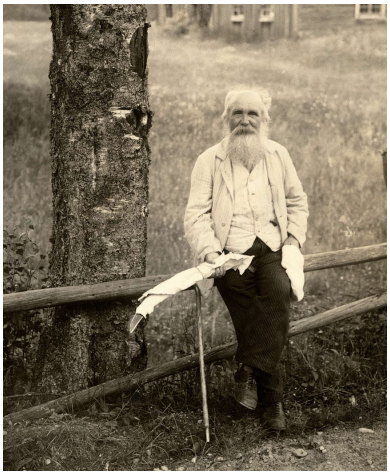
December 2023, No. 10

☆ The Värmland-Hedmark Cluster ☆

About the VHC Newsletter



The VHC newsletter is published twice a year, in July and December. It provides updates on a genetic-genealogy project that carries the same name, "The Värmland-Hedmark Cluster" (or VHC for short). This 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). Among the questions that we ask are: What can be said about the ancestors' whereabouts before they start to appear in the written records (so 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 following Y-DNA haplogroup (and some of its surrounding branches):

> R1b → M269 → U106 → Z18 → S11601 → Y112538 → Y130179.

The newsletter is written by Johan N.M. Lagerlöf (email address in the page footer). This issue and all the previous ones are downloadable at www.johanlagerlof.com/gengen. Thoughts and opinions about the content of the newsletters are very welcome. A good forum for discussion is the weblog called "The VHC Blog," available at www.johanlagerlof.com/the-vhc-blog.

The newsletter is written in LaTeX. The layout is borrowed from www.overleaf.com, which cites howtotex.com (a now discontinued website), September 2011, as its source.

En svensk sammanfattning av det viktigaste i nyhetsbrevet finns på sista sidan.

Contents

The Värmland-Hedmark Cluster and a Neighboring Branch (Dec. 2023)

Confidence intervals for age estimates

The age estimates for A1-A9 in the tree are from YFull (YTree v11.05.00), and those for A3 and A10-A11 are from FTDNA (Jan 1, 2024); thus, for A3, age estimates from both companies are provided. Unless otherwise indicated, all years shown are A.D. Below are confidence intervals at the 95% level:

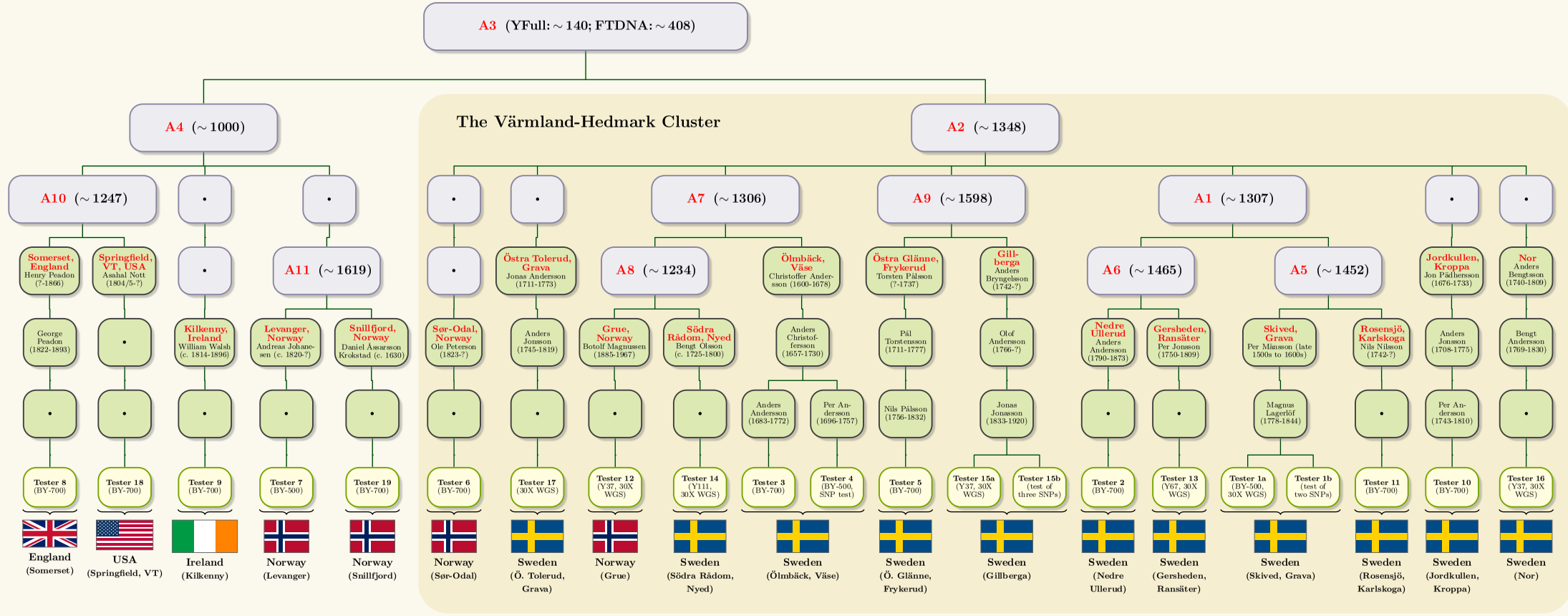
	95% CI
◊ **A1:**	923 — 1623
◊ **A2:**	1173 — 1523
◊ **A3:**	477 B.C. — 673 (YFull) 73 B.C. — 790 (FTDNA)
◊ **A4:**	323 — 1273
◊ **A5:**	923 — 1748
◊ **A6:**	923 — 1773
◊ **A7:**	1173 — 1523
◊ **A8:**	1173 — 1523
◊ **A9:**	1123 — 1848
◊ **A10:**	762 — 1581
◊ **A11:**	1285 — 1833

SNPs that define the branches

The Värmland-Hedmark Cluster is a twig on the R1b branch of the human Y-DNA 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.[a]

	Defining SNPs
◊ **A1:**	Y86344, Y107658*
◊ **A2:**	Y100873*, Y128033, Y101814*, Y103246, Y130179, Y83455, Y125815*
◊ **A3:**	Y112538
◊ **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)*
◊ **A10:**	FT5016, FT5166, FT5167, FT5193, FT5729
◊ **A11:**	BY106437, BY112147, BY134583

[a] 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.



Tester	YFull ID	Oldest known patrilineal ancestor	Type of test	# of private SNPs
1a	YF71553 (=YF10028)	Per Månsson (late 1500s to 1600s). Skived, Grava parish, Värmland	Big Y-500, DL 30X WGS	n.a.
1b	n.a.	Same as Tester 1a	3 SNPs at YSEQ	n.a.
2	YF65575 (=YF11441)	Anders Andersson (1790–1873), Nedre Ullerud parish, Värmland	Big Y-500, Big Y-700	2
3	YF70514 (=YF13065)	Christoffer Andersson (1600–1678), Ölmbäck, Väse parish, Värmland	Big Y-500, Big Y-700	n.a.
4	YF13845	Same as Tester 3	Big Y-500, 2 SNPs at YSEQ	n.a.
5	YF83719 (=YF14610)	Torsten Pålsson (?–1737), Östra Glänne, Frykerud parish, Värmland	Big Y-500, Big Y-700	2
6	YF072349 (=YF014751)	Ole Peterson (1823–?), Sør-Odal, Norway	Big Y-500, Big Y-700	4
7	YF15653	Andreas Johannesen (c. 1820–?), Levanger, Norway	Big Y-500	4
8	YF70654	Henry Peadon (?–1866), Somerset, England	Big Y-700	11
9	YF85325 (=YF10028)	William Walsh (c. 1814–1896), Kilkenny Ireland	Big Y-700	7
10	YF64392	Jon Pädhersson (1676–1733), Jordkullen, Kroppa parish, Värmland	Big Y-700	3
11	YF66826 (=YF11441)	Nils Nilsson (1742–?), Rosensjö, Karlskoga parish, Värmland	Big Y-700	5
12	YF75623	Botolf Magnussen (1885–1967), Grue, Norway	DL 30X WGS	6
13	YF74441	Per Jonsson (1750–1809), Gersheden, Ransäter parish,Värmland	DL 30X WGS	4.86
14	YF80309	Bengt Olsson (c. 1725–1800), Södra Rådom, Nyed parish, Värmland	DL 30X WGS	4
15a	YF87292	Anders Bryngelsson (1742–?), Gillberga parish, Värmland	DL 30X WGS	3
15b	n.a.	Same as Tester 15a	3 SNPs at YSEQ	n.a.
16	YF93936	Anders Bengtsson (1740–1809), Nor parish, Värmland	DL 30X WGS	1
17	not subm.	Jonas Andersson (1711–1773), Östra Tolerud, Grava parish, Värmland	DL 30X WGS	3
18	not subm.	Asahal Nott (b. 1804/5), Springfield, Vermont, USA	Big Y-700	not known
19	not subm.	Daniel Åssarsson Krokstad (c. 1630), Snillfjord STR, Norway	Big Y-700	not known

Table 1: Information about the testers in the project. The numbers in the first column refer to the numbering of testers in the tree on page 2. The indicated number of private SNPs in the last column is the count according to YFull and it refers to the combBED region (although for Tester 17, this piece of information comes from YSEQ). The reason why Tester 13's SNP count is not an integer is, I believe, that YFull uses a particular weight when it is unsure about whether to include a SNP or not. I use this number for the time being, and I hope to be able to investigate this issue more carefully some time in the future.

HURRAH, HURRAH, hurrah! This is a Jubilee Number of the VHC Newsletter—Issue No. 10, in fact.

The very first issue of the newsletter was published four and a half years ago, in July 2019. I then thought of it as an experiment. My hope was that a newsletter—uploaded to my website and sent out as an email attachment—would be a convenient way of updating the project members about developments and new results, relative to writing a group email (which I had done for some time before that).

I think the experiment has worked out reasonably well. The newsletter helps me keep in touch with the project members, and the fact that I "have" to write it ensures that I continuously document events in the project. The newsletter format is not, however, ideal for all kinds of purposes. As a complement to the newsletter, I would like to like to get time to write a short essay that introduces beginners to the questions we ask in the project and what we think we have learned so far. Hopefully I can do that in a not too distant future.

The Jubilee Issue is fairly short—partly because I had too many other things to do this time, partly because there are not that many new developments to report on. Section 1, as usual, provides information about the cover picture. Section 2 explains what has changed in our part of the haplotree, relative to last time. There are not that many changes—the single one being that the so-called Gillberga branch has a new tester (Tester 15b), who helps us confirm that the way we thought the patriline of that branch looks like is indeed correct.

Section 3 discusses a very promising new feature of the autosomal test sold by the American company Family Tree DNA. The new feature, which is available to male testers only, consists of information about the tester's Y-DNA haplogroup—at a level that is fairly crude but still precise enough to be of great use when we look for new branches of the Värmland-Hedmark Cluster.

1 The Cover: An Old Man in Lekvattnet

THE PHOTOGRAPH on page 1 is part of the collections of *Nordiska Muséets arkiv* (i.e., the archive of the "Nordic Museum"). At its website, the museum describes itself as follows:[1] "Nordiska museet is Sweden's largest museum of cultural history and stories about the life and people of the Nordic region. It is home to over one and a half million objects." I found the photograph at the website digitaltmuseum.se.[2]

The photograph is, according to the information from Nordiska Muséet, from 1927, and the name of the photographer is C.G. Rosenberg. The same source states that the photograph shows "An old man leaning against a fence" and that the place is Lekvattnet. Lekvattnet is a village in the northern part of Värmland. In our project, we have so far no testers with patrilineal ancestors from that area—if they are not from Hedmark i Norway, all patrilineral ancestors of the VHC testers are from a parish in the south (or south-east) of Värmland. Thus, it seems unlikely that the unknown man pictured in the photograph was a member of our cluster. Still, it is a nice picture that, I think, makes a good cover.

2 The Latest Version of the VHC Tree

AS USUAL, the most recent version of the VHC haplotree can be found on page 2. This time there is only one (substantial) change in the tree. This is the addition of Tester 15b (and Tester 15 has, as a consequence, been relabeled Tester 15a).

Tester 15b is a man who lives in Stockholm, Sweden. He has earlier, at my request, taken an autosomal test at Family Tree DNA, with the purpose of helping us identify Tester 15a's paternal great grandfather. This is an unknown-father investigation that I have been working on for some time (an essay in which I will document the findings is in progress), and by now I feel quite confident that we know who Tester 15a's paternal great grandfather is.

If we indeed assume that this family connection is correct, Tester 15a's grandfather's grandfather (along the direct male line) is identical to Tester 15b's grandfather's father (again along the direct male line). The name of this man was Jonas Jonasson (1833-1920); he was born in Gillberga parish in Värmland and later moved to the nearby parish Tveta. His name is shown in the tree on page 2. As also indicated there, we believe we know the patrilineal ancestors of Jonas Jonasson a few generations back in time. The oldest one we can track is Anders Bryngelsson, who was born in 1742 and lived, as several of his descendants, in Gillberga.

In addition to letting Tester 15b do an autosomal test, I wanted to let him test a few selected SNPs on the Y chromosome, all of which I knew that Tester 15a is positive for. In September I ordered, on Tester

[1] See https://www.nordiskamuseet.se/en/about-us/.
[2] Specifically this page: https://digitaltmuseum.se/011013841556/en-gammal-man-lutad-mot-ett-staket-lekvattnet-varmland.

15b's behalf, a test of four SNPs at the German DNA-testing company YSEQ (this company is to some extent specialized in Y-DNA testing, although they also sell WGS tests and tests of one's mitochondrial DNA).

The four SNPs that I chose are all so-called novel SNPs for Tester 15a; that is, so far (among all tested male individuals on the planet) only Tester 15a has tested positive for these SNPs, and they have therefore not yet given rise to a branch in the Y-DNA haplotree. Even if Testers 15a and 15b share a common patrilineal ancestor in Jonas Jonasson, as we believe is the case, it could happen that Tester 15b is negative for all four of the chosen SNPs (if so, this would be because they have arisen *after* Jonas Jonasson and somewhere along Tester 15a's line). I thus took a small gamble when selecting only these SNPs (given that one of my objectives was to obtain further confirmation that the family connection was as we believed it to be).

We have so far received results from YSEQ for three of the four SNPs. The results show that Tester 15b is positive for *one* of these SNPs (my gamble paid off!); the name of this SNP is A29539. We can conclude two things: (i) we now have further evidence that we have found the right unknown father and (ii) the two testers' youngest common patrilineal ancestor Jonas Jonasson must have been positive for the SNP A29539.

The results also show that Tester 15b is negative for *two* of the SNPs (the names of these SNPs are A29536 and A29537). That is, these two SNPs must have arisen after Jonas Jonasson and somewhere along Tester 15a's line. As mentioned, we do not yet have any results for the fourth SNP (the name of this one is A29535).

In December, we almost accidentally received further confirmation that Testers 15a and 15b belong to the same patriline (and that their lineages intersect quite recently). As mentioned above, Tester 15b has taken an autosomal test at Family Tree DNA. This company has recently launched a new feature associated with that test, which involves providing relatively crude information about the Y-DNA haplogroup of any male who takes the test. The information we received said that Tester 15b is positive for the SNP ZP30, which is located upstream of the Värmland-Hedmark Cluster in the tree, although still fairly close to it. This information thus amounts to yet more evidence in favor of the proposition that Testers 15a and 15b belong to the same patriline (and that their lineages intersect quite recently).

The next section explains more about the new feature of Family Tree DNA's autosomal test.

3 Autosomal Tests and Y-DNA Haplogroups

The American DNA-testing company Family Tree DNA (FTDNA) is, for readers of this newsletter, perhaps best known for selling the tests called Big Y-700, Y37, and Y111—all of which investigate the test person's Y chromosome. While the two latter tests look at a selection of so-called STR markers (37 and 111 of them, respectively), the Big Y-700 test *in addition* investigates whether the tester is positive or negative for a very large number of so-called SNPs located on the Y chromosome. (Readers who would like to be reminded about what we mean by STRs and SNPs, please have a look at the box on the next page.)[3]

The Y-chromosome haplotree is constructed on the basis of such SNPs, and therefore we need tests that look also for these kinds of markers to be able to learn more about the tree and its branches. Indeed, results from such tests are required to be able to expand the tree and thus learn more about migration paths and how the testers are connected to each other.

In the early days of genetic genealogy, tests that look only for STR markers were the only ones available to purchase. Although these tests cannot tell us, for sure, whether a tester is positive or negative for a particular SNP, the tester's STR results are fairly highly correlated with his SNP results. Therefore, an STR test can be used to *predict* where in the haplotree the tester *probably* belongs (i.e., which Y-chromosome SNPs that the tester is likely to be positive/negative for). In addition, a person who purchases one of FTDNA's STR tests gets access to a list of matches—that is, a list of other testers with similar STR results.

These lists have been very useful for us in the VHC project, as they have helped us identify individuals who are likely to belong to our part of the tree, although they have not yet taken a Big Y-700 or some other test that investigates SNPs—like a whole genome sequencing (WGS) test, which is sold by several other companies. If also the geography of the match's oldest known patrilineal ancestor is in line with what we expect (meaning, typically, that this ancestor lived in Värmland), then we have felt confident enough to be willing to pay for a more ambitious test for this person (in one or two cases a Big Y-700, but typically a WGS test as these are less expensive). Many of the branches in the Värmland-Hedmark Cluster, as shown in the tree on page

[3] I used an almost identical box in No. 5 of the newsletter.

2, have been created in this way.

In the last few years, however, the number of new STR matches in our project has dropped dramatically. Indeed, the most recent STR match arrived on April 2020, which is almost four years ago (see the discussion in No. 8, Section 3, of the VHC Newsletter). In light of that sad development, it is particularly gratifying to learn that FTDNA recently has started to launch a new feature associated with the company's autosomal test (i.e, the test that the company calls called Family Finder).

An *autosomal test* is a test that investigates SNPs on the 22 pair of chromosomes that are *not* sex chromosomes (although some such tests, like FTDNA's, also include the X chromosome). Autosomal tests for genealogy purposes are sold by about half a dozen large companies. Apart from FTDNA, these include Ancestry, 23andMe, My Heritage, and Living DNA.

About STR markers and SNPs

Our DNA consists of a long series of "letters" A, C, G, and T (to call them letters is a simplification but is good enough now for our genealogy purposes). A segment of our DNA (say, on the Y chromosome) may thus look like this:

AGCCTACAGGCAGGCAGGCAGGCTGGACAGTACTGA

A SNP (single-nucleotide polymorphism), pronounced "snip," is simply a change of one of these letters to another letter. For example, the first letter above, an A, may change to a T.

What is an STR (short tandem repeats) marker? Study the series of letters above. If you look carefully, you will see that the combination of letters AGGC is repeated four times in the middle of the series (below the same sequence is shown again, but with the four appearances of AGGC being highlighted):

AGCCTACAGGCAGGCAGGCAGGCTGGACAGTACTGA

An STR marker is the number of such repeats (so, in the example, the value of the STR marker is 4). The reason why a certain combination of letters is repeated several times is that there was a DNA copying error. It would have sufficed if Mother Nature had included the combination once, but by mistake it was added a few additional times (without affecting anything biologically with the body, as far as I understand).

The value of an STR marker tends to change quite often. Sometimes the number of repeats goes up and sometimes it goes down. A SNP, in contrast, is much more likely to stay put, once it has occurred. For example, at the conception of some patrilineal ancestor of the individuals in the tree on page 2, the SNP Z18 occurred (this is a change from a G to a A at position $\#12,879,820$ on the Y chromosome, if we use the Hg38 reference genome). This happened about 3000 or 4000 years ago, and the SNP has not reverted in any of the generations after that ancestor. As the SNPs are more stable and reliable, they are used for building the tree. The STR markers have historically been easier and less expensive to test, which is one reason why they have been used a lot over the years in forensic science, genealogy, and other fields. They are also useful for us in the project, partly because they help us identify people who are likely to belong to the Värmland-Hedmark Cluster. Yet, to confirm this and to be able to put these individuals in the tree, a fairly advanced SNP test is needed (e.g., a Big Y-700 or a 30X WGS test).

The autosomal tests investigate a very large selection of SNPs (typically around 700,000-800,000; see Rae-Venter (2023, p. 252)). These SNPs have almost exclusively been chosen for genealogy purposes, although some of the companies have in addition included a small number of key SNPs that can help answer medical questions. Furthermore, for male customers, FTDNA has included some SNPs on the Y chromosome. Until recently, however, a customer has not been able to learn from the company about which SNPs on the Y chromosome he is positive for. The new feature that FTDNA has just started to launch, as a part of their Family

[4]For information about the new feature, see the following two blog posts: https://blog.familytreedna.com/y-dna-haplogroups-family-finder/ and https://dna-explained.com/2023/11/30/familytreedna-provides-y-dna-haplogroups-from-family-finder-autosomal-tests/.

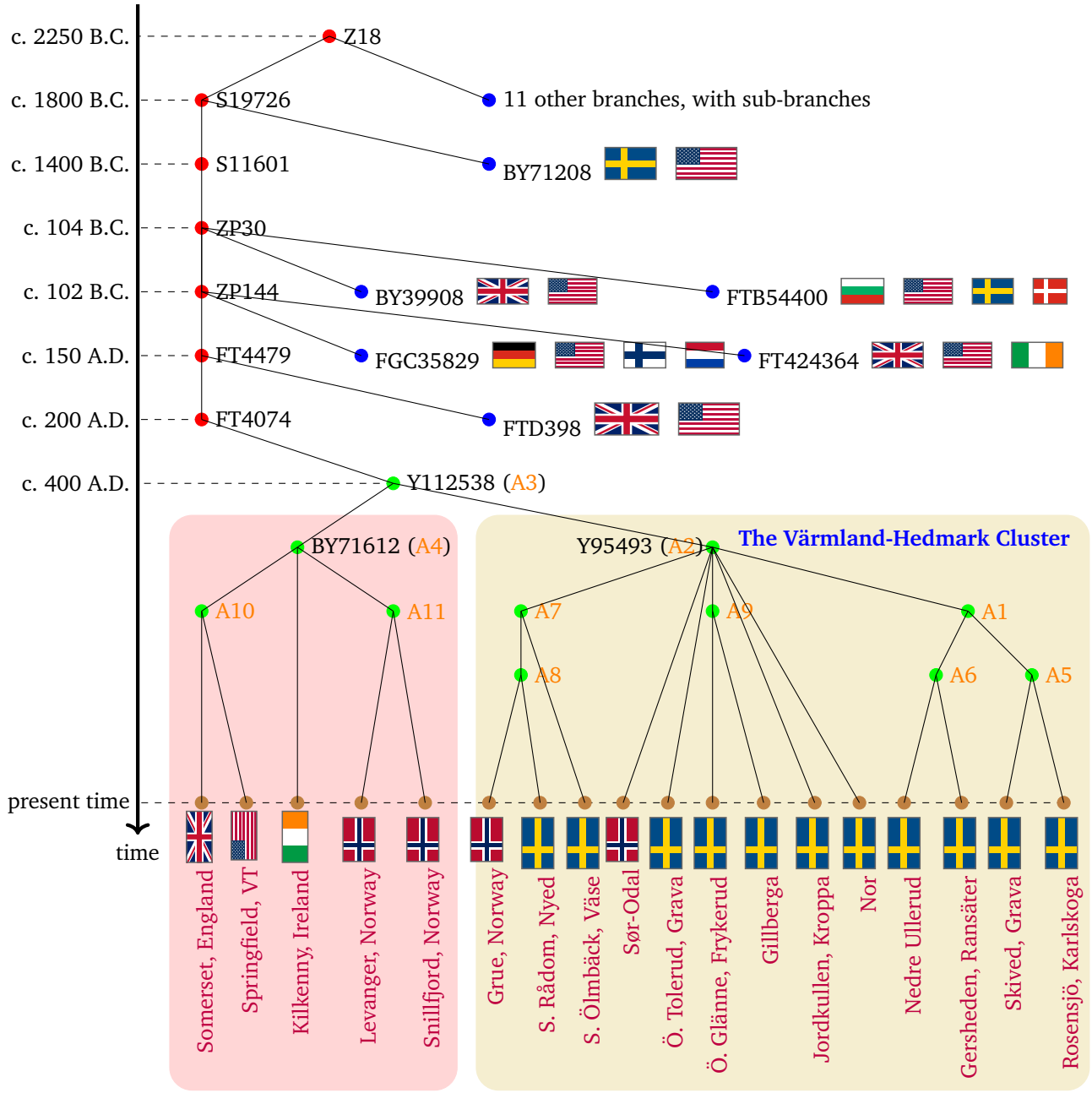


Figure 1: The figure shows a partially truncated version of the Y-DNA haplotree under R-Z18. The blue nodes represent branches with sub-branches that have been left out. The red nodes, in contrast, are exactly as shown in FTDNA's tree. The green nodes also show the complete, known haplotree (given information from both FTDNA and YFull, in addition to some things known only within the project); moreover, the part of the tree with green nodes coincides with the tree shown on page 2.

Finder test, provides exactly that information.[4]

The new feature will gradually become available for (male) customers. First out are people who have purchased a Family Finder test relatively recently (since March 2019). In fact, at least some of these customers already have access to the new feature. In a couple of projects that I am working on, I have during the summer of 2023 tested four male individuals using FTDNA's Family Finder test. These testers all received information about their (relatively crude) Y-DNA haplogroup on December 6. One of the four testers belongs to the Värmland-Hedmark Cluster—indeed, he is Tester 15b (see the preceding section for more information). The haplogroup that was reported for this tester is R-ZP30.

The SNP ZP30 is located upstream of the ancestor labeled A3

in the tree shown on page 2. In that sense, the haplogroup R-ZP30 is somewhat crude. It is, however, not *very* crude and, indeed, this haplogroup assignment is more precise than I and many others had expected when we first heard of FTDNA's plans to launch the new feature. Figure 1 illustrates this. It shows that the SNP ZP30 is, according to FTDNA's haplotree, four "steps" upstream of Y112538, which is the SNP that defines the ancestor A3 at the top of the tree on page 2. In terms of time, the distance between ZP30 and Y112538 is (according to FTDNA's age estimations) believed to be about 500 years: the estimate for ZP30 is 100 B.C., whereas that for Y112538 is 400 A.D.

FTDNA's Y-DNA haplogroup assignment based on the autosomal test has, I would argue, the potential of being amazingly useful for us in the project. The reason for this, as I think of it, is threefold. First, the number of people, not least in Sweden, who do an autosmal test at FTDNA is very large—much larger, by several multiples, than the number of people who purchase an STR test at the same company. Second, there seems to be a reasonably good chance of finding many of these autosomal testers—e.g., by posting in Facebook groups about genetic genealogy, by reaching out to genealogy associations, by providing information in a blog post (which hopefully can be easily found by search engines), and by searching for "ZP30" in the match lists of our autosomal FTDNA tests (I have verified that this is possible). Third, the information we obtain when learning that a test person is positive for the SNP ZP30 is reasonably precise; in addition, we can ask the tester about what he knows about his patrilineal ancestors' geographical origin. A person with an ancestral origin from, say, Värmland, and who also is known to be positive for ZP30, should have a very good chance of indeed being a member of the Värmland-Hedmark Cluster.

At the stage where we have managed to identify an autosomal tester who seems likely to belong to the Värmland-Hedmark Cluster, we can, to start with, provide him with information about our project and we can investigate whether the test person possibly belongs to a branch in our tree that is already known to us (and, thus, that this tester's connection to one or more of the existing testers in the project can be confirmed by church records). Next, depending on the outcome of that investigation, we can explain to the tester what the possible options for more ambitious Y-DNA testing are. Some people might then become interested in upgrading, at their own expense, to a Big Y-700 test or a WGS test. I will also consider to fund some WGS tests for likely members of the Värmland-Hedmark Cluster.

Suppose we have identified an autosomal tester who is positive for ZP30. With access to only that information, how likely is it that this individual is also positive for Y112538—meaning that he could be inserted in the tree on page 2 if he were to do a more ambitious test (a Big Y-700 or a WGS test)? We can obtain a rough sense of the magnitude of that probability by noting that, according to FTDNA, 179 of the testers in the company's tree are positive for ZP30, and a subset consisting of 13 testers are in addition positive for Y112538.[5] That is, conditional on having learned that one is positive for ZP30 (but not knowing anything more), the likelihood of being positive for Y112538 would be about 7 percent (13/179).

This number might sound somewhat low. But, in practice, the tester would typically also have information about the geographic origin of his patrilineal ancestors. If these ancestors were known to be from, say, the south of Värmland, then we should feel significantly more confident that the tester will indeed turn out to belong to the Värmland-Hedmark Cluster. To upgrade to a Big Y-700 or a WGS test in that situation would be a lottery with a very decent chance of winning (in the sense of learning that one belongs to our cluster).

In addition, even if it turns out that one does *not* belong to the Värmland-Hedmark Cluster, from a broader perspective the upgraded test is of course not a waste. Any other outcome would just mean that the tester belongs to some other branch, and he can then try to learn about that one instead.

I have not yet started the recruitment process, by writing blog posts and Facebook posts, etcetera. But I will try to do that as soon as I get a chance.

References

Rae-Venter, Barbara. 2023. *I Know Who You Are: How an Amateur DNA Sleuth Unmasked the Golden State Killer and Changed Crime Fighting Forever*. New York, NY: Ballantine Books.

[5] Information found in FTDNA's Y-DNA haplotree on December 30, 2023.

Svensk sammanfattning

Värmland-Hedmark-klustret (förkortat VHC) är benämningen på en – vad det verkar – väldigt stor släkt som levde i Värmland och Hedmark under medeltiden och kanske även 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 pågår kontinuerligt med att samla mer kunskap om Värmland-Hedmark-klustret. Det här nyhetsbrevet har utkommit i juli och december varje år sedan 2019, 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?

✔Fotografiet på omslaget är från 1927 och föreställer en äldre man i Lekvattnet i norra Värmland. Vi har hittills inte stött på någon gren i Värmland-Hedmark-klustret där anorna kommer från den delen av Värmland, utan jag tyckte bara att bilden nog skulle pryda sin plats på omslaget. Fotograf är C.G. Rosenberg och källa är Nordiska Muséets samlingar (via digitaltmuseum.se).

✔Den senaste versionen av vårt haploträd återfinns som vanligt på sidan 2 i nyhetsbrevet. Denna gång är det inga större förändringar. Den enda modifikationen är att Tester 15b har tillkommit (och Tester 15:s nummer har ändrats till 15a). Den nytillkomna personen har, hos YSEQ i Berlin, testat några utvalda SNP:er på Y-kromosomen som vi vet att Tester 15a är positiv för. Testresultaten bekräftar (ytterligare) att de två personerna är släkt på det sättet vi trodde; resultaten ger oss dessutom kunskap om vilka av de testade SNP:erna som testtagarnas yngsta gemensamma patrilinjära ana – Jonas Jonasson (1833-1920) – var positiv respektive negativ för.

✔Det amerikanska bolaget Family Tree DNA (FTDNA) har nyligen börjat lansera en tjänst som kommer följa med det autsomala testet som bolaget säljer (men även rådata som är överförda till FTDNA från något annat bolag omfattas av tjänsten). Den nya tjänsten innebär att manliga testtagare kommer få information om sina Y-DNA-haplogrupper – om än på en ganska grov och oprecis nivå. Informationen kommer dock vara tillräckligt specifik för att vi i projektet bör kunna få väldigt stor hjälp av den när vi letar efter ännu ej upptäckta grenar i Värmland-Hedmark-klustret. Den nya tjänsten kommer att introduceras gradvis, och bolaget börjar med de personer som har testat sig relativt nyligen (jag testade några personer i somras, och de fick del av den nya tjänsten i början av december).

En person som tillhör Värmland-Hedmark-klustret kommer (i alla fall om dennes test är gjort tidigast i mars 2019) av den nya tjänsten att få sig tilldelad följande haplogrupp: R-ZP30. Att av den nya tjänsten få sig tilldelad haplogruppen R-ZP30 är alltså ett *nödvändigt* (men icke tillräckligt) villkor för att tillhöra vårt kluster. Men om man dessutom vet att ens patrilinjära anor kommer från Värmland eller Hedmark, då är oddsen väldigt goda!