offer this kind service, TotheletterDNA based in Australia (`https://www.totheletterdna.com/`) and the American company KeepsakeDNA (`https://www.keepsakedna.com/`).

Another recent paper that I liked was published in Nature and titled "Paths and Timings of the Peopling of Polynesia Inferred from Genomic Networks " (Ioannidis, 2021). Here is the abstract of the article:

> Polynesia was settled in a series of extraordinary voyages across an ocean spanning one third of the Earth, but the sequences of islands settled remain unknown and their timings disputed. Currently, several centuries separate the dates suggested by different archaeological surveys. Here, using genome-wide data from merely 430 modern individuals from 21 key Pacific island populations and novel ancestry-specific computational analyses, we unravel the detailed genetic history of this vast, dispersed island network. Our reconstruction of the branching Polynesian migration sequence reveals a serial founder expansion, characterized by directional loss of variants, that originated in Samoa and spread first through the Cook Islands (Rarotonga), then to the Society (Totaiete ma) Islands (11th century), the western Austral (Tuhaa Pae) Islands and Tuamotu Archipelago (12th century), and finally to the widely separated, but genetically connected, megalithic statue-building cultures of the Marquesas (Te Henua Enana) Islands in the north, Raivavae in the south, and Easter Island (Rapa Nui), the easternmost of the Polynesian islands, settled in approximately AD 1200 via Mangareva.

It was written quite extensively about this article also in the popular press, and one easily find these texts by googling.

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Svensk sammanfattning

Värmland-Hedmark-klustret är benämningen på en – vad det verkar – väldigt stor släkt som levde i Värmland och Hedmark under medeltiden och kanske även ännu längre tillbaka i tiden. Idag är det många människor, inte minst i Värmland, som härstammar från denna släkt på sitt raka fäderne – och ännu fler, förstås, längs andra linjer. En av Värmland-Hedmark-klustrets många grenar leder till exempel till den värmländska släkten Lagerlöf (som författaren till de här raderna råkar tillhöra).

Dessa saker har vi upptäckt med hjälp av DNA-test av nu levande personer. Framförallt har vi varit behjälpta av test av Y-kromosomen, som bara män har och som ärvs från far till son. Arbetet är i full gång med att samla mer kunskap om Värmland-Hedmark-klustret. Det här nyhetsbrevet utkommer med jämna mellanrum (hittills har det blivit i juli och december varje år), och det rapporterar och diskuterar vad som har hänt inom projektet sedan sist.

Exempel på frågor som vi försöker förstå: Hur stor var den här släkten? Var i Värmland och Hedmark fanns den? Hur långt tillbaka i tiden har medlemmar i släkten funnits i Värmland och/eller Hedmark? Varifrån kom släktmedlemmarna när de anlände dit? Kan resultaten hjälpa oss att förstå frågor kring social mobilitet?

- ✔ Återigen har Värmland-Hedmarks-klustret fått en ny gren, jämfört med det föregående numret av nyhetsbrevet. Den nya grenen kopplar ihop testare med äldsta kända patrilinjära anor från Frykerud och Gillberga. Man kan se den senaste versionen av trädet på sidan 2 i nyhetsbrevet. Anfadern som bildar en ny gren har där fått beteckningen A9. Punktskattningen för hans födelse är början av 1600-talet, men ett 95%-igt konfidensintervall går tillbaka ända till 1200-talet (så stor osäkerhet med andra ord).
- ✔ Den testare med anor i Gillberga som nu har bildat en ny gren (se ovan) har haft en okänd farfars far. Vi tror att vi nu har lyckats identifiera den personen (och det är skälet till att jag vågar säga att anorna kommer från just Gillberga). Vi kan dock inte vara säkra ännu, och en del ytterligare DNA-test återstår att göra.
- ✔ Vi har ytterligare en ny testperson i trädet (Tester 16), som även han har visat sig tillhöra Värmland-Hedmark-klustret. Testpersonens äldsta kända patrilinjära ana levde i Nors socken i Värmland.
- ✔ Jag har arbetat med mina egna åldersuppskattningar, och jag kan äntligen presentera en del resultat. Skälet till att jag vill göra egna åldersuppskattningar är att jag i alla avseenden inte är riktigt nöjd med det sätt som YFull gör dem på. (Man kan göra den statistiska analysen bättre, menar jag. Det är också önskvärt att inkorporera våra genealogiska data i estimationen. Dessutom skulle jag vilja utföra formella statistiska test av olika hypoteser som vi formulerar, och detta är inte möjligt enbart genom att använda YFulls analys.)
- ✔ Genetiker har på sistone gjort framsteg med att kartlägga (sekvensera) delar av det mänskliga genomet som tidigare inte har varit kartlagda. Dessa framsteg har utnyttjats av några haplogruppsforskare, för att försöka undersöka om det går att göra haploträden mer detaljerade (med hjälp av nya SNP:er som kan upptäckas med hjälp av den nya tekniken). Det är i praktiken inte aktuellt för personer som tillhör vår haplogrupp (R1b) att använda dessa metoder, men det är en intressant och potentiellt viktig utveckling att följa.
- ✔ Det här numret av nyhetsbrevet innehåller också några lästips.