Journal of Genetic Genealogy

CASE STUDIES USING GENEALOGICAL JUNCTIONS AMONG UNPLACED DNA MATCHES TO IDENTIFY UNKNOWN ANCESTORS[1]

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Abstract

The present paper describes case studies where the purpose was to identify two unknown ancestors: the author's paternal grandfather [FF] and his paternal grandmother's maternal grandfather's father [FMMFF]. A four-step method was used: (1) The author's and his brother's closest atDNA matches were identified, and the genealogical relationships to these matches were searched for by a comparison with their family trees. Those atDNA matches for which no explanatory genealogical relationship could be found were named *unplaced* DNA matches. Nineteen unplaced DNA matches were found who shared more than 100 cM with the two brothers. (2) The family trees of these unplaced DNA relatives were compared to each other, and common ancestors who recurred in the family trees of at least two unplaced DNA relatives were referred to as *genealogical junctions*. The four "strongest" genealogical junctions were focused (involving, eight, four, three, and three unplaced DNA matches, respectively). (3) An analysis of the *connectedness* between these genealogical junctions (e.g., marriages between descendants) were used to generate two hypotheses: the FF Norberg hypothesis, and the FMMFF Jon Pehrsson hypothesis. (4) The FF Norberg hypothesis was tested in collaboration with four descendants of the Norberg family who tested their atDNA, and one of them who also tested his Y-DNA, and the results fully supported the hypothesis. The FMMFF Jon Pehrsson hypothesis was tested by segment triangulation methods, to see if DNA segments shared with descendants of Jon Pehrsson's (*1795) children overlapped with DNA segments shared with descendants of the author's FMMF. Support for such DNA sharing was found on seventeen of the chromosomes, and the most conclusive support was found on chromosome 16. The results are discussed in terms of the distinction between proofs and evidence, the sensitivity of the genealogical junctions method, the importance of having one's siblings DNA tested, the confounding factor of the number of descendants of a hypothesized ancestor, and the choice of cut-off for identifying the set of unplaced DNA matches.

Key words: unknown ancestors, atDNA, Y-DNA, segment triangulation, genealogical junctions

[1] I wish to thank Sven-Erik Johansson and Robert Eckeryd for invaluable help during the years that I have been working on this project. Without having access to Sven-Erik Johansson's carefully organized genealogical database *Kråken.se*, I would probably never have embarked on the project. And if I had, it would most certainly have taken me much longer to complete. Sven-Erik Johansson has also been helpful in answering all kinds of questions during the process. Without Robert Eckeryd's doctoral thesis on unmarried mothers in this part of Sweden during the relevant periods, and his generous sharing of data about my paternal grandmother collected during his doctoral work, crucial information about her had been missing. I am also very grateful to my brother and my newly discovered cousins for their willingness to contribute to the process by testing their DNA; without their help this study could not have been completed. Finally, I want to thank anonymous reviewers for very valuable comments on a previous version of the manuscript.

1. INTRODUCTION

The present author's father (here referred to as F) was born in 1913 in Nordmaling parish, Västerbotten county, in northern Sweden. His mother Nanny Elina Ekholm (here referred to as FM) was unmarried and already had one child, a daughter born in 1910. She worked as a milkmaid on a farm, and as she found it difficult to take care of two small children, she left F in a foster family where he was raised. According to the birth records F's father (here referred to as FF) was unknown.

There had been many ideas over the years of who FF could be. For example, some had guessed that FF was a father or a son in the foster family. Another lead was followed by the municipality's poor welfare board when they initiated a paternity trial in 1916 against a sawmill worker (here referred to as JL) who had once claimed to be the father. The municipality's poor welfare board made a monthly contribution to the foster family for their expenses raising F, and now they wanted the biological father to take his responsibility and pay. During the trial, however, JL retracted his confession and denied ever having been sexually involved with FM.

During the paternity trial, which was extended over more than three years (as JL repeatedly failed to attend the court hearings), FM got married and moved to another parish together with her daughter. Her new husband, who was a widower with four children of his own, did not want to take responsibility for raising F, who stayed with his foster family. As has been documented by Eckeryd (2017) in his doctoral thesis on unmarried mothers in this part of Sweden, this was typical of the fate of unmarried mothers at that time: If they eventually found a man to marry, with whom they had not conceived a child prior to the marriage, they were allowed to take with them at most one child to the new household.

1.1. Prologue to the present study

In a first attempt to identify the FF, the author wanted to test the possibility that the father was indeed JL (who had once claimed to be the father, but then denied it) or one of the men in F's foster family, or possibly some other man in FM's vicinity. For this purpose, the author tested both his atDNA and Y-DNA, and his strongest atDNA matches were identified. The genealogical relationship to these DNA matches were then explored by comparing the known branches of the author's family tree (i.e., his mother's branch and the known part of the FM branch) with the family trees of his atDNA matches, in a search for genealogical relationships that could explain the amount of DNA shared. As the author's FM, MF and MM and their family branches were relatively well known, it was possible to tie most of the closest DNA matches to these family branches. This was facilitated by the fact that the author's mother's family came from another part of Sweden, with a low probability of overlaps between her family tree and that of the author's father. In this way, genealogical relationships were identified for most of these DNA matches that were sufficiently close to explain the amount of DNA shared (according to data from Bettinger's [2020] Shared cM Project 4.0.].

Left, however, was a subgroup of relatively strong DNA matches where no sufficiently close genealogical relationships were found that could explain the amount of shared DNA. They were referred to as the *unplaced* DNA matches, and it was assumed that they were probably related to the author via his unknown FF.

At this stage of the research, it was still assumed that the FF was probably identical to one of the already designated candidates (i.e., either JL or one of the males in the foster family), or alternatively some man who was living or working in the FM's vicinity at the time of conception in 1912. Several such hypotheses were tested by

searching these persons' family trees for genealogical connections to the families of the unplaced DNA matches, but without success. In this way, both JL and the males in the foster family could be excluded as extremely unlikely FF candidates. The father in the foster family came from another part of Sweden, and no ancestors from his family could be found in any of the unplaced DNA matches' family trees. Although JL did have his roots closer to Västerbotten county, the same was true with regards to his family tree: no single overlap could be found between his family tree and the family trees of any of the unplaced DNA matches within a genealogical distance of six generations back in time.

The exclusion of JL as a possible FF candidate was all the more remarkable in view of the fact that the paternity trial reached an end in 1920 when FM swore on the Bible that she had been sexually involved with JL during the relevant period and that he could therefore be the father (Eckeryd, 2017; Nordmaling District Court, Fall Session 1920, § 14, 133). Although there are many possible explanations of why she did this, one plausible explanation is that she sincerely believed that JL was the father, although she had also been sexually involved with someone else during the relevant period but did not want to disclose this because she was newly married and feared for the consequences if her husband would find out.

Another approach that was tried at this early stage of the process was to search for a likely FF candidate among men who were living or working in FM's vicinity. A search for candidates were made by consulting the parish book for Nordmaling. Among a tenfold of men who appeared to be possible candidates, because they were in FM's vicinity at the time of conception in 1912, only one could be shown to be genealogically relatively closely related to *some* of the unplaced DNA matches, although not to such an extent that it made him appear as a likely FF candidate.

This lack of success led to a re-start with a new approach, where all previous suggestions about the identity of the FF were abandoned in favor of a procedure that involved an *analysis of genealogical junctions among the unplaced atDNA matches* without any presuppositions of the identity of FF. One purpose of the present paper is to describe this procedure and how it was used to identify the FF's family.

1.2. Genealogical junctions

The basic idea was that an exploration of how the unplaced DNA matches were *genealogically related to each other* would make it possible to identify *genealogical junctions*, in the form of couples (i.e., a man and a woman) probably no longer than 5 generations back in time that were common ancestors to subsets of these unplaced DNA matches. The original assumption was that these couples were likely to be ancestors to FF, and that the identification of FF would require the identification of at least two independent subsets of unplaced DNA matches defined by two different genealogical junctions, where one would represent the FF's mother's family and the other would represent the FF's father's family. If more than two genealogical junctions were identified it was expected that an analysis of the *connectedness* between these genealogical junctions (e.g., in the form of marriages between descendants) would make it possible to form a hypothesis about the identity of the FF, which could then be tested by DNA analyses. More specifically, the assumption was that the lines forward in time from the genealogical junctions would converge in a new couple that would be hypothetically identifiable as the FF's parents, and the idea was to test this hypothesis by asking living descendants of theirs to test their DNA. Partly similar methods have been used successfully in forensic contexts (e.g., Tillmar et al., 2021).

A complication, however, was that although the author's father's biological mother (FM) was known there were some gaps also in her family tree. Of special importance, her MF Carl Johan Forssén's (*1828) father was

unknown (see Figure 1). This meant that some of the unplaced atDNA matches might alternatively be explained by genealogical relationships via the unknown FMMFF. It was therefore concluded that the search for genealogical junctions in the family trees of the unplaced DNA matches had to include the identification of at least three different genealogical junctions. This might make possible also the formulation of a hypothesis about the identity of the FMMFF.

Figure 1.
The author's father's pedigree, as known at the start of the investigation[2].

TWO GENERATIONS BACK FROM THE AUTHOR
FF: Unknown
FM: Nanny Elina Ekholm *1883-11-10 Nordåker, Vännäs, Västerbotten. †1948-09-03 Robertsfors, Västerbotten

THREE GENERATIONS BACK
FFF/FFM: Unknown
FMF: Erik Ekholm *1845-12-12 Östanå, Vännäs, Västerbotten. †1920-11-13 Hörneå, Hörnefors, Västerbotten
FMM: Maria Kristina Forssén *1855-03-16 Överboda, Umeå, Västerbotten. †1915-09-16 Hörneå, Hörnefors, Västerbotten

FOUR GENERATIONS BACK
FFFF/FFFM/FMFF/FFMM: Unknown
FMFF: Johan Georg Ekholm *1821-06-13 Gumboda, Nysätra, Västerbotten. †1905-02-05 Nordåker, Vännäs, Västerbotten
FMFM: Anna Anna Elisabet Lundberg *1820-09-19 Norrmjöle, Umeå, Västerbotten. †1886-11-18 Nordåker, Vännäs, Västerbotten
FMMF: Carl Johan Forssén *1828-02-15 Björnlandsbäck, Vännäs, Västerbotten. †1865-06-08 Granlund, Vännäs, Västerbotten
FMMM: Susanna Forssén *1826-06-24 Överboda, Umeå, Västerbotten. †1897-02-01 Granlund, Vännäs, Västerbotten

FIVE GENERATIONS BACK
FFFFF/FFFFM/FFFMF/FFFMM/FFMFF/FFMFM/FFMMF/FFMMM: Unknown
FMFFF: Göran Johansson Ekholm *1789-12-31 Forsa, Hälsingland. †1859-04-14 Östanå, Vännäs, Västerbotten
FMFFM: Margareta Larsdotter *1779-01-14 Gumboda, Nysätra, Västerbotten. †1841-07-29 Östanå, Vännäs, Västerbotten
FMFMF: Fredrik Lundberg *1777-08-12 Korsholm, Vasa, Finland † 1837-10-19 Norrmjöle, Umeå, Västerbotten
FMFMF: Lisa Greta Persdotter *1779-09-14 Gubböle 2, Umeå, Västerbotten. † 1851-02-14 Norrmjöle, Umeå, Västerbotten
FMMFF: Unknown
FMMFM: Greta Stina Olofsdotter *1800-01-29 Hjuken, Vindeln, Västerbotten. †1890-09-11 Nylandsnäs, Vännäs, Västerbotten
FMMMF: Erik Eriksson Forssén *1786-02-07 Nyåker, Nordmaling, Västerbotten. †1867-12-12 Överboda, Umeå, Västerbotten
FMMMM: Charlotta Andersdotter *1790-05-22 Överboda, Umeå, Västerbotten

It was assumed that any hypothesis about the identity of FMMF's father would have to be tested in another way than the FF hypothesis. Testing the hypothesized identity of an unknown ancestor two generations back in time typically requires access to new atDNA data from his children or grandchildren. In the case of the unknown FF this would be a real possibility if children or grandchildren of a hypothetical FF could be identified and were willing to test their DNA. In the case of the FMMFF, however, no living children or grandchildren, or even great-grandchildren could realistically be expected to be found. On the other hand, the probability of finding great-great-grandchildren or great-great-great-grandchildren *who had already tested their atDNA* was judged to be relatively good. If so, it might be possible to test the hypothesis by means of *an analysis of DNA segments shared*

[2] In 19th century Sweden, family names were still uncommon and instead patronymics were in common use. This meant that both boys and girls got their surnames after their father's given name. For example, if the father's name was Olof Jonsson his sons got the surname Olofsson (i.e., Olof's son) and his daughters got the surname Olofsdotter (i.e., Olof's daughter). The latter was the case with Carl Johan Forssén's (*1828) mother, Greta Stina Olofsdotter (*1800); her father's name was Olof Jonsson, and her brothers accordingly got the surname Olofsson, whereas she bore the name Olofsdotter. So-called illegitimate children did not naturally receive any surname. The author's FMMF was given the name Carl Johan when baptized but acquired the surname Forssén first upon getting married; this was actually his wife's surname. Forssén was originally a soldier's name that her father Erik Eriksson Forssén (*1786) got while serving in the army, and that was then preserved as a family name in later generations. This was a typical origin of many family names at that time; the family name Ekholm of the FMF branch of the family was originally also a soldier's name given to the FMFFF Göran Johansson Ekholm (*1789) while serving in the army.

by descendants of FMMF Carl Johan Forssén and his hypothesized father. As a complement to searching for descendants of Carl Johan who had already tested their DNA, it was also possible to contact first and second cousins of the author who were his descendants and ask if they were willing to test their DNA.

To summarize, if a hypothetical FMMFF could be identified by the analysis of genealogical junctions, it was assumed that *segment triangulation* could be used to test this hypothesis. More specifically: If the hypothesis was correct, the author would be likely (1) to share DNA segments with DNA matches who were descendants of this hypothetical FMMFF and that (2) *also* were shared with DNA matches who were descendants of FMMF Carl Johan Forssén (*1828).

1.3. Segment triangulation

Segment triangulation is defined by Bettinger (2016) as a technique used to identify the ancestor or ancestral couple potentially responsible for a DNA segment shared by three or more descendants of that ancestor or ancestral couple. As Thomas (2021) formulates it, this is especially relevant to establishing distant relationships and "involves finding three or more persons that share an identical atDNA segment (HIR) and that also have genealogies that show a single common ancestor is uniquely shared among them" (p. 29). The procedure starts with the identification of an atDNA segment that the person A shares with at least two persons: B and C. A basic requirement is that all the included matches match each other (e.g., A-B, A-C, and B-C); this is essential to rule out the possibility that what looks like an apparent segment triangulation may be spurious because A shares the segment on one chromosome with B and the segment in the same location on the other chromosome in the chromosome pair with C.

The persons who share a given DNA segment are referred to as a triangulated group (TG), and when such a group has been identified the next step is to use genealogical research to identify common ancestors (CA) to the members of this TG. As pointed out by Thomas (2021), *independent lineages* are a key consideration when triangulating: "The lineages to the common ancestor need to be independent. Having three (or more) independent lineages to the common ancestor are what gives triangulation its power to prove relationships" (p. 71). Applied to the present research question, this means that descendants of FMMF Carl Johan Forssén (*1828) must share DNA segments to a hypothetical FMMFF via descendants of at least two of that hypothetical FMMFF's other children if the triangulation is to count as evidence of paternity.

Yet another consideration when using segment triangulation is that the strongest evidence for common ancestry is to be found when a series of *intermediate MRCAs* (most recent common ancestors) can be identified for DNA matches in each generation back in time (Bartlett, 2016). With a large TG, the ideal goal may even be described as *tracing the history of the DNA segment*, rather than as identifying one common ancestor or ancestral couple. Although this procedure involves genealogical research for the purpose of identifying MRCAs with each individual in the TG, these MRCAs will usually be found at different genealogical distances for different individuals. If the TG is sufficiently large, it may ideally be possible to identify a succession of MRCAs, generation for generation back in time, that provides a hypothetical historical reconstruction of how the DNA segment has "travelled" in time from ancient times to the present.

The important thing here is not to find matches who share strictly *identical* DNA segments, but rather who show *overlapping* of DNA segments that may be of different lengths. For example, the DNA segments shared with relatively close cousins typically tend to be larger than the segments shared with more distant cousins. The genealogical distance to the MRCAs with each individual in the TG can be expected to correlate with the size of

the DNA segments; the larger the DNA segment shared, the closer in time the MRCA may be expected to be found. No perfect correlation should be expected, however, as the transmission of DNA between generations involves a lot of randomness.

1.4. Purpose of the present study

To summarize, the purpose of the present study was

- to search for genealogical junctions (GJ) among unplaced atDNA matches
- to analyze the connectedness between these GJs in order to formulate hypotheses about the FF and FMMFF, and
- to test these hypotheses by means of further atDNA tests, Y-DNA testing, and segment triangulation.

2. MATERIAL AND METHODS

2.1. Genealogical data

There are systematic population registers in Sweden since the 16th century. In addition, a new kind of population register was introduced by a church law in 1686, whereby the country's priests were required to visit all the roots (districts) in the parish every autumn. All residents of the parish were required to participate in these house interrogations. Failure to attend could be punished with a fine and, if it was repeated, by having to sit in the church log outside the church. The purpose of the new church law was to gain better control over the population, both to ensure that people had the correct Christian doctrine and to facilitate the selection of soldiers for war service. In connection with these house interrogations, the priests were obliged to keep books of the residents of the parish, so-called parish household records.

These parish household records show variations in form but are generally organized in books, with one line for each individual and columns for the individual's name, date and place of birth, marriage, death, and migration from one parish to another. Sometimes these books also contain notes about reading or writing skills, an account of when each individual took communion, and a separate column about conduct, such as for example being convicted of a crime. These parish household records are now digitalized and are available online. The author had access to these via a subscription to *ArkivDigital* (https://www.arkivdigital.se), which is Sweden's largest and most extensive online archive of digitalized original records for genealogists.

The author, however, primarily used the full version of the genealogical database *Kråken.se*, because it provided quick access to large amounts of systematically organized genealogical information of the kind that was of primary interest in this study. This database, which was developed by the genealogist Sven-Erik Johansson, contains genealogical data on more than 600 000 persons from southern Västerbotten and northern Ångermanland (i.e., the most important geographical area for the present study). *Kråken.se* is the most complete existing genealogical database covering this part of Sweden from earliest documented time to the end of the 19th century. These data are arranged familywise with information about the time and place of birth, death, and marriage of the individual, and also contain references to the volumes and pages of the parish household books from which genealogical data were retrieved.

Pedigrees in Word format (of the form illustrated in Figure 1) were developed based on the information that the DNA matches provided themselves, in combination with information from *Kråken.se* and *ArkivDigital*. All

information was checked by consulting the digitalized archives in *ArkivDigital* before being included in the present study. Names and birth dates were entered as they were spelled and organized in *Kråken.se* to make the pedigrees easily searchable to find specific persons by using the search function in Word.

Information from US censuses, passenger lists from ships going between Sweden and the US, American muster cards from the first and second world, and other genealogical information from the US were accessed via a subscription to *Ancestry* (https://www.ancestry.se).

2.2. DNA data

The author tested his atDNA at three companies: *MyHeritage, Family Tree DNA* and *Ancestry*. On September 1st, 2023, he had 30,073 matches at *MyHeritage*, 11,282 matches at *Ancestry*, and 9,122 matches at *Family Tree DNA*. To get more complete information about the F's DNA, the author's brother was also asked to test his atDNA. Because MyHeritage produced the most matches, he tested his atDNA at *MyHeritage*; on September 1st, 2023 he had 27,713 matches. When other relatives were asked to test their atDNA this was also done on MyHeritage. As to Y-DNA it was tested by a Big-Y test at *Family Tree DNA*, both for the author and for one relative.

2.3. Procedure

The investigation proceeded in four steps: (1) the identification of unplaced DNA matches; (2) the search for genealogical junctions; (3) the generation of hypotheses, and (4) the testing of hypotheses.

2.3.1. The identification of unplaced DNA matches

In the first step, the two brothers' closest atDNA matches were identified, and the genealogical relationships to them were searched for by a comparison of the brothers' pedigree to the DNA matches' pedigrees. The closest DNA matches were defined as those who shared the most DNA with the two brothers *in combination*. This was computed as the total cM of all the DNA segments (with a size of at least 6 cM) that each DNA match shared with the two brothers. To illustrate: If a certain DNA match shared 50 cM with Brother 1 on chromosome 1 and 50 cM with Brother 2 on chromosome 2, the total shared sum would be 100 cM. But if a DNA match shared 50 cM with each brother on the same segment of chromosome 1, the total shared sum would be 50 cM.

Those of the closest DNA matches (>100 cM combined for both brothers) for which there were available family trees, but for which no explanatory genealogical relationship could be found by a comparison with the known branches of the author's family tree (i.e., his FM, MF and MM branches) within at least six generations back in time, were named *unplaced DNA matches*. To facilitate the detection of common ancestors between DNA matches, all family trees were organized in the form of Word documents in the same way as in Figure 1, to make them easy to search by entering the name and birth date of ancestors in the search field of the Word program.

2.3.2. The identification of genealogical junctions

In the second step, the family trees of the unplaced DNA matches were compared to each other, to find common ancestors no longer than five or six generations back in time. Ancestors who were common to at least two of the unplaced DNA matches were referred to as *genealogical junctions*. The task was set at finding *at least* three such genealogical junctions, the three "strongest" ones. The *strength* of genealogical junction was defined in terms of the number of unplaced DNA matches who had them in their family trees.

Here it is important to note that the strength of a genealogical junction depends also on the number of descendant branches, and that this is a potential source of error that needs to be taken account of. For example, it is quite possible that a certain couple will be identified as a genealogical junction simply because they have *a very large number of now living descendants* that have tested their DNA, despite their not being the source of the shared cM (which might instead lie one or more generations back in time).

At the other end of the spectrum, the analysis of genealogical junctions may also fail if an ancestral couple that is highly relevant to the research in question has *very few* descendants. The fewer descendants an ancestral couple has, the less likely they are to turn up as a genealogical junction in the comparison between the family trees of DNA matches, simply because they have so few descendants that can test their DNA. An ancestral couple with very few descendants is therefore less likely to be identified by an analysis of genealogical junctions. These limitations to the method are discussed further in section 4.2 of the Discussion.

2.3.3. The generation and testing of hypotheses

In the third stage the genealogical junctions that had been identified were used to generate hypotheses about the unknown ancestors. Hypotheses were generated by searching primarily for (1) convergent lines from the genealogical junctions forward in time in the form of marriages between their descendants, and if no such convergent lines could be found for (2) geographical affinities between places of residence of persons that were relevant to the investigation.

In the fourth stage the hypotheses were tested. This was done in two different ways. In the case of the author's FF the hypothesis was tested by contacting descendants of the hypothesized FF, asking them if they would like to test their atDNA and Y-DNA. In the case of the author's FMMFF the hypothesis was primarily tested by segment triangulation methods, as described below. To increase the likelihood of finding segment triangulations, two close relatives in the FM branch of the family were asked to test their atDNA.

2.3.4. Segment triangulation

A basic requirement in segment triangulation is that all the included matches match each other on the relevant DNA segment (e.g., A-B, A-C, and B-C). MyHeritage provides each tested person A with access not only to information about the segments that A shares with B and C, but also information about the segments that B and C share with each other (provided that B and C have explicitly chosen to make that information available to their DNA matches).

As implemented in the present study to test the FMMFF hypotheses, two sets of DNA matches were identified: (1) DNA matches who were descendants of Carl Johan Forssén (*1828), and (2) DNA matches who were descendants of his hypothesized father. The basic assumption was that to the extent that atDNA segments could be found that were shared *both* with descendants of Carl Johan Forssén *and* with his hypothesized father, this would count as evidence in favor of the hypothesis. The more such segments that could be found, the larger they were, and the better the conditions of independent lineages and intermediate MRCAs were satisfied (see above in section 1.3), the stronger would the evidence be.

MyHeritage provides information not only about how much DNA one shares with the DNA matches (and on which chromosomes) but also about how much DNA these matches share with each another (and on which chromosomes). To find as many descendants as possible of both the FMMF and the hypothesized FMMFF, an iterative search process was used where DNA matches who had the FMMF or the hypothesized FMMFF in their family trees were searched for their closest DNA matches in turn, comparing their family trees to see which of them also had the FMMF or the hypothesized FMMFF in their family trees. In this way, the number of descendants of both the FMMF and the hypothesized FMMFF was successfully multiplied.

The chromosome browser in MyHeritage includes detailed information about DNA segments with a size of at least 6 cM that are shared with one's atDNA matches. Information about atDNA segments of interest was exported to the program DNA Painter (https://dnapainter.com) to provide an illustrative view of how these DNA segments overlapped with each other at each chromosome. The cut-off for including DNA segments in DNA Painter was set at the size of 7 cM.

2.3.5. Ethical considerations

To preserve confidentiality, all DNA matches were given code names. These code names were constructed as a combination of a quasi-randomly generated name and the totally shared cM. To illustrate: The code name *Brian-100* would mean (1) that the person's real name was *not* Brian, and (2) that the author and his brother together shared 100 cM with him.

In addition, because the degree of anonymity of the relatives at 1st and 2nd cousin level were lower than for the other DNA matches, they were asked for their consent to refer to them under these specific code names. The manuscript was sent to them, and they were asked if they wanted to change anything to increase their degree of anonymity; all of them gave their consent to referring to them by the given code name.

When individuals test their atDNA at MyHeritage, they choose how much information they want to make available to their DNA matches. For example, they can choose if they want to make information available about the DNA segments that are shared with their matches. They also choose if they want to make genealogical information available about their family tree. For some of the author's DNA matches no family tree information was made available at MyHeritage, and for some no information about DNA segments was available; they were not included in the study.

3. RESULTS

The results are presented in five sections, of which the first four describe the results of the four different steps in the research process. In the first section, the list of the closest unplaced DNA-matches is presented. In the second section the four "strongest" genealogical junctions (GJ) are described and analysed to see if they represent independent lineages. The third section contains an exploration of the possible connectedness between these GJs in the form of marriages between their descendants and describes how this connectedness was used to generate hypotheses. The fourth section describes the testing of these hypotheses by means of atDNA, Y-DNA-testing, and segment triangulation methods. The fifth and final section contains an evaluation of the genealogical junctions method.

3.1. The closest unplaced DNA matches

A cut-off of 100 cM was chosen for how much atDNA the unplaced DNA matches had to share with the author and his brother together. In total, nineteen DNA matches who passed this cut-off were found at MyHeritage (see Table 1). The author also tested his DNA at Family Tree DNA and Ancestry, but this resulted in few strong DNA matches, and no additional match that passed the cut-off. To explore the usefulness of this cut-off and whether it might be more useful with a lower cut-off, an alternative cut-off set at 90 cM was also tested; this, however, did not contribute to any new findings of importance for the results.

Table 1 lists the nineteen unplaced DNA matches. The table also describes the amount of atDNA they shared with each brother and the two brothers in common, as well as the size of the two largest shared DNA segments, and the number of shared segments larger than 6 cM.

Table 1.
The closest unplaced DNA matches of the two brothers, and the amount of atDNA they shared in cM, the size of the two largest shared segments, and the number of shared segments, as reported by MyHeritage.

Code namn	**Brother 1 cM**	**Brother 2 cM**	**Total cM**	**Two largest shared segments (cM)**	**Number of shared segments (> 6 cM)**
Sofia-150	55	119	150	39 and 32	11
Thore-147	106	113	147	64 and 28	9
Eivor-144	89	83	144	33 and 20	11
Maja-132	52	102	132	24 and 18	11
Cesar-128	117	54	128	34 and 34	7
Willy-124	59	118	124	27 and 24	9
Igor-124	68	112	124	42 and 37	7
George-122	75	58	122	25 and 24	10
Austin-120	91	82	120	23 and 21	12
Tora-116[a]	95	74	116	16 and 14	12
Clara-114	24	114	114	40 and 18	7
Elisabeth-115	44	88	111	31 and 24	7
Axel-112	33	112	112	35 and 24	7
Marcus-111	65	79	111	39 and 16	9
Bruno-108	56	68	108	51 and 19	5
Ellie-106	59	63	106	33 and 15	9
Bianca-102	102	61	102	62 and 40	2
Ludvig-101	67	95	102	55 and 11	7
Elvira-101	40	85	101	17 and 15	10

Note. Brother 1 = the author; Brother 2 = the author's brother.
[a] *Tora-116* also tested her DNA at *Family Tree DNA*, where she was reported to share 90 cM with Brother 1.

3.2. Genealogical junctions (GJ)

The aim here was to find at least three ancestral couples no longer than five or six generations back in time who were common to at least two unplaced DNA matches (i.e., had a "strength" of at least 2), and in this sense constituted genealogical junctions (GJ). This was done by searching the Word family tree documents for persons with a specific name and birth date. Four GJs were found that had a strength of 3 or more (i.e., who had three or more of the unplaced DNA matches in their family trees). Some additional GJs were also identified that had two

unplaced DNA matches in their trees. But because four GJs had already been identified with a strength of 3, the choice was made to stay with these four. They were the following:

3.2.1. Genealogical junction 1 (GJ-1)

The strongest genealogical junction (in terms of the number of unplaced DNA matches who shared it) was a couple from southern Nordmaling born in the first decade of the 19th century: Matts Olofsson (*1806) and Maja Greta Andersdotter (*1803). Eight of the 19 unplaced DNA matches had this couple in their family tree: *Sofia-150, Maja-132, Igor-124, Tora-116, Clara-114, Elisabeth-115, Marcus-111,* and *Ludvig-101.*

Matts Olofsson (*1806) was a farmer in Ava, Nordmaling, but he was born in Bodum, a small village in Grundsunda parish, south of Nordmaling. His wife Maja Greta Andersdotter (*1803) was born in Långed, a village in the southern part of Nordmaling. After being married they moved to Ava, where they had ten children during the years 1829-1848. Of these, eight survived into adulthood and formed their own families. All in all, they had 58 grandchildren.

3.2.2. Genealogical junction 2 (GJ-2)

The next strongest genealogical junction was a couple from another part of the Nordmaling parish: Erik Olofsson (*1782) and Anna Katarina Jakobsdotter (*1788). They were found in the family trees of four of the unplaced DNA matches: *Eivor-144, George-122, Austin-120* and *Elvira-101.* Erik Olofsson (*1782) was a farmer in Mullsjö. He married a woman from the neighbouring village of Örsbäck in 1805, and they had fifteen children in Mullsjö during a 27-year period from 1806 to 1833. Ten of their children grew up to form families of their own. All in all, they had 67 grandchildren.

Interestingly, there was no overlap between the two subsets of DNA matches from GJ-1 and GJ-2 in terms of the DNA matches that had these couples in their family trees. In other words, these two subsets of DNA matches obviously represented two *independent* genealogical junctions.

3.2.3. Genealogical junction 3 (GJ-3)

The third strongest genealogical junction was a farmer couple from Ava in southern Nordmaling: Johan Petter Johansson (*1819) and Maria Karolina Mattsdotter (*1829). They had three children, of which two formed their own families, and altogether they had 25 grandchildren. This couple was found in the family trees of three of the unplaced DNA matches: *Sofia-150, Igor-124,* and *Clara-114.*

Here it may be noted that this subset of DNA matches overlapped with that from GJ-1. They actually constituted a subset of the DNA matches from GJ-1: three of the eight DNA matches from GJ-1. This meant that it did not constitute an *independent* genealogical junction. A look for genealogical connections revealed that the woman in this couple, Maria Karolina Mattsdotter (*1829), was a daughter of the couple from GJ-1.

3.2.4. Genealogical junction 4 (GJ-4)

The fourth strongest genealogical junction was a couple from Vännäs, which is about 50 kilometers to the north of Nordmaling. This couple, Jon Pehrsson (*1795 in Berg, Vännäs) and Anna Beata Vilhelmsdotter Berggren (*1791 in Vännäs) was found in the family trees of three of the unplaced DNA matches: *Cesar-128, Bruno-108*

and *Bianca-102*. If the cut-off was lowered to 90 cM one further DNA match was added. There was no overlap between this subset of DNA matches and any of the other three; it thus constituted an independent genealogical junction.

In contrast to the three previous couples, this couple was not very stationary. Jon Pehrsson (*1795) was born in the village of Berg, close to Vännäs, but in his youth he moved to the neighbouring village of Kolksele, where he worked as a servant on a farm. Eighteen years old he married one of the farmer's daughters, the four-year older Anna Beata (*1791). They later moved to Pengsjö, another small village close to Vännäs, and then to Högland, another neighbouring village. Jon Pehrsson worked as a farmer but was also involved in building the church in Vännäs in the 1820s. All in all, this couple had 13 children over a 21-year period from 1814 to 1835, ten of which grew up to have their own families, and they had 64 grandchildren. After the death of his wife, Jon Pehrsson re-married at an age of 81 years, and had 12 years with his second wife, until he died in 1889 at an age of 93.

3.3. The generation of hypotheses

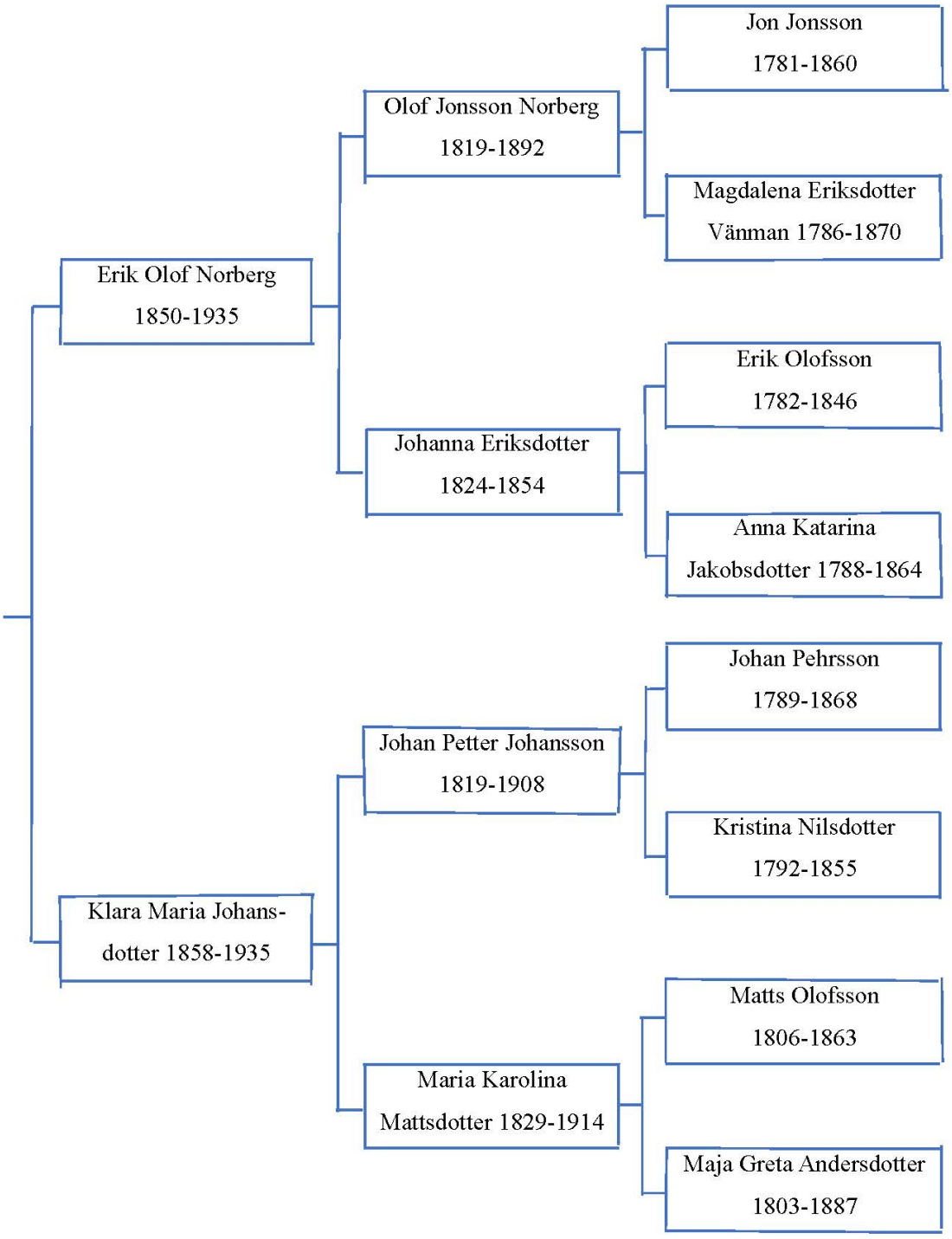
3.3.1. The FF Norberg hypothesis

To generate hypotheses about the identity of the author's FF, convergent lines from the four genealogical junctions were searched for, in the form of marriages between descendants. As already described in section 3.2.3, GJ-3 was not independent from GJ-1, as the three DNA matches whose family trees converged in GJ-3 was a subset of the eight DNA matches from GJ-1. The woman in the GJ-3 couple, Maria Karolina Mattsdotter (*1829 in Ava, Nordmaling), actually was daughter of the couple from GJ-1.

The next question was if a connection between these two hierarchically related genealogical junctions GJ-1 and GJ-3 could also be established with two other genealogical junctions GJ-2 and GJ-4, or at least one of them. A search for marriages between descendants of these GJs resulted in the discovery that a daughter of the couple in GJ-3, Klara Maria Johansdotter (*1858), on June 30th in 1878 married a grandson of the couple from GJ-2, Erik Olof Norberg (*1850). Here the family lines, in other words, converged between descendants from genealogical junctions 1, 2 and 3.

No similar convergence of family lines could be found with genealogical junction 4. It therefore seemed logical to formulate the following hypothesis about the identity of the author's biological FF: he was probably a son of Klara Maria Johansdotter (*1858) and Erik Olof Norberg (*1850), farmers in Lögdeå, Nordmaling. If this was correct the FF would have the family name of Norberg, and the hypothesis was accordingly named *the Norberg hypothesis*. The genealogical relationships between the people in genealogical junctions 1-3 are shown in Figure 2.

Figure 2.
*Erik Olof Norberg (*1850) and Klara Maria Johansdotter (*1858), their parents and grandparent, and the relationships between the genealogical junctions 1, 2 and 3. Klara Maria Johansdotter's parents represent GJ-3, whereas her maternal grandparents represent GJ-1. Erik Olof Norberg's maternal grandparents represent GJ-2.*



3.3.2. The FMMFF Jon Pehrsson hypothesis

When the author's FMMFM, Greta Stina Olofsdotter (*1800) got pregnant with her son Carl Johan (*1828; the author's FMMF) in May 1827, she worked as a maid in the small village of Pengsjö, south of Vännäs. A first conjecture, therefore, was that the father could have been a man who lived in Pengsjö at that time. This small village at that time contained five farms (numbered from 1 to 5), a soldier's croft, and a saltpetre smelter. Greta Stina worked as a maid at Pengsjö 1. Living at Pengsjö 2 were Jon Pehrsson (*1795) and Anna Beata Vilhelmsdotter Berggren (*1791), the couple in genealogical junction 4, and their children who were at that time eight in number and aged from 1 to 13 years.

This demographic information in combination with Jon Pehrsson's appearance in GJ-4 made it natural to hypothesize that Jon Pehrsson (*1795) was the author's FMMFF. First, he was living at the right place at the right time. Second, he was a common ancestor of three of the author's closest unplaced DNA matches: *Cesar-128, Bruno-108,* and *Bianca-102*. Third, some additional genealogical research revealed that, although Jon Pehrsson and his family stayed in Pengsjö only for about five years, from 1824 to 1829, he and Greta Stina Olofsdotter (*1800) might have known each other from earlier on. During the spring in 1820 Greta Stina's brother Hans Olofsson (*1798) had married one of Jon Pehrsson's first cousins, Ulrika Pehrsdotter (*1792). It seemed quite likely that Greta Stina had been present at her brother's wedding in 1820, because she and her brother seemed to be rather close as siblings (as suggested by her being one of the witnesses when her brother's first child was baptized one year after the wedding). Quite possibly, Jon Pehrsson (*1795) was also present at the same wedding, as it was one of his first cousins who got married. This indirect kinship might possibly have served as a context and excuse for Jon and Greta Stina to get acquainted during their time in Pengsjö.

3.4. Testing the FF Norberg hypothesis

To test the Norberg hypothesis, all sons in the Norberg family were identified, and a search was made for their descendants. Five such descendants (grandchildren of sons in the Norberg family) were identified and four of them were asked if they were willing to test their atDNA. All four did. The author's relationship to three of the Norberg descendants (*Viveka-509, Mattias-304*, and *Niklas-290*) went via their maternal grandfather, whereas the relationship for the fourth (*Steve-168*) went via his paternal grandfather. This meant that the hypothesis could undergo additional testing by asking *Steve-168* if he was willing to test his Y-DNA, which he was. The present section starts with a summary description of the seven brothers in the Norberg family and their known descendants, and then proceeds with a description of the results of the DNA tests.

3.4.1. The seven Norberg brothers

Erik Olof Norberg (*1850) was a farmer in Lögdeå in Nordmaling parish. He and his wife Klara Maria Johansdotter (*1858) had fifteen children during a 23-year period from 1879 to 1902. Among them were ten sons. According to the Norberg hypothesis, one of their ten sons was probably the author's FF. The youngest one was born in 1902 and since he was only eleven years when the author's father was born in 1913, he could be excluded, as could also two other sons who died as children. This left seven sons for more detailed exploration. They are referred to below as candidates 1-7.

*Candidate 1: Johan Norberg (*1879).* The oldest son, Johan Norberg (*1879) emigrated to the US in 1902 and arrived in Boston, Massachusetts on April 24th. When he applied for American citizenship in 1927, he was 48 years old and had already lived in the US for 25 years. He had worked as a miner and as a sailor/engineer on ships

going to Siberia, and he had participated in the Norwegian explorer Roald Amundsen's Maud expedition through the Northeast Passage 1918-1925. But he was still unmarried. In 1938 he married a Russian woman who was a widow with two children from an earlier marriage. She was 18 years younger, but they did not get any common children. He had no known children and therefore no descendants that could test their DNA. A study of passenger lists indicated that he had visited Sweden in 1929, but nothing indicated that he had been in Sweden in 1912 at the time when the author's father was conceived.

*Candidate 2: Eric Adolph Norberg (*1881)*. The second son, Eric Adolph (*1881) also emigrated to the US in 1902. He worked as a carpenter in Minneapolis, Minnesota and married an American woman in 1905. They had three children, born in 1907, 1910, and 1916. Only the youngest of them had children of his own, one boy and one girl. Here there were descendants that could test their DNA. But there were no indications from any passenger lists or any other documents that Eric Adolph (*1881) ever returned to Sweden.

*Candidate 3: Gustaf Fritz Norberg (*1885)*. The third son Gustaf Fritz (*1885) stayed in Sweden and took over half of the homestead in Lögdeå after his parents. He married in 1914, the year after the birth of the author's father. This meant that he was still a bachelor when the author's father was conceived, and that he was a possible FF candidate. His marriage, however, remained childless, so there were no descendants that could possibly test their DNA.

*Candidate 4: August Norberg (*1887)*. The fourth son August (*1887) emigrated to the US in April 1906 and should according to the parish book in Nordmaling have stayed there until 1921, when he returned to Lögdeå and took over half of the homestead after his parents. He settled in Lögdeå and married a woman from another family in the same village. They had one daughter, who in turn had two children, which meant that there were descendants who could test their DNA. Because he was believed to have been in US from 1906 to 1921 he seemed to be a very unlikely FF candidate. However, no documents could be found from his stay in the US, apart from his name on the passenger list of the ship Caledonia that arrived in New York on May 26th, 1906. This was in stark contrast to the wealth of information that was found for his two elder emigrating brothers Johan (*1879) and Eric Adolph (*1881): information from censuses, muster cards from the first world war, etc. The possibility could not be ruled out that he had returned to Sweden earlier than 1921.

*Candidate 5: Olov Albin Norberg (*1891)*. The fifth son, Olov Albin (*1891) married in 1930, at an age of 39 years, with a woman who had two children from previous relationships, but they had no children in common. Olov Albin stayed in Nordmaling, where he was a forest worker and ditch worker. He could not be ruled out as a FF candidate, but had no descendants who could test their DNA.

*Candidate 6: Karl Elof Norberg (*1893)*. The sixth son, Karl Elof (*1893) emigrated to the US in April 1913, four months before the birth of the author's father. He stayed in the US until 1933, when he returned to Nordmaling. In this case, just as for his two oldest brothers Johan (*1879) and Eric Adolph (*1881), it was easy to find documents referring to his life in the US: registration cards from the First World War, censuses, etc. He lived in Hennepin, Minnesota, where he worked as a clerk on a firm called Sash & Door. He never married and had no descendants that could test their DNA, but he could not be ruled out as an FF candidate.

*Candidate 7: Axel Nikanor Norberg (*1896)*. The seventh son, Axel Nikanor (*1896) stayed in Lögdeå, Nordmaling and married a teacher from the neighbouring village Mo, where they settled. They had one daughter, and she in turn married and had a son, so here there was one descendant who could test his DNA.

3.4.2. Testing atDNA

Apparently, only three of the seven brothers had descendants that could test their atDNA: Eric Adolph (*1881), August (*1887) and Axel Nikanor (*1896). The author approached the two known descendants of August (*1887), the only known descendant of Axel Nikanor (*1896), and one descendant of Eric Adolph (*1881), and asked if they were willing to test their DNA, and all of them did. The results from their DNA testing, in terms of the amount of DNA shared with the author and his brother, and between themselves, is shown in Table 2.

Table 2.
The amount of DNA(in cM) shared between brothers 1 and 2 and descendants of the Norberg brothers.

	Brother 1	Brother 2	*Viveka-509*	*Mattias-309*	*Niklas-290*	*Steve-168*
Brother 1	-					
Brother 2	2728 cM	-				
Viveka-509	286 cM	372 cM	-			
Mattias-304	167 cM	208 cM	2761 cM	-		
Niklas-290	204 cM	113 cM	214 cM	203 cM	-	
Steve-168	101 cM	102 cM	162 cM	98 cM	146 cM	-

Note. *Viveka-509* and *Mattias-304* are siblings and descendants of August Norberg (*1887). *Niklas-290* is descendant of Axel Nikanor Norberg (*1896). *Steve-168* is descendant of Eric Adolph Norberg (*1881).

As seen in Table 2, *Viveka-509* was the one who shared the most atDNA with her second cousins and with brothers 1 and 2: At an average she shared 188 cM with her 2nd cousins *Niklas-290* and *Steve-168*, and 329 cM with brothers 1 and 2. Her brother *Mattias-304* shared at an average 151 cM with his 2nd cousins *Niklas-290* and *Steve-168* and 188 cM with brothers 1 and 2. That is, both grand-children of August Norberg shared even more atDNA with brothers 1 and 2 than they did with their 2nd cousins *Niklas-290* and *Steve-168.* This clearly supported the Norberg hypothesis.

As to *Niklas-290* he shared at an average 188 cM with his three 2nd cousins *Viveka-509, Mattias-304*, and *Steve-168*. He shared at an average a little less than so, 159 cM, with brothers 1 and 2. *Steve-168* was the one who shared the least atDNA with the others: at an average 135 cM with his three 2nd cousins *Viveka-509, Mattias-304*, and *Niklas-290*, and a little less than so with the two brothers: 101,5 cM. Interestingly, the amount of DNA that brothers 1 and 2 shared with their four hypothesized 2nd cousins fell well within the range of shared DNA among the Norberg descendants: an average of 190 cM for Brother 1, and 199 cM for Brother 2. This was clearly consistent with the Norberg hypothesis: both brothers shared as much DNA as could be expected to be shared with the Norberg descendants if they were their 2nd cousins.

A crucial question was if any of these three Norberg brothers could be identical with the author's FF. If so, grandchildren of that brother would be the author's *half first cousin*, whereas grandchildren of the other brothers would be the author's *second cousins*. A correct interpretation of these results requires empirical data on how much DNA one tends to share with one's half first cousins versus one's second cousins. Data on this was taken from Bettinger's (2020) Shared cM Project 4.0 and are shown in Table 3.

Table 3.
Amount of DNA shared with half first cousins and second cousins, according to Bettinger's (2020) Shared cM Project 4.0.

Genealogical relationship	**Average shared DNA**	**Range (low to high; 99th percentile)**
Half first cousins	449	156-979
Second cousins	229	41-592

First, these data indicate that neither Axel Nikanor Norberg (*1896) nor Eric Adolph Norberg (*1881) were likely FF candidates. The reason for this is that Brother 2 shared only 113 cM with *Niklas-290*, which was below the range for half first cousins (i.e., less than 156 cM), and that both Brother 1 and 2 shared even less with *Steve-168.*

Second, although it could not be conclusively ruled out that August Norberg (*1887) was the FF, this did not seem very likely. The amount of DNA that the two brothers shared with August's grandchildren *Viveka-509* and *Mattias-304* was clearly within the range for half first cousins (156-979 cM), but it was also clearly within the range for second cousins (41-592). What primarily spoke against August Norberg being the FF, however, was the results for *Mattias-304*; the amount of DNA that he shared with both Brother 1 and 2 (167 cM and 208 cM, respectively) was lower even than the average for second cousins (229 cM).

3.4.3. Y-DNA

Of the four Norberg descendants, the author was related to three via their maternal grandfathers and to one, *Steve-168*, via his paternal grandfather. *Steve-168* was therefore asked if he would be willing to test his Y-DNA. He did this by taking a Big-Y test at Family Tree DNA, and the results were classified as an "exact match". *Steve-168* belonged to the same haplogroup as the author, R-YP4123. The comparison of STRs showed that only 1 of 653 differed, and the matching of private SNPs showed only two non-matching variants. This meant that the Norberg hypothesis was corroborated also by the testing of Y-DNA.

To conclude, this first part of the analysis clearly indicated that one of the Norberg brothers was the author's biological FF, but it was not possible to decide which of them. The most likely candidates were Gustaf Fritz (*1885), Olov Albin (*1891) and Karl Elof (*1893), but none of them had any known children and therefore no descendants that could test their DNA. Although August (*1887) could not be excluded, he did not seem to be a very likely candidate.

3.4.4. Segment triangulation

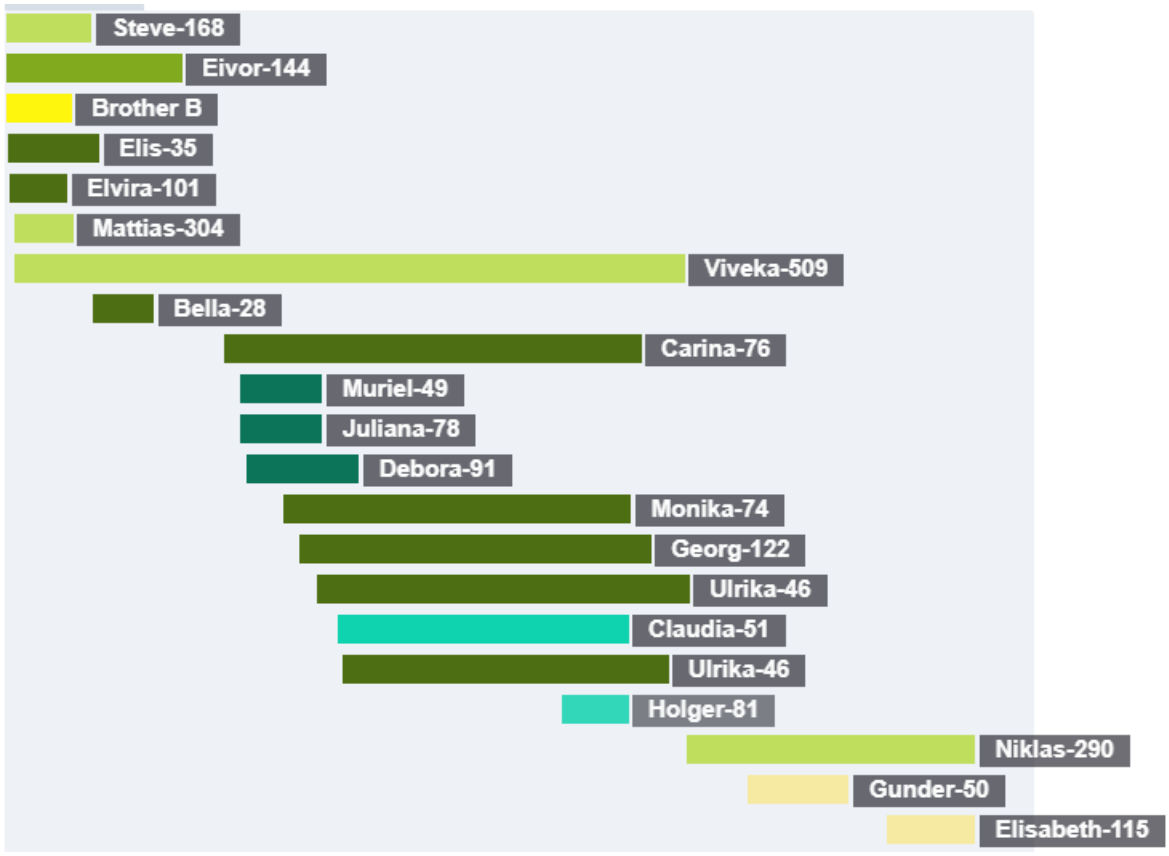
Finally, the Norberg hypothesis was tested also by means of segment triangulation. The reasoning was as follows: If the Norberg descendants *Viveka-509, Mattias-304, Niklas-290* and *Steve-168* were 2nd cousins to brothers 1 and 2, this should (1) result in the sharing of some relatively large DNA segments between the Norberg descendants and the two brothers, which (2) should also be shared (at least in part) by other DNA matches who had either Erik Olof Norberg's (*1850) or Klara Maria Johansdotter's (1858) parents or grandparents in their family trees (cf. the pedigree in Figure 2).

The testing of the hypothesis was made in the following steps: (1) The chromosome browser in MyHeritage was used to identify eleven relatively large (>30 cM) DNA segments where Brother 1 and/or Brother 2 shared DNA with at least one of the Norberg descendants. (2) The largest of these DNA segments was selected for more detailed analysis. This was a segment found on chromosome 16, where Brother 1 shared 78 cM with *Viveka-509*. (3) The chromosome browser in MyHeritage was used to identify DNA matches who shared this DNA segment (or part of it) and had ancestors to the Norberg brothers in their family trees. (4) This information was exported into DNA Painter to get an illustrative picture of the way these individuals shared DNA on chromosome 16 (see Figure 3).

As can be seen in Figure 3, of the Norberg descendants *Viveka-509*'s brother *Mattias-304* also shared 11 cM of this segment, and their 2nd cousin *Steve-168* shared 18 cM of it, both at the very beginning of the segment. Brother

2 also shared 12 cM of the segment at its very beginning. The only one among the Norberg descendants who did not share any part of this segment was *Niklas-290*; on the other hand, as seen in Figure 3, *Niklas-290* shared a relatively large segment with the author that started right where the larger segment ended and stretched almost to the end of the chromosome.

Figure 3.
*DNA segments on chromosome 16 shared between Brother 1 and descendants of Erik Olof Norberg (*1850) and Klara Maria Johansdotter (1858), as depicted by DNA Painter based on data from the chromosome browser in MyHeritage.*



MRCA: FFF Erik Olof Norberg (*1850) and FFM Klara Maria Johansdotter (*1858)
MRCA: FFFF Olof Norberg Jonsson (*1819) and FFFM Johanna Eriksdotter (*1824)
MRCA: FFFMF Erik Olofsson (*1782) and FFFMM Anna Katarina Jakobsdotter (*1788)
MRCA: FFFMFF Olof Isaksson (*1746) and FFFMFM Margareta Olofsdotter (*1755)
MRCA: FFFMMF Jakob Jakobsson (*1760) and FFFMMM Brita Persdotter (*1765)
MRCA: FFMMF Matts Olofsson (*1806) and FFMMM Maja Greta Andersdotter (*1803)

As depicted in Figure 3, Brother 1 shared almost this entire chromosome with Norberg descendants, which indicates that he had received almost the entire chromosome from his FF. In contrast, Brother 2 shared only a small part with Brother 1 on this chromosome (12 cM at the very beginning). Brother 2, in fact, had inherited almost all DNA on his corresponding chromosome 16 from the FM branch of the family (see below in section 3.5.2).

If the Norberg hypothesis were correct, the origin of this large DNA segment on chromosome 16 should be possible to trace to ancestors of the father and/or the mother in the Norberg family. As seen in Figure 3, the results were clearly in line with the hypothesis. The large segment shared with *Viveka-509* seemed to have come from the Norberg brothers' paternal grandmother, Johanna Eriksdotter (*1824), who had received part of it from her father and part of it from her mother. This is indicated by the following findings:

1. First, a relatively large part of this segment, 33 cM, was shared with the author's 3rd cousin *Eivor-144.* Because her MRCA were Erik Olof Norberg's (*1850) parents Olof Norberg Jonsson (*1819) and Johanna Eriksdotter (*1824), this suggested that at least part of the segment originated from this ancestral couple.

2. Second, among the author's 4th cousins that have already been mentioned previously in this paper (because they belonged to the author's closest unplaced DNA matches), 23 cM of the segment was shared by *Georg-122,* and another 10 cM was shared by *Elvira-101*. Their MRCA were Erik Olof Norberg's (*1850) maternal grandparents Erik Olofsson (*1782) and Anna Katarina Jakobsdotter (*1788). This indicated that the segment, or at least parts of it, came from this ancestral couple. This hypothesis was further strengthened by the fact that several other 4th cousins with the same MRCA also shared parts of this DNA-segment: *Carina-76* (32 cM), *Monika-74* (23 cM), *Ulrika-46* (26 cM), *Elis-35* (19 cM), and *Bella-28* (12 cM).

3. Five additional DNA matches were found who had the *parents* of Erik Olofsson *1782 or Anna Katarina Jakobsdotter *1788 in their family trees. Three of these (*Deborah-91, Juliana-78* and *Muriel-49*) had Erik Olofsson's (*1782) parents Olof Isaksson (*1746 in Mullsjö, Nordmaling) and Margareta Olofsdotter (*1755 in Mullsjö, Nordmaling) among their ancestors, whereas two others (*Holger-81* and *Claudia-51*) had his wife Anna Katarina Jakobsdotter's (*1788) parents Jakob Jakobsson (*1760 in Örsbäck, Nordmaling) and Brita Persdotter (*1765 in Ängersjö, Nordmaling) in their trees. This suggested that different parts of the segment might have their origin in these two ancestral couples.

Finally, as a contrast, it can be seen in Figure 3 that the segment on chromosome 16 that was shared with *Niklas-290* (as seen in the right part of the figure) was shared also with two other DNA matches (*Elisabeth-115* and *Gunder-50*) whose family trees contained another ancestral couple: the Norberg brothers' mother's maternal grandparents Matts Olofsson (*1806) and Maja Greta Andersdotter (*1803). This suggested that the segment that was shared by *Niklas-290* probably had its origin in that branch of the family.

To summarize: the Norberg hypothesis had now been tested in three different ways, and all results were clearly in line with the hypothesis. Everything pointed to one of the Norberg brothers as being the FF.

3.5. Testing the FMMFF Jon Pehrsson hypothesis

The Jon Pehrsson hypothesis was more difficult to test, partly because the searched-for ancestor was five generations back in time, whereas the Norberg hypothesis was about an ancestor two generations back in time. In this case the hypothesis was tested primarily by segment triangulation methods, although the process was facilitated by contacting relatives in the FM branch and asking them if they were willing to test their atDNA. Two such relatives were addressed, and both were willing to collaborate: a half first-cousin one step removed (*Valter-261*) and a second cousin (*Ramona-420*). This added more DNA matches who were descendants of Carl Johan Forssén (*1828) for segment triangulation purposes.

The chromosome browser in MyHeritage presents detailed information about the overlapping of one's DNA with that of the DNA matches at each chromosome. This made it possible to explore to what extent the DNA segments that Brother 1 and/or Brother 2 shared with descendants of Carl Johan Forssén (*1828) were also shared by descendants of his hypothesized father Jon Pehrsson (*1795). If such overlapping between DNA segments were found this would count as support for the hypothesis.

To test the hypothesis, a search was first made for (1) all DNA matches who were descendants of Carl Johan Forssén (*1828), and (2) as many DNA matches as possible who were descendants of Jon Pehrsson (*1795). (See also section 2.3.4 under Methods and materials.) Table 4 lists the DNA matches who were descendants of Carl Johan Forssén, how much DNA was shared with them, the nature of the author's genealogical relationship to them, and their lineage to Carl Johan Forssén (i.e., which of his children they descended from). As seen in the table, the matches included descendants of five of Carl Johan Forssén's children: Katarina Charlotta (*1851), Maria Kristina (*1855), Susanna Sofia (*1857), Karl (*1860), and Johan Petter (*1862).

Table 4.
*DNA matches who were descendants of FMMF Carl Johan Forssén (*1828), the amount of DNA shared with them (in cM, as reported by MyHeritage) and the nature of their genealogical relationship to the FMMF.*

Code name	Brother 1 cM	Brother 2 cM	Total cM	Genealogical relationship	Descendant of
Ramona-420	339[a]	254	420	Second cousin	FFMF's daughter Maria Kristina *1855
Valter-261	149	187	261	Half first cousin one step removed	FFMF's daughter Maria Kristina *1855
Robin-219	181	190	219	Second cousin one step removed	FFMF's daughter Maria Kristina *1855
Henrik-175	68	130	175	Third cousin one step removed	FFMF's daughter Susanna Sofia *1857
Amanda-147	99	77	147	Third cousin	FFMF's daughter Susanna Sofia *1857
Ella-129	98	129	129	Third cousin one step removed	FFMF's son Karl *1860
Abigail-125	24	101	126	Third cousin two steps removed	FFMF's son Karl *1860
Ingeborg-119	112	45	119	Third cousin	FFMF's daughter Katarina Charlotta *1851
Erik-101	48	84	105	Third cousin	FFMF's daughter Susanna Sofia *1857
Elof-99	49	50	99	Third cousin	FFMF's son Johan Petter *1862
Beata-70	42	64	70	Third cousin	FFMF's son Johan Petter *1862
Jesper-56	33	43	56	Third cousin one step removed	FFMF's daughter Susanna Sofia *1857
Kerstin-53	45	18	53	Third cousin two steps removed	FFMF's daughter Katarina Charlotta *1851
Arthur-50	35	15	50	Third cousin one step removed	FFMF's son Johan Petter *1862
Cilla-46	46	0	46	Third cousin two steps removed	FFMF's daughter Katarina Charlotta *1851
Isa-24	24	0	24	Third cousin two steps removed	FFMF's son Johan Petter *1862

[a] *Ramona-420* also tested her DNA at Ancestry, where she was reported to share 324 cM with Brother 1.
Note. Brother 1 = the author; Brother 2 = the author's brother.

Table 5 similarly shows a list of DNA matches who were descendants of Jon Pehrsson (*1795), how much DNA was shared with them, and how these DNA matches were genealogically related to Jon Pehrsson (i.e., which of his children they descended from).

Table 5.

*DNA matches who were descendants of Jon Pehrsson's (*1795) children (their names depicted in different colours) in his marriage with Anna Beata Vilhelmsdotter Berggren (*1791), and the amount of DNA shared with these matches (in cM) as reported by MyHeritage.*

Code name	Brother A	Brother B	Total cM	Jon Pehrsson's genealogical relationship to the DNA matches and name of the children they were descendants of
Cesar-128	117	54	128	FFFFF via Erik (*1820)
Bruno-108	56	68	108	MMFF via Johan (*1835)
Bianca-102	102	61	102	FMFFFF via Johan (*1835)
Jessica-92	74	34	92	FFFFF via Johan (*1835)
Kasper-83	9	74	93	FMFFF via Erik (*1820)
Oscar-80	48	40	80	FMFFF via Erik (*1820)
Elsy-78	0	78	78	FFMFFF via Erik (*1820)
Anne-74	74	--[a]	74	MFFFFF via Erik (*1820)
Jerry-69	0	69	69	FFMFFF via Erik (*1820)
Malin-69	30	39	69	MFFMFF via Vilhelm Petter (*1814) and MFMFFF via Johan (*1835)
Jörgen-68	0	68	68	MFMMF via Sofia Helena (*1834)
Erling-65	0	65	65	MFFFFF via Erik (*1820)
Liv-64	27	37	64	FFFF via Johan (*1835) and MFMFF via Vilhelm Petter (*1814)
Eileen-64	38	43	65	FFFFF via Erik (*1820)
Benjamin-62	62	0	62	FFFF via Erik (*1820)
Timmy-61	39	41	61	FMFMFF via Vilhelm Petter (*1814)
Anny-60	33	48	60	FMMMFF via Johan (*1835)
Martin-60	0	60	60	MFFFFF via Erik (*1820)
Derek-59	36	39	59	FFFMFF/ MFFMFF via Vilhelm Petter (*1814)
Hellen-56	48	39	56	FMFMMF via Sofia Helena (*1834)
Lucy-55	47	32	55	MFFMFF via Vilhelm Petter (*1814)
Blenda-49	49	12	49	MFFFMF via Maria Kristina (*1818)
Hedda-45	0	45	45	FMMFF via Vilhelm Petter (*1814)
Ragnhild-43	16	27	43	FMFMMF via Maria Kristina (*1818)
Kinna-42	42	0	42	MFMFMF via Cajsa Lisa (*1828)
Rasmus-41	0	41	41	FFFFMFF via Vilhelm Petter (*1814)
Kicki-40	40	0	40	MMMFMF via Cajsa Lisa (*1828)
Pamela-40	40	0	40	MMFMF via Cajsa Lisa (*1828)
Bertram-39	30	22	37	FMMMF via Barbro Magdalena (*1823)
Hildegard-39	39	25	39	MFFMFF via Vilhelm Petter (*1814)
Bernarda-38	37	22	37	FFFMMMF via Barbro Magdalena (*1823)
Tullia-38	38	0	38	FFMMFF/ MMFMFF via Erik (*1820)
Vicky-38	24	38	38	MFMFFFF via Erik (*1820)
Li-37	0	37	37	MMFFMFF via Vilhelm Petter (*1814) and MMFMFFF via Johan (*1835)
Mats-37	37	22	37	FMMMF via Barbro Magdalena (*1823)
Joe-33	18	33	33	MMMFF via Johan (*1835)
Rodney-32	29	26	32	MFMFF via Barbro Magdalena (*1823)
Quinn-29	29	0	29	MMFMF via Cajsa Lisa (*1828)
Marian-28	28	0	28	MFMFMF via Cajsa Lisa (*1828)
Sofie-28	28	0	28	FMMMF via Barbro Magdalena (*1823)
Andres-27	14	29	27	MFFFFF via Johan (*1835)
Joanna-23	23	0	23	MFFFFF via Johan (*1835)
Gregor-20	20	0	20	FMFFF via Erik (*1820)
Katrin-20	20	0	20	MFMFFF via Erik (*1820)
Lukas-19	19	0	19	FFMMMF via Anna Margareta (*1821)
Malena-19	0	19	19	MMFMFF via Erik (*1820)
Sture-18	18	0	18	FMFFF via Erik (*1820)
Matti-17	17	0	17	FMMFF via Johan (*1835)
Bernie-16	16	0	16	MFMFMMF via Maria Kristina (*1818)

[a] *Anne-74* had only tested her DNA at Family Tree DNA, and Brother 2 had not tested his DNA there.

Note. Brother 1 = the author; Brother 2 = the author's brother.

As seen in Table 5, the matches included descendants of eight of Jon Pehrsson's children: Vilhelm Petter (*1814), Maria Kristina (*1818), Erik (*1820), Cajsa Lisa (*1820), Anna Margareta (*1821), Barbro Magdalena (*1823), Sofia Helena (*1834), and Johan (*1835). The names of the children are depicted in different colours; this information is important to establish independent lineages (Thomas, 2021) in the segment triangulations described below. More detailed information about the lineage from each of these DNA matches to Jon Pehrsson is also found in the table; as seen on the first row, for example, Jon Pehrsson was *Cesar-128's* FFFFF.

Common to all the DNA matches in Table 4 are that they are descendants of Carl Johan Forssén (*1828; the author's FMMF), and common to all DNA matches in Table 5 are that they are descendants of Jon Pehrsson (*1795) children in his marriage with Anna Beata Vilhelmsdotter Berggren (*1791). If Jon Pehrsson (*1795) was the father of Carl Johan Forssén (*1828), they would be expected to share a substantial amount of DNA, and a substantial number of atDNA segments. Accordingly, their respective descendants would also be expected to share some of these DNA segments with each other. By implication, the author and his brother (as being descendants of Carl Johan Forssén) would also be expected to share some of the segments that these two sets of DNA matches share with each other. It should be noted that this procedure requires a segment triangulation involving *three* different sets of individuals: (1) Brother 1 and/or 2; (2) other descendants of Carl Johan Forssén; and (3) descendants of Jon Pehrsson's other children.

The hypothesis was tested in the following way: First, information about DNA segments (>7 cM) shared with the DNA matches in Table 4 (descendants of Carl Johan Forssén) and the DNA matches in Table 5 (descendants of Jon Pehrsson) that was available in the chromosome browser at MyHeritage was exported to the program DNA Painter (https://dnapainter.com). This provided an illustrative view of how these DNA segments overlapped with each other at each chromosome. Second, all chromosomes were searched for segments where Brother 1 and/or Brother 2 had an overlap of DNA *both* with descendants of Carl Johan Forssén *and* with descendants of Jon Pehrsson's children. Third, to make sure that this overlapping was on the same chromosome (and not on the other chromosome in the pair) it was ensured that the matches who shared segments with brothers 1 and/or 2 also shared these segments (or at least part of these segments) with each other.

*3.5.1. Overview of the segment triangulations between descendants of Carl Johan Forssén (*1828) and descendants of Jon Pehrsson (*1795)*

Table 6 shows atDNA segments that were shared *both* with descendants of Carl Johan Forssén (*1828) *and* with descendants of Jon Pehrsson's (*1795) children. Only triangulations that involved segments where at least one DNA match shared more than 15 cM with Brother 1 or Brother 2 were included. (For example, a triangulation on segment 2 with two descendants of Carl Johan Forssén and two descendants of Jon Pehrsson was excluded, as all four segments measured only between 7 and 13 cM). The names of the descendants of Jon Pehrsson are written in different colours, depending on which children they descendent from (cf. Table 5); this makes it easier to see to what extent independent lineages were involved in the various triangulations.

Table 6.

*Segment triangulations between Brother 1 and/or Brother 2 and DNA matches who were descendants of Carl Johan Forssén (*1828) and DNA matches who were descendants of Jon Pehrsson (*1795) children. The chromosome number, segment size (cM) and start and end location for each segment is included. The different colours indicate which of Jon Pehrsson's children they were descendants of:* Vilhelm Petter (*1814), Maria Kristina (*1818), Erik (*1820), Anna Margareta (*1821), Barbro Magdalena (*1823), Cajsa Lisa (*1828), Sofia Helena (*1834),or Johan (*1835).

Chromosome No. (Brother 1 and/or 2)	Descendants of Carl Johan Forssén (*1828); segment size (cM); start and end location	Descendants of Jon Pehrsson' (*1795) children
1 (A+B)	*Ramona-420:* 41 cM [107,825,866-162,252,097] *Robin-219*: 7 cM [162,357,707-167,403,625]	*Hannes-39:* 39 cM [88,794,011-146,672,906] *Jessica-92*: 16 cM [88,794,011 - 107,823,943] *Bianca-102:* 62 cM [100,864,133-173,376,184] *Lucy-55:* 12 cM [103,756,707-113,288,057] +8 cM [154,814,917-160,678,721 *Hildegard-39*: 27 cM [154,814,917 - 176,446,394]] *Anne-74:* 8 cM [161,919,011-167,103,268] *Derek-59:* 13 cM [165,125,851 - 177,342,651]
2 (B)	*Henrik-175:* 21 cM [169,010,659-192,417,747] *Valter-261:* 14 cM [169,427,769-180,693,147] *Erik-105:* 20 cM [175,333,632-202,897,049] *Beata-70:* 21 cM [193,472,864-217,414,502] *Arthur-50:* 15 cM [196,051,485-212,888,988]	*Malin-69:* 25 cM [171,075,730-199,419,373] *Timmy-61: 26 cM:* [171,358,785 - 202,897,049] *Vicky-38:* 7 cM [191,800,905-200,930,815]
3 (A)	*Ramona-420:* 32 cM [148,317,504 - 181,443,42] + 12 cM [188,430,230 - 193,962,67]	*Bruno-108:* 17 cM [180,633,485 - 189,583,705] *Cesar-128*: 17 cM [181,692,310 - 189,948,515] *Anne-74*: 15 cM [182,372,828 - 189,590,825] *Elmar-38*: 12 cM [185,447,038 - 189,948,515]
4 (A)	*Amanda-147:* 28 cM [5,794,904-22,396,295] *Arthur-50:* 9 cM [5,794,904-8,031,590] *Ramona-420:* 15 cM [8;774,285-21,183,041]	*Kinna-42:* 27 cM [5,920,389-21,816,328]
6 (A)	*Ramona-420:* 41 cM [123,805,429-155,763,508] *Henrik-175:* 23 cM [123,805,429-143,702,113]	*Cesar-128:* 9 cM [124,975,861-133,614,576] *Derek-59:* 9 cM [124,975,861-134,090,307] *Anny-60:* 8 cM [125,219,805-133,077,063]
7 (A+B)	*Valter-261:* 22 cM [43,748 - 11,597,743]	*Bernarda-38*: 12 cM [43,748 - 6,495,017] *Verna-17*: 10 cM [915,678 - 6,026,607] *Mats-37*: 11 cM [915,678 - 6,933,726]
9 (B)	*Elof-99:* 29 cM [114,636,015 - 134,717,69] *Ramona-420*: 11 cM [125,075,782 - 133,351,106]	*Malin-69:* 15 cM [99,448,564 - 112,271,779] *Liv-64*: 18 cM [100,270,846 - 115,103,266] *Eileen-64*: 18 cM [100,507,445 - 115,430,157] *Vicky-38*: 7 cM [110,383,797 - 115,430,157]
10 (A)	*Robin-219:* 24 cM [83,286,025 - 108,878,616]	*Bernie-16*: 16 cM [83,739,866 - 99,268,810] *Ragnhild-43*: 16 cM [83,790,207 - 99,551,326] *Timmy-61*: 22 cM [90,101,723 - 114,197,642]
12 (A)	*Ramona-420:* 17 cM [52,374,207-68,138,077]	*Benjamin-62:* 55 cM [5,383,579-54,593,124] *Bianca-102:* 40 cM [23732165- 67,920,566] *Jessica-92:* 38 cM [23,732,165-67,066,115] *Sture-18*: 18 cM [29,762,556 - 53,175,287] *Lukas-19:* 19 cM [42,068,852-62,103,023]
13 (A)	*Robin-219:* 14 cM [38,363,047-48,376,814] *Ingeborg-119:* 7 cM [44,249,607 - 49,798,391]	*Jessica-92:* 19 cM [38,363,047-57,054,331] *Bruno-108:* 19 cM [38,551,272-57,054,331] *Marian-28:* 14 cM [38,551,272-49,434,635]

		Mulle-15: 15 cM [38,363,047 - 49,798,391] *Elmar-38:* 12 cM [46,287,707-61,160,649] *Eberhard-39*: 10 cM [46,655,501 - 60,218,409]
15 (B)	*Robin-219:* 26 cM [85,939,032 - 96,900,999]	*Hellen-56*: 25 cM [8,543,639 - 93,885,108]
16 (B)	*Henrik-175:* 55 cM [5,488,091-53,137,282] *Ramona-420:* 30 cM [11,930,337-34,786,294] *Valter-261:* 27 cM [12,430,207- 27,887,780] + 39 cM [77,447,299-90,233,487] *Abigail-125:* 81 cM [20,419,699-85,659,155] *Amanda-147:* 30 cM [46,538,105- 71,961,906] *Elof-99:* 14 cM [78,197,287-82,866,767]	*Elsy-78:* 14 cM [4,171,701-9,173,143] + 51 cM [17,338,502-69,892,430] *Martin-60:* 13 cM [4,388,655- 9,173,143] + 46 cM [17,338,502- 63,545,556] *Jerry-69:* 14 cM [4,388,655-9,551,490] + 55 cM [17,338,502-73,752,262] *Kasper-83:* 14 cM [4,388,655-9,366,359] + 21 cM [17,950,096-34,786,294] + 33 cM [46,538,105-73,752,262] *Malena-19:* 11 cM [5,294,643-9,173,143] + 8 cM [56,737,620-62,268,125] *Bruno-108:* 51 cM [9,184,894-56,594,499] *Hedda-45:* 9 cM [6,082,553- 9,173,143] + 21 cM [58,867,991-78,883,118] *Rasmus-41:* 10 cM [6,082,553-9,366,359] +18 cM [59,888,170-78,041,865] *Erling-65:* 9 cM [6,164,478-9,173,143] + 44 cM [21,288,101-67,409,180]
17 (A)	*Amanda-147:* 29 cM [13,222,160-38,447,569]	*Oscar-80:* 20 cM [17,570,827-38,447,569] *Anne-74:* 20 cM [18,566,664-38,955,833] *Liv-64:* 19 cM [18,626,014-38,447,569] *Cesar-128:* 19 cM [18,626,014-38,447,569]
18 (B)	*Ramona-420:* 21 cM [0,582,838-7,339,906] *Robin-219:* 13 cM [0,582,838-5,069,982]	*Jörgen-68*: 11 cM [3,042,297-6,260,004]
19 (A)	*Erik-105:* 20 cM [48,760,229-55,069,964] *Beata-70:* 17 cM [51,595,182-56,596,815] *Isa-24:* 18 cM [51,595,182-56,762,676]	*Blenda-49*: 12 cM [49,171,593-53,577,419]
20 (B)	*Abigail-125:* 21 cM [31,859,221 - 48,913,503]	*Jörgen-68*: 37 cM [14,559,429-47,778,602]
22 (A)	*Ingeborg-119* 27 cM [22,235,510 - 37,033,264] *Kerstin-53:* 12 cM [22,910,416-27,647,065] *Cilla-46:* 11 cM [23,262,118-27,647,065]	*Matti-17*: 17 cM [21,363,306-28,074,256] *Bruno-108:* 14 cM [23,262,118-29,390,049] *Jessica-92*: 17 cM [27,647,289 - 38,164,106] *Katrin-20*: 20 cM [36,241,136 - 45,772,802] *Gregor-20*: 20 cM [36,241,136 - 45,772,802] *Oscar-80*: 21 cM: [37,966,060 - 49,067,699]

Note. Brother 1 = the author; Brother 2 = the author's brother.

As seen in Table 6, segment triangulation with descendants of Carl Johan Forssén (*1828) *and* descendants of Jon Pehrsson's (*1795) children was found on 17 chromosomes. Six of these (on chromosomes 4, 7, 15, 18, 19, and 20), however, failed to include independent lineages as each of them included only one of Jon Pehrsson's children. Six others did include independent lineages with two of Jon Pehrsson's children. In the following, however, the focus is only on the five of the triangulations that involved three of Jon Pehrsson's children: those on chromosome 1, 6, 12, 13 and 16. Because the strongest evidence of the hypothesis was found on chromosome 16, this is analysed first.

As an additional check of the Jon Pehrsson hypothesis, the possibility was considered that the important genealogical junction might lie one or more generations back in time. This was not relevant with regards to the genealogical junctions 1-3, because of their interconnectedness and their forward convergence in the Norberg family. The fourth genealogical junction, Jon Pehrsson (*1795) and his wife, however, was a "singleton" in this regard; here there was no interconnectedness with other genealogical junctions that contributed to the confirmation of the hypothesis. This, for example, left the possibility that it was not Jon Pehrsson who was the important genealogical junction but rather his parents. A search was therefore also made for DNA matches where his parents represented the MRCA, to see if this presented a viable alternative hypothesis.

3.5.2. Segment triangulation on chromosome 16

The strongest evidence in support of the hypothesis was found on chromosome 16, and more specifically on Brother 2's version of this chromosome. This was a chromosome where the two brothers shared very little DNA with each other. Brother 1, who shared only 15 cM of the segment at its very end, in fact had inherited almost all DNA on his corresponding chromosome 16 from the FF branch of the family (see above in section 3.4.4).

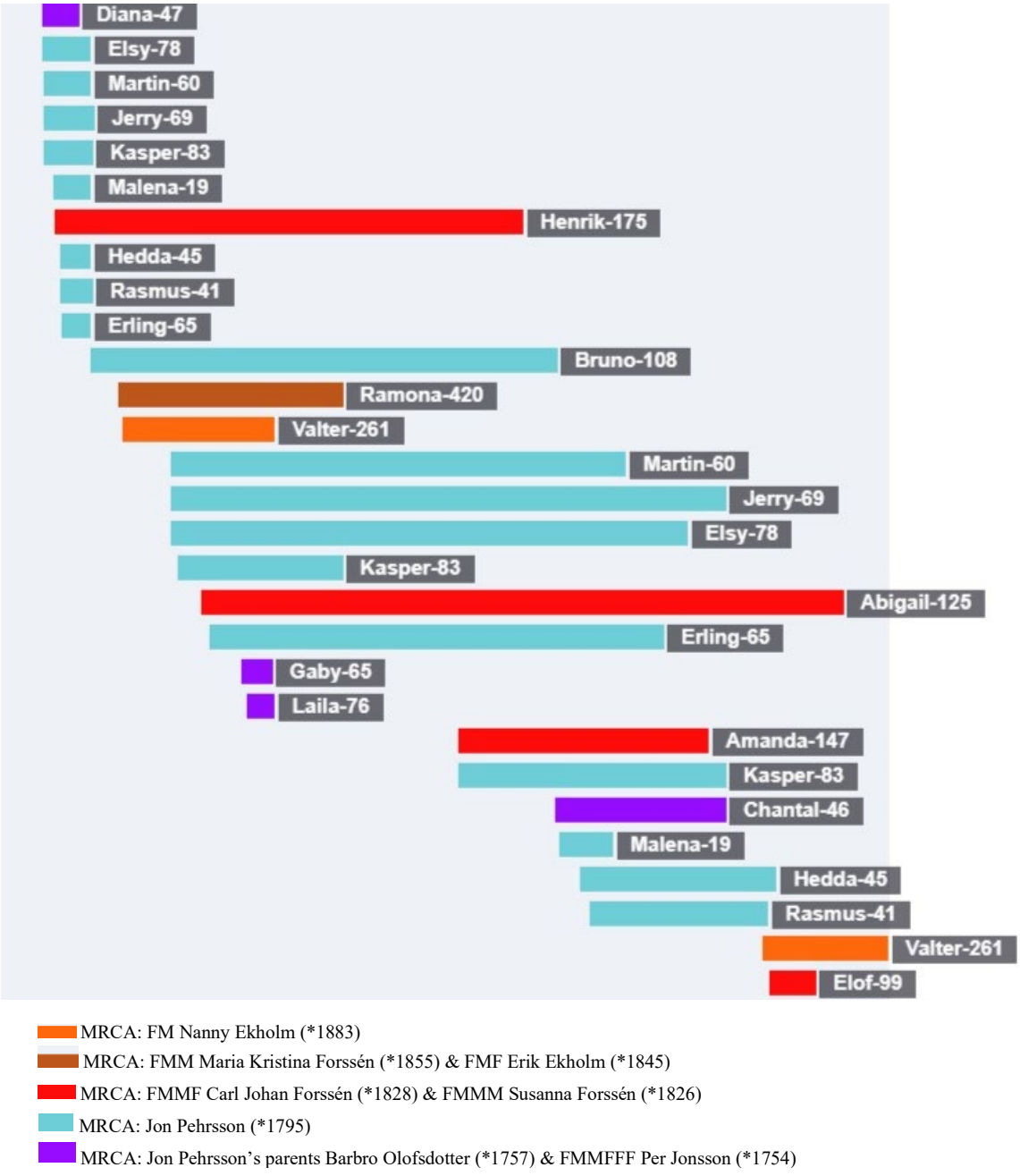
As seen in Table 6 and as illustrated in Figure 4, overlaps of DNA with six of Carl Johan Forssén's (*1828) descendants were found to *also* overlap with DNA of nine of Jon Pehrsson's (*1795) descendants on chromosome 16. Figure 4 shows the DNA segments shared with descendants of Jon Pehrsson (*1795) in blue colour (and his parents in purple), and segments shared with descendants of Carl Johan Forssén (*1828) in red (third cousins), brown (second cousin) or orange colour (first cousin level). As can be seen, the overlaps with these two groups of DNA matches cover a major part of chromosome 16, more specifically from location 4,171,701 to location location 78,883,118 (see also Table 6). The only two bits that are not covered by DNA segments that could be linked to descendants of *both* Jon Pehrsson and Carl Johan is the very first short part of the chromosome, from location 0 to location 4,171,701, and the very last part of the chromosome (from location 78,883,118 to the end of the chromosome). Although one of Carl Johan Forssén's descendants, *Valter-261*, shared this latter part of the chromosome with Brother 2 (and the very last part of it also with Brother 1), there was no evidence that any of Jon Pehrsson's children did.

The figure also shows some DNA matches with additional descendants of Jon Pehrsson's *parents* (*Diana-47, Gaby-65, Laila-76,* and *Chantal-46*) who shared small parts of these DNA segments on chromosome 16. They all turned out to be descendants of one of Jon Pehrsson's sisters. The relatively small number of these DNA matches, however, together with the relatively small DNA segments that were shared with them, gave no support for the possibility that his parents represented the most relevant genealogical junction.

The requirement of independent lineages among the DNA matches who shared segments on chromosome 16 was very well met. The nine descendants of Jon Pehrsson descended from three of his children (cf. table 6):

*Vilhelm Petter *1814* [*Hedda-45, Rasmus-41*]
*Erik *1820* [*Kasper-83, Elsy-78, Jerry-69, Erling-65, Martin-60, Malena-19*]
*Johan *1835* [*Bruno-108*]

Figure 4.
DNA segments on chromosome 16 (from location 4,171,701 to location 90,233,487) shared between Brother 2 and descendants of Jon Pehrsson (in blue) and his siblings (in purple) and descendants of Carl Johan Forssén (in shades of red, orange and brown depending on their most recent common ancestors [MRCA]), as depicted by DNA Painter based on data from the chromosome browser in MyHeritage.



The six descendants of Carl Johan Forssén similarly could be divided into independent lineages via four of his children (cf. table 5):

*Maria Kristina *1855* [*Ramona-420, Valter-261*]
*Susanna Sofia *1857* [*Henrik-175, Amanda-147*]
*Karl *1860* [*Abigail-125*]
*Johan Petter *1862* [*Elof-99*]

The hypothesis was further strengthened by the fact that this segment triangulation involved intermediate MRCAs (Bartlett, 2016) covering three generation before reaching Jon Pehrsson (*1795) at generation 5:

Generation 2 [*Valter-261*; MRCA the author's FM]
Generation 3 [*Ramona-420*; MRCA the author's FMF/FMM]
Generation 4 [*Henrik-175, Amanda-147, Abigail-125, Elof-99*; MRCA the author's FMMF/FMMM]

This makes it possible to construct a hypothetical history of the major part of this chromosome from location 4,171,701 to location 78,883,118, as Brother 2 shared DNA *both* with descendants of Jon Pehrsson (*1795) and with descendants of Carl Johan Forssén (*1828) on this entire part of the chromosome. If this hypothesis were correct it would mean that the major part of this chromosome was derived from Jon Pehrsson (*1795) and had been transferred to his son Carl Johan Forssén (*1828), and from him to his daughter Maria Kristina Forssén (*1855), and in turn to her daughter Nanny Elina Ekholm (*1883), to her son (the author's F), and to his son Brother 2. Almost none of this DNA, however, was transferred to Brother 1, who instead received almost the whole of his corresponding chromosome 16 from the author's FF (see above in section 3.4.4).

In other words, if this were true it would mean that a large DNA segment covering a major part of this chromosome had been transferred relatively intact during five generations from Jon Pehrsson (*1795) to Brother 2 but had been completely lost to Brother 1 in the last stage of this process. Although Brother 1 shared 15 cM with Brother 2 on this chromosome, this small segment was located at the very end of the chromosome (from location 85,206,943 to 90,233,487) and although it was shared with *Valter-261* it showed no evidence of being shared with any descendant of Jon Pehrsson.

Although these results are entirely in line with the hypothesis, it is important to note that they do not in any way *prove* that Jon Pehrsson was the father of Carl Johan Forssén. For example, the results of the segment triangulation as such are equally theoretically compatible with the possibility that Jon Pehrsson was the father of Carl Johan's wife Susanna Forssén (*1826). All six descendants of Carl Johan Forssén that were presented in Figure 4 were of course, also descendants of Susanna Forssén. The DNA data presented in Table 4 can in no way differentiate between the hypothesis that Jon Pehrsson was the father of Carl Johan and the alternative hypothesis that he was the father of Susanna. *In combination with other data*, however, it appears that the Carl Johan hypothesis is much more likely to be true than the Susanna hypothesis. Most importantly, (1) Carl Johan's father was unknown, whereas Susanna's father is given in the population registers as Erik Eriksson Forssén (*1786); (2) Jon Pehrsson was a close neighbour to Carl Johan's mother in Pengsjö at the time when she got pregnant, whereas Susanna was from another village, Överboda, about ten kilometers to the east of Pengsjö. These demographic data make it much more *likely* that Jon Pehrsson was the father of Carl Johan than the father of Susanna.

Before leaving the analysis of the DNA segment at chromosome 16 it may be noted that of the three originally unplaced DNA matches, *Cesar-128, Bruno-108* and *Bianca-102,* who had Jon Pehrsson (*1795) as their ancestor (see Table 1 above, and section 3.2.4), only one (*Bruno-108*) shared DNA on chromosome 16 (a large segment of 51 cM). *Cesar-128* and *Bianca-102,* on the other hand, shared large segments with both brothers on

chromosome 1 and with Brother 1 on chromosome 12. The segment triangulations on these two chromosomes are described in the next two sections. Because there was some evidence that the DNA segment on chromosome 16 could be traced further back in time to Jon Pehrsson's parents, the family trees of other DNA matches who shared part of the segments on chromosomes 1 and 12 were also studied to see if they included close ancestors to Jon Pehrsson (*1795).

3.5.3. Segment triangulation on chromosome 1

Figure 5 depicts a large part of chromosome 1, from location 88,794,011 to the end of the chromosome. On this part of the chromosome, DNA segments were shared with two of Carl Johan Forssén's descendants (*Ramona-420* and *Robin-219;* marked in brown) and with several descendants of Jon Pehrsson (including the two strongest DNA matches, *Cesar-128* and *Bianca-102;* marked in blue), and also with some descendants of Jon Pehrsson's close maternal ancestors (marked in other shades of blue). In total, 16 descendants of Jon Pehrsson were found who shared segments on this part of the chromosome. Segment triangulations in support of the hypothesis were found for seven of them, including *Bianca-102,* who shared a large DNA-segment (62 cM) with brothers 1 and 2, parts of which were also shared with *Ramona-420* and *Robin-219* (see also Table 6). For *Cesar-128* and eight other Jon Pehrsson-descendants in the right part of the figure, however, no Carl Johan-descendants could be found that shared DNA with them on that part of the chromosome.

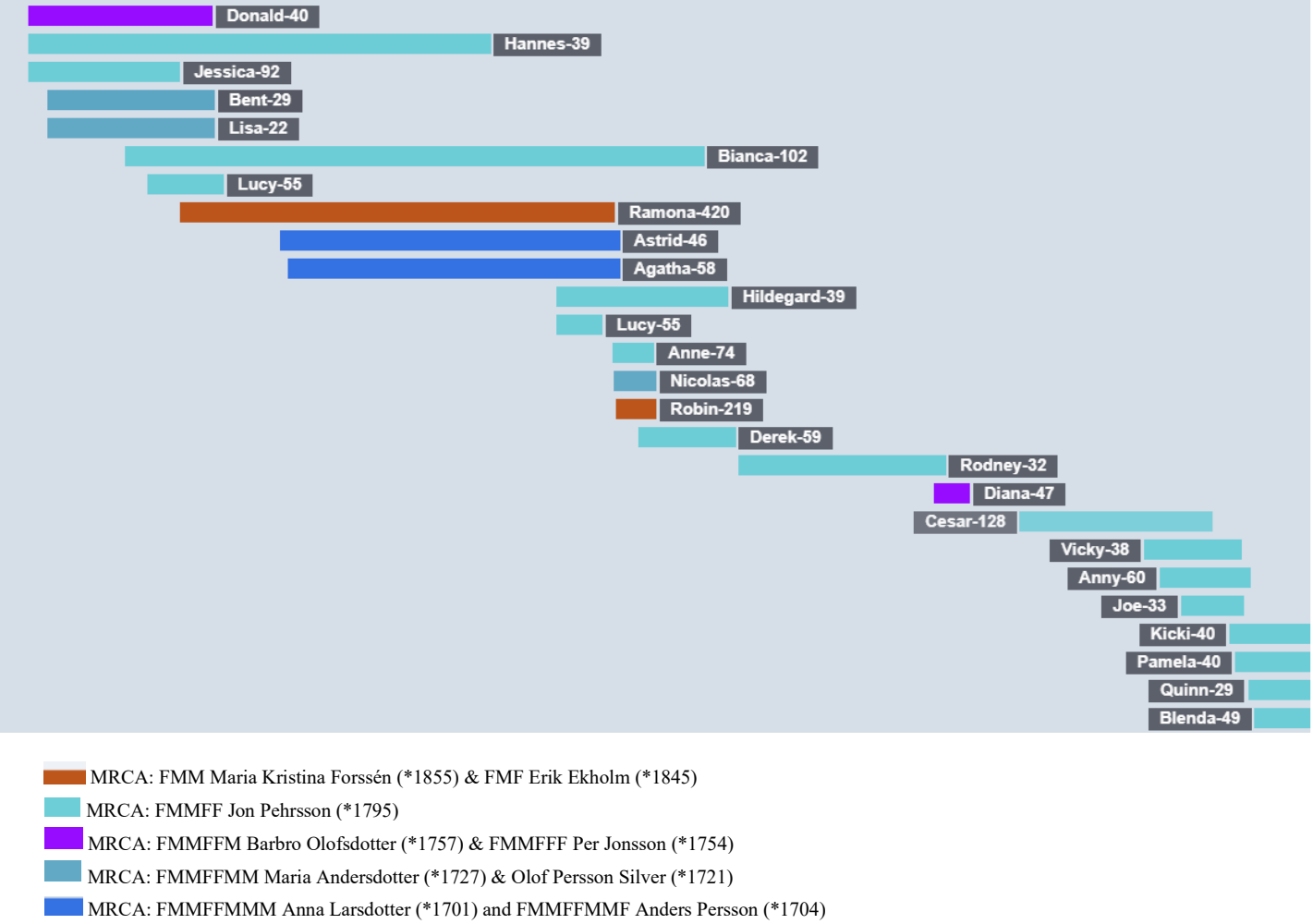
This means that, although the segment triangulation on chromosome 1 is clearly in line with the hypothesis, it does not provide equally strong evidence. Only two descendants of Carl Johan (*Ramona-420* and *Robin-219*) were found that shared the segment with *Bianca-102* and the six other Jon Pehrsson-descendants in the left part of the figure, and they were both related to the author at the second cousin level. No third cousin descendants of Carl Johan Forssén were found who shared DNA on this part of the chromosome. This leaves a gap of one generation in the analysis of this DNA segment, which theoretically makes room for other alternative hypotheses, as for example that Jon Pehrsson was an ancestor of the author's FMF Erik Ekholm (*1845). In other words, *the range of alternative hypotheses* are larger here than for the DNA segment on chromosome 16 (which was shared by four matches at the third cousin level).

In combination with other kinds of data (e.g., Jon Pehrsson being a neighbor to Carl Johan Forssén's mother in Pengsjö at the time she got pregnant), these alternative hypotheses still appear much less likely. Also, despite this increased uncertainty about how to interpret the segment triangulation in this case, the picture given in Figure 5 suggests the possibility that the entire chromosome from location 88,794,011 (where the segment shared with *Hannes-39* starts; see Table 6) to its end might derive from Jon Pehrsson (*1795). Sixteen of his descendants were found that "cover" that entire part of the chromosome, and Jon Pehrsson was the MRCA in all these cases.

The condition of independent lineages was well met. The seven descendants of Jon Pehrsson (*1795) that were part of the segment triangulation (in the left part of Figure 5) descended from three different children of his (cf. Table 6):

*Vilhelm Petter *1814* [*Derek-59, Lucy-55, Hannes-39, Hildegard-39*]
*Erik *1820* [*Anne-74*]
*Johan *1835* [*Bianca-102, Jessica-92*]

Figure 5.
DNA segments on chromosome 1 that the two brothers shared with descendants of Carl Johan Forssén (in red) and/or with descendants of Jon Pehrsson's children and his maternal ancestors (in various shades of blue depending on their most recent common ancestors [MRCA]), as depicted by DNA Painter based on data from the chromosome browser in MyHeritage.



Some evidence also suggested that at least part of this DNA segment could be traced further back in time. As seen in Figure 5, Jon Pehrssons parents Barbro Olofsdotter (*1757) and Per Jonsson (*1754) were found to be the MRCAs of two DNA matches who shared part of the segment: *Donald-40* and *Diana-47*. Also, one generation further back in time, John Persson's maternal grandparents Maria Andersdotter (*1727) and Olof Persson Silver (*1721) were found to be the MRCAs of two additional DNA matches: *Astrid-46* and *Agatha-58*. And yet another generation back in time, two other matches were found to have Jon Pehrsson's mother's maternal grandparents Anna Larsdotter (*1701) and FMMFFMMF Anders Persson (*1704) in their pedigrees: *Bent-29* and *Lisa-22*. This is not only consistent with the hypothesis that the DNA segment on chromosome 1 derived from Jon Pehrsson (*1795), but it also suggests that it might be quite possible to trace DNA segments many generations back in time, at least in some cases.

Further corroboration of this possibility was found when a systematic search was engaged in for DNA matches who shared more than 15 cM of the segment from location 88,129,038 to location 146,672,906 on chromosome

1. The reason for engaging in this "side project" was that some rather strong DNA matches who bordered on the category of "closest unplaced DNA matches" (see section 3.1) shared rather large DNA segments with brothers 1 and 2 on this part of the chromosome. Most notably, *Filip-95* shared 38 cM of this segment. A search of his pedigree showed that the MRCA with *Filip-95* seemed to be Anna Larsdotter's (*1701) parents Märeta Mattsdotter *(1678 in Armsjö, Nordmaling) and Lars Olofsson (*1675 in Bergsjö, Nordmaling). This couple was Jon Pehrsson's (*1795) MMMM and MMMF, and in other words nine generations back in time from the author.

Surprisingly, a systematic search for other DNA matches who shared more than 15 cM of the segment shared with *Filip-95* led to the identification of 43 additional matches. Of these 32 had Märeta Mattsdotter (*1678) and Lars Olofsson (*1675) in their pedigrees (in most cases as the MRCA), and ten further matches had Märeta Mattsdotter's (*1675) father Matts Hindersson (*around 1618)[3]. Only one of the 43 matches fell outside the picture, as no CA with her could be found (possibly because her mother's paternal grandfather was unknown). Figure 6 describes these DNA segments. This figure represents an expansion of Figure 5 with a focus on the specific region of chromosome 1 from location 88,129,038 to location 146,672,906, and including DNA matches with MRCAs two more generations back in time.

Typically, the size of DNA segments shared with *closer* cousins tend to be larger than the segments shared with more *distant* cousins. But here the size of the segments shared with descendants of Märeta Mattsdotter (*1678) and her husband tended to be *larger* than those shared with her daughter Anna Larsdotter (*1701), her granddaughter Maria Andersdotter (*1727), and her great granddaughter Barbro Olofsdotter (*1757). So many as 12 of the 32 DNA matches where Märeta and her husband appeared as MRCA were larger than 30 cM. Furthermore, many more DNA matches were found who shared this DNA segment with Märeta Mattsdotter than with her descendants in Jon Pehrsson's (*1795) maternal ancestral line: 32 matches as compared with only a few in each generation after her. This raises several questions for further research.

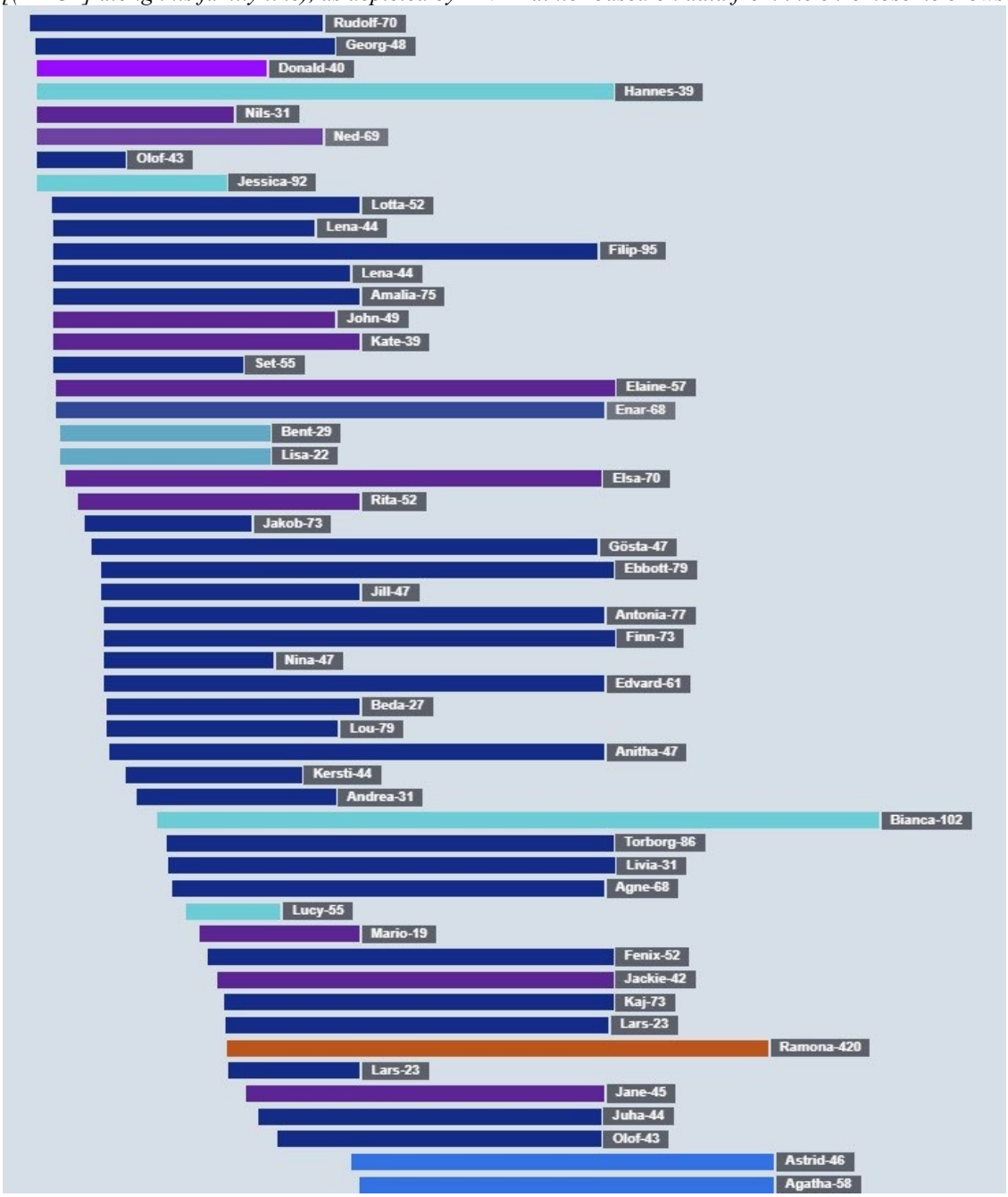
One possible contributing factor would be pedigree collapse among the DNA matches. Examples of this were found among several of these DNA matches. To take one of the more extreme examples: *Ebbott-79* shared 33 cM of this DNA segment, and Märeta Mattsdotter (*1678) and Lars Olofsson (*1675) were the most recent common ancestors (MRCA) that could be found in his pedigree. Moreover, this couple was found in nine places (eight generations back in four cases, and nine generations back in five cases) in his pedigree. In terms of genealogical relationships with *Ebbot-79* this means that he was a 4 x 7th cousin-1R and 5 x 8th cousin via Märeta Mattsdotter and her husband. In addition, Märeta's siblings and half siblings were found in 14 more places in his pedigree, which means that *Ebbott-79* was also the author's cousin via Matts Hindersson (*1618) in fourteen additional cases. This might have contributed to the amount of DNA shared with *Ebbot-79* both on chromosome 1 (33 cM) and in total (79 cM).

This could hardly be the full explanation of the present findings, however, because several other of these DNA matches apparently had only one lineage to Märeta Mattsdotter and her husband. For example, *Filip-95* who was the DNA match in this group who shared the largest amount of DNA with the author and his brother, apparently had Märeta Mattsdotter and her husband only at one place in his pedigree.

[3] Only her father, not her mother, is mentioned here because the lineages from Matts Hindersson (*1618) involved children from his two marriages.

Figure 6.

DNA segments on chromosome 1 that Brothers 1 and 2 shared with descendants of Carl Johan Forssén (in brown) and descendants of Jon Pehrsson's children and his maternal ancestors (in various shades of blue depending on their most recent common ancestors [(MRCA] along this family line), as depicted by DNA Painter based on data from the chromosome browser in MyHeritage



MRCA: FMM Maria Kristina Forssén (*1855) & FMF Erik Ekholm (*1845)
MRCA: FMMFF Jon Pehrsson (*1795)
MRCA: FMMFFM Barbro Olofsdotter (*1757) & FMMFFF Per Jonsson (*1754)
MRCA: FMMFFMM Maria Andersdotter (*1727) & Olof Persson Silver (*1721)
MRCA: FMMFFMMM Anna Larsdotter (*1701) & FMMFFMMF Anders Persson (*1704)
MRCA: FMMFFMMMM Märeta Mattsdotter (*1678) & FMMFFMMMF Lars Olofsson (*1675)
CA: FMMFFMMMMF Matts Hindersson (*around 1618)

Another possibility in terms of pedigree collapse would be that Märeta Mattsdotter (*1678) and Lars Olofsson (*1675) were ancestors to the author also via some additional linages/lineages. Although this couple could not be found anywhere else in the author's pedigree, Märeta's half-sister Elisabet Mattsdotter (*1661) was found in his FF branch as the FF's FMFFMFM, which means that their father Matts Hindersson (*around 1618) was an ancestor both to the author's FF and his FM at ten generations distance.

Perhaps even more relevant here was the possibility that Märeta Mattsdotter and her husband might have an additional place somewhere in the author's pedigree, via unknown ancestors further back in time. Most notably, the father of Carl Johan Forssén's (*1828) MMF Hans Jonsson Tiger (*1742) was unknown, as were also the parents of his wife Magdalena Eriksdotter (*around 1742). The possibility of a connection here was suggested by the fact that three of the DNA matches in Figure 6 (*Elaine-57, John-49*, and *Kate-39*) had the Hans/Magdalena couple as MRCA in their pedigrees. They are depicted in the figure as having Matts Hindersson (*around 1618) as their CA (*not* MRCA), but in view of the relatively large segments they shared (37 cM, 31 cM, and 30 cM, respectively) it seemed more likely that the explanation might go via their MRCA, who were three generations closer in time. If so, however, this would require some genealogical connection between the Hans/Magdalena couple and the Märeta/Lars couple.

3.5.4. Segment triangulation on chromosome 12

Figure 7.
DNA segments on chromosome 12 that Brother 1 shared with descendants of Jon Pehrsson's children and his maternal ancestors (in various shades of blue depending on their most recent common ancestors [MRCA]) and descendants of Carl Johan Forssén (in brown), as depicted by DNA Painter based on data from the chromosome browser in MyHeritage.

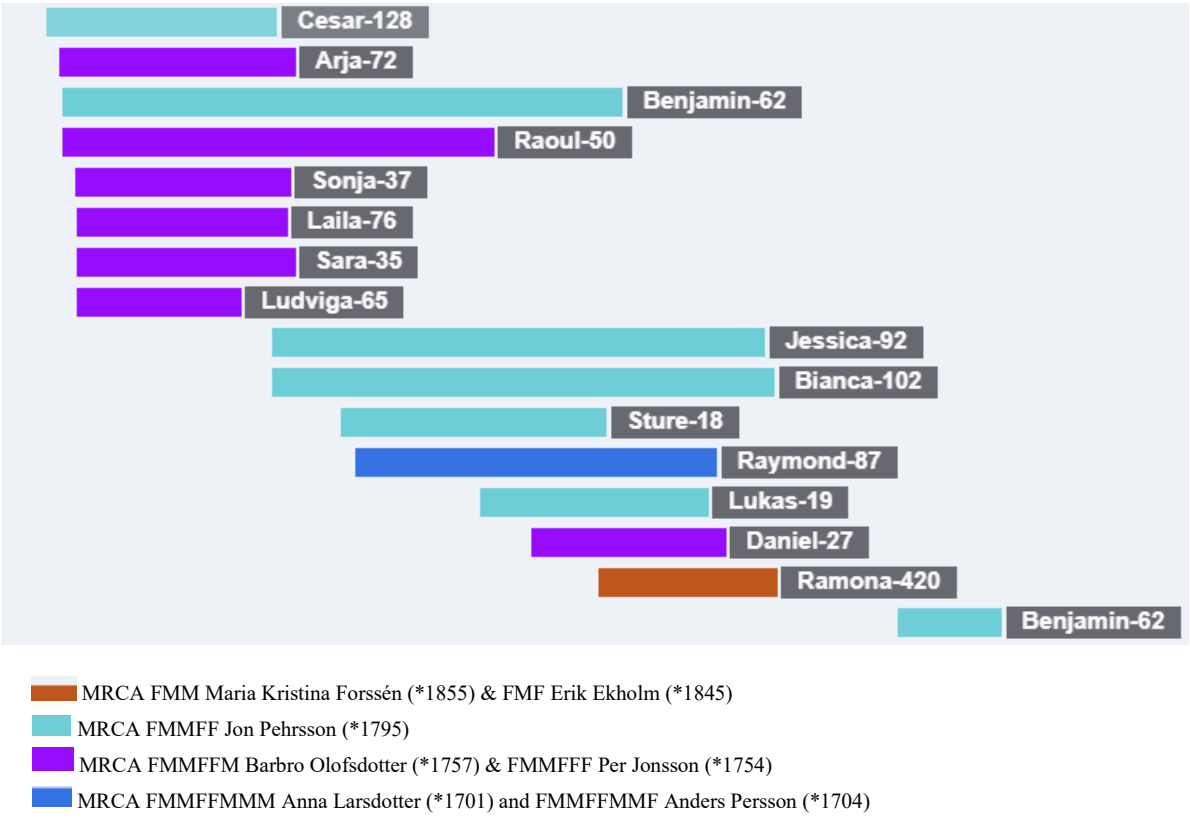


Figure 7 describes the segment triangulation on chromosome 12. As shown in the figure, this segment triangulation involved only one descendant of Carl Johan Forssén (*1828), *Ramona-420,* who shared a relatively small part of the segment (17 cM). This was in stark contrast to the relatively large segments shared with descendants of Jon Pehrsson (*1795): 55 cM with *Benjamin-62*, 40 cM with *Bianca-102*, 38 cM with *Jessica-92*, and 34 cM with *Cesar-128*.

Yet the condition of independent lineages was well met also here; the six descendants of Jon Pehrsson (*1795) who were part of the segment triangulation descended from three of his children (cf. Table 6):

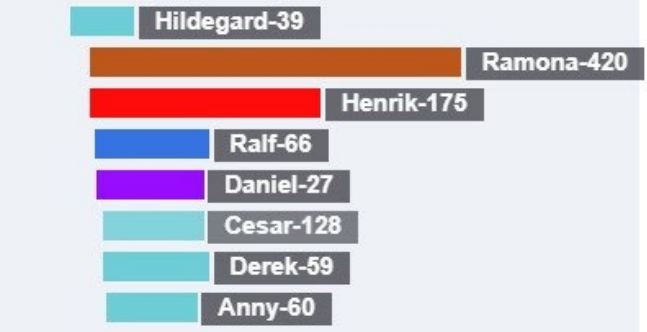
*Erik *1820* [*Cesar-128, Benjamin-62, Sture-18*]
*Anna Margareta *1821* [*Lukas-19*]
*Johan *1835* [*Bianca-102, Jessica-92*]

As seen in Figure 7, the triangulations also involved several DNA matches who had Jon Pehrsson's parents and maternal grandparents as their MRCAs, which was consistent with the hypothesis. On the other hand, the condition of intermediate MRCAs was not met (no 3rd cousins were found who shared parts of the segment), which means that this segment triangulation considered in isolation represented rather weak evidence of the hypothesis.

3.5.5. Segment triangulation on chromosome 6

Figure 8 shows the segment triangulation on chromosome 8. Here the condition of intermediate MRCAs was met, as the segment was shared by both second and third cousins.

Figure 8.
DNA segments on chromosome 6 that Brother 1 shared with descendants of Jon Pehrsson and his maternal ancestors (in various shades of blue depending on their most recent common ancestors (MRCA) and with descendants of Carl Johan Forssén (in red and brown), as depicted by DNA Painter based on data from the chromosome browser in MyHeritage.



MRCA: FMM Maria Kristina Forssén (*1855) & FMF Erik Ekholm (*1845)
MRCA: FMMF Carl Johan Forssén (*1828) & FMMM Susanna Forssén (*1826)
MRCA: FMMFF Jon Pehrsson (*1795)
MRCA: FMMFFM Barbro Olofsdotter (*1757) & FMMFFF Per Jonsson (*1754)
MRCA: FMMFFMMM Anna Larsdotter (*1701) and FMMFFMMF Anders Persson (*1704)

As to the segment triangulation on chromosome 6 (see Figure 8) it also met the condition of independent lineages quite well. The four descendants of Jon Pehrsson (*1795) who were part of the segment triangulation descended from three different children of his (cf. Table 6):

*Erik *1820* [*Cesar-128*]
*Vilhelm Petter *1814* [*Hildegard-39, Derek-59*]
*Johan *1835* [*Anny-60*]

Further, some DNA matches with Jon Pehrsson's (*1795) maternal ancestors were also found to share DNA on this segment, which was clearly in line with the hypothesis.

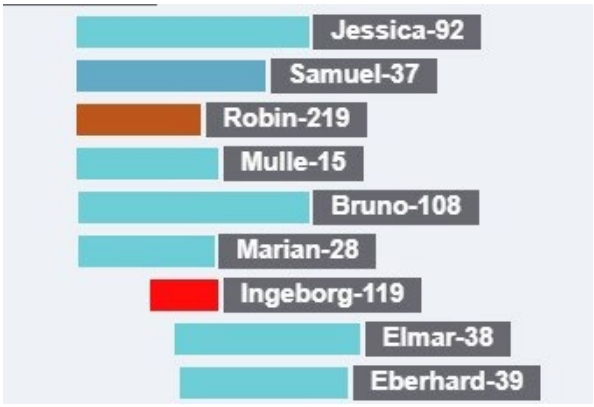
3.5.5. Segment triangulation on chromosome 13

Finally, as to the segment triangulation on chromosome 13, the situation was rather similar to that on chromosome 6. The condition of independent lineages was well met as the six descendants of Jon Pehrsson (*1795) who were part of the segment triangulation descended from three different children (cf. Table 6):

*Erik *1820* [*Elmar-38, Eberhard-39*]
*Cajsa Lisa *1828* [*Mulle-15, Marian-28*]
*Johan *1835* [*Jessica-92, Bruno-108*]

The condition of intermediate MRCAs was also met. As seen in Figure 9, the triangulation involved descendants of Carl Johan Forssén (*1828) at both the second cousin and third cousin level.

Figure 9.
DNA segments on chromosome 13 that Brother 1 shared with descendants of Jon Pehrsson and his maternal ancestors (in various shades of blue depending on their most recent common ancestors [MRCA] and with descendants of Carl Johan Forssén (in red and brown), as depicted by DNA Painter based on data from the chromosome browser in MyHeritage.



MRCA: FM Nanny Ekholm (*1883)
MRCA: FMM Maria Kristina Forssén (*1855) & FMF Erik Ekholm (*1845)
MRCA: FMMF Carl Johan Forssén (*1828) & FMMM Susanna Forssén (*1826)
MRCA: FMMFF Jon Pehrsson (*1795)
MRCA: FMMFFMM Maria Andersdotter (*1727) & Olof Persson Silver (*1721)

To summarize, the segment triangulations contributed considerable evidence in support of the FMMFF Jon Pehrsson hypothesis. In combination with demographic data showing that Jon Pehrsson was a close neighbour to Greta Stina Olofsdotter (*1800) at the time when she got pregnant with her son Carl Johan (*1828), the large number of segment triangulations (and especially the triangulation on chromosome 16) presents a strong case for Jon Pehrsson being the father of Carl Johan.

3.6. Evaluation of the genealogical junctions method

In the present study, the analysis of genealogical junctions led to the identification of genealogical relationships to previously unplaced DNA matches, and to the filling of several gaps in the author's pedigree. But it did not lead to the identification of the genealogical relationships to *all* unplaced DNA matches, and it did not *directly* identify all ancestors that were searched for. The present section focuses on these apparent shortcomings, first with regards to the unplaced DNA matches, and then with regards to the newly identified ancestors.

3.6.1. The previously unplaced DNA matches

Table 1 above contained a list of 19 unplaced DNA matches. Table 7 describes the genealogical relationships that were discovered to these persons as results of the analysis.

Table 7.
The previously unplaced DNA matches of the two brothers, and genealogical relationships that were established to them.

Code namn	*Genealogical relationship*	*Most recent common ancestors (MRCA)*
Sofia-150	3rd cousin	Johan Petter Johansson (*1819) & Maria Karolina Mattsdotter (*1829)
Thore-147		
Eivor-144	3rd cousin	Erik Olofsson (*1782) & Anna Katarina Jakobsdotter (*1788)
Maja-132	3rd cousin 1R	Matts Olofsson (*1806) & Maja Greta Andersdotter (*1803)
Cesar-128	half 4th cousin	Jon Pehrsson (*1795)
Willy-124		
Igor-124	3rd cousin	Johan Petter Johansson (*1819) & Maria Karolina Mattsdotter (*1829)
George-122	4th cousin	Erik Olofsson (*1782) & Anna Katarina Jakobsdotter (*1788)
Austin-120	4th cousin	Erik Olofsson (*1782) & Anna Katarina Jakobsdotter (*1788)
Tora-116	4th cousin	Matts Olofsson (*1806) & Maja Greta Andersdotter (*1803)
Clara-114	3rd cousin 1R	Johan Petter Johansson (*1819) & Maria Karolina Mattsdotter (*1829)
Axel-112		
Elisabeth-115	4th cousin	Matts Olofsson (*1806) & Maja Greta Andersdotter (*1803)
Marcus-111	4th cousin	Matts Olofsson (*1806) & Maja Greta Andersdotter (*1803)
Bruno-108	half 3rd cousin 1R	Jon Pehrsson (*1795)
Ellie-106		
Bianca-102	half 5th cousin 1R	Jon Pehrsson (*1795)
Ludvig-101	4th cousin 1R	Matts Olofsson (*1806) & Maja Greta Andersdotter (*1803)
Elvira-101	4th cousin	Erik Olofsson (*1782) & Anna Katarina Jakobsdotter (*1788)

As can be seen in Table 7, fifteen of these 19 previously unplaced DNA matches were found to be either 3rd, 4th, or 5th cousins, one step removed at most. Four of them, however, remained unplaced: *Thore-147, Willy-124, Axel-112,* and *Ellie-106*. As to *Thore-147,* this was most probably due to his FFF being unknown. *Thore-147*'s FF and FFM, however, were from Nordmaling parish, and he shared considerable amounts of DNA with several other of the author's closest matches on the FF side: 102 cM with *Niklas-290*, 138 cM with *Maja-132*, 109 cM with *Ludvig-101*, and 154 cM with *Saga-91*. A reasonable hypothesis was that the relationship with *Thore-147* went

via his unknown FFF, which in that case probably would make him a 2nd cousin-1R, a 3rd cousin, or maybe a 3rd cousin-1R.

A closer investigation of the family trees of *Willy-124* and *Axel-112* also led to the identification of genealogical relationships that might explain the amount of DNA shared with them. As to *Willy-142*, he turned out to be related to the author in multiple ways. First, he was the author's 5th cousin one step removed via *the parents of* Anna Katarina Jakobsdotter (*1788) from GJ-2. Second, *Willy-142* was the author's fourfold 7th cousin via one couple from the author's FM branch (i.e., a case of pedigree collapse, as this couple appeared at four slots in *Willy-142's* family tree). A close inspection of the DNA segments that were shared with *Willy-142* revealed that the author shared DNA with him both via FF and FM. These multiple genealogical relationships seemed to be a reasonable explanation of the total amount of DNA that was shared.

As to *Axel-112*, he turned out to be the author's 5th cousin in two different ways: (1) *via the parents* of Erik Olofsson (*1782) from GJ-2, and (2) *via the maternal grandparents* of Johan Petter Johansson (*1819) from GJ-3. This double 5th cousin relationship seemed to be a reasonable explanation of the total amount of DNA that was shared. Because these relationships were at the level of 5th cousins they could, by definition, not be detected by the analysis of genealogical junctions as it was defined in the present study.

Finally, as to *Ellie-106*, it was more difficult to find a likely explanation of the amount of DNA shared with her. No genealogical relationships even at a 5th cousin level could be found. The search for an MRCA with *Ellie-106* led to Jon Pehrsson's maternal grandparents, Maria Andersdotter (*1727) and Olof Persson Silver (*1721). The largest DNA segment shared with her (33 cM on chromosome 20) was shared by one descendant of FMMF Carl Johan Forssén (*Abigail-125*) and another descendant of Jon Pehrsson (*Jörgen-68*), which suggested that at least part of the DNA shared with *Ellie-106* came from Jon Pehrsson's mother's branch of the family tree. More specifically this meant that *Ellie-106* was the author's sixth cousin one step removed, but this seemed too far back in time to be a sufficient explanation of all the amount of DNA shared. A close inspection of her family tree also revealed some examples of pedigree collapse; for example, she was a threefold 7th cousin via the author's FMMFMFFF/ FMMFMFFM, who were found at three slots in her family tree. This suggested the possibility that the DNA shared with her resulted from multiple genealogical relationships via the FM branch.

3.6.2. The newly identified ancestors

One main result was that the many empty slots in the author's pedigree, as shown in Figure 1, were now filled. The resulting new pedigree is seen in Figure 9.

Figure 9.
The author's father's pedigree, as known at the end of the investigation

TWO GENERATIONS BACK FROM THE AUTHOR
FF: One of the Norberg brothers
FM: Nanny Elina Ekholm *1883-11-10 Nordåker, Vännäs †1948-09-03 Robertsfors

THREE GENERATIONS BACK
FFF: Erik Olof Norberg *1850-10-31 Lögdeå, Nordmaling †1935-02-14 Nordmaling
FFM: Klara Maria Johansdotter *1858-04-25 Ava, Nordmaling †1935-01-20 Lögdeå, Nordmaling
FMF: Erik Ekholm *1845-12-12 Östanå, Vännäs †1920-11-13 Hörneå, Hörnefors
FMM: Maria Kristina Forssén *1855-03-16 Överboda, Umeå †1915-09-16 Hörneå, Hörnefors

FOUR GENERATIONS BACK
FFFF: Olof Norberg Jonsson *1819-02-03 Pengsjö, Vännäs †1892-03-22 Lögdeå, Nordmaling

FFFM: Johanna Eriksdotter *1824-05-25 Mullsjö, Nordmaling †1854-03-20 Lögdeå, Nordmaling
FFMF: Johan Petter Johansson *1819-11-26 Ava, Nordmaling †1908-09-03 Ava, Nordmaling
FFMM: Maria Karolina Mattsdotter *1829-05-29 Ava, Nordmaling †1914-02-12 Ava, Nordmaling
FMFF: Johan Georg Ekholm *1821-06-13 Gumboda, Nysätra †1905-02-05 Nordåker, Vännäs
FMFM: Anna Anna Elisabet Lundberg *1820-09-19 Norrmjöle, Umeå †1886-11-18 Nordåker, Vännäs
FMMF: Carl Johan Forssén *1828-02-15 Björnlandsbäck, Vännäs †1865-06-08 Granlund, Vännäs
FMMM: Susanna Forssén *1826-06-24 Överboda, Umeå †1897-02-01 Granlund, Vännäs

FIVE GENERATIONS BACK
FFFFF: Jon Jonsson *1781-11-09 Pengsjö, Vännäs †1860-03-15 Pengsjö, Vännäs
FFFFM: Magdalena Eriksdotter Vänman *1786-07-20 Vännäs †1870-03-18 Pengsjö, Vännäs
FFFMF: Erik Olofsson *1782-09-05 Mullsjö, Nordmaling †1846-05-20 Mullsjö, Nordmaling
FFFMM: Anna Katarina Jakobsdotter *1788-03-24 Örsbäck, Nordmaling †1864-07-04 Mullsjö, Nordmaling
FFMFF: Johan Persson *1789-09-26 Gideåbacka, Grundsunda †1868-07-30 Ava, Nordmaling
FFMFM: Kristina Nilsdotter *1792-09-07 Rönnholm, Nordmaling †1855 Ava, Nordmaling
FFMMF: Matts Olofsson *1806-08-30 Bodum, Grundsunda †1863-06-18 Bodum
FFMMM: Maja Greta Andersdotter *1803-08-25 Långed, Nordmaling †1887-09-12 Ava, Nordmaling
FMFFF: Göran Johansson Ekholm *1789-12-31 Forsa †1859-04-14 Östanå, Vännäs
FMFFM: Margareta Larsdotter *1779-01-14 Gumboda, Nysätra †1841-07-29 Östanå, Vännäs
FMFMF: Fredrik Lundberg *1777-08-12 Korsholm, Vasa, Finland † 1837-10-19 Norrmjöle, Umeå
FMFMF: Lisa Greta Persdotter *1779-09-14 Gubböle 2, Umeå † 1851-02-14 Norrmjöle, Umeå
FMMFF: Jon Pehrsson *1795-09-24 Berg, Vännäs †1889-03-03 Brännland, Bjurholm
FMMFM: Greta Stina Olofsdotter *1800-01-29 Hjuken, Vindeln †1890-09-11 Nylandsnäs, Vännäs
FMMMF: Erik Eriksson Forssén *1786-02-07 Nyåker, Nordmaling †1867-12-12 Överboda, Umeå
FMMMM: Charlotta Andersdotter *1790-05-22 Överboda, Umeå

Focusing on the sixteen ancestors five generations back in time, as seen in Figure 9, only seven of them were known before this study (see Figure 1), whereas nine were missing. Of these nine previously unknown ancestors seven appeared in the analysis of genealogical junctions: FFFMF/FFFMM Erik Olofsson (*1782) and Anna-Karin Jakobsdotter (*1788) in GJ-2; FFMFF/FFMFM Johan Persson (*1789) and Kristina Nilsdotter (*1792) as being the parents of the Johan Petter Johansson (*1819) in GJ-3; FFMMF/FFMMM Matts Olofsson (*1806) and Maja Greta Andersdotter (*1803) in GJ-1; and FMMFF Jon Pehrsson (*1795) in GJ-4. The fact remains, however, that one of the couples at the distance of 5 generations was *not* found in the analysis of genealogical junctions: the couple FFFFF/FFFFM Jon Jonsson (*1781) and Magdalena Eriksdotter Vänman (*1786).

This gives rise to some questions of relevance for understanding the reliability and sensitivity of the analysis of genealogical junctions. A first question is why the FFFFF/FFFFM couple was not found in this analysis. A second question is if they could have been found with a lower cut-off for including unplaced DNA matches (i.e., lower than 100 cM).

One possible explanation why a certain couple is not found in this kind of analysis is that they have fewer descendants that could test their DNA and is therefore less likely to appear in the family trees of DNA matches. This, however, did not seem to the case here. The couple FFFFF/FFFFM Jon Jonsson (*1781) and Magdalena Eriksdotter Vänman (*1786) had eight children, of which seven formed their own families, and altogether they had 62 grandchildren. This was not lower than those of the couples in genealogical junctions 1-4 (see section 3.2).

An exploration of the family trees of the unplaced DNA matches showed that only one of them, *Eivor-144*, did have the FFFFF/FFFFM couple Jon Jonsson (*1781) and Magdalena Eriksdotter Vänman (*1786) in her family tree. This did not pass the cut-off for genealogical junctions, which required that at least two unplaced DNA matches should have the couple in their family trees. In fact, the cut-off would have to be lowered all the way to 86 cM to make this couple a genealogical junction. With such a lowered cut-off, *Lola-86* had also been included among the unplaced DNA matches, as she had the FFFFF/FFFFM couple at two different places in her family tree.

On the other hand, a lowering of the cut-off to 86 cM would probably also have led to the identification of other genealogical junctions that might not be relevant to the author's family tree. In other words, it would probably have led to false positives (i.e., the identification of couples who were common ancestors to two or more unplaced DNA matches without having any place in the author's family tree).

Finally, the method of analyzing genealogical junctions was also tested by exploring if it could have identified ancestors on the FM side, if that had been the task. This was clearly so in the case of the FM's mother's family, as eight of the closest DNA matches (with a cut-off of 100 cM) had FMMF Carl Johan Forssén (*1828) and FMMM Susanna Forssén (*1826) in their family trees. This was not equally clear, however, with the FM's father's family. Two of the closest DNA matches (>100 cM), *Linnea-112* and *Olivia-105*, did have the FMFMF/FMFMM couple Fredrik Lundberg (*1777) and Lisa Greta Persdotter (*1779) in their family trees. But only one of them, *Olivia-105*, also had the FMFFF/FMFFM couple Göran Johansson Ekholm (*1789) and Margareta Larsdotter (*1779) in her tree.

This means that the latter couple would not have been identified by an analysis of genealogical junctions. Moreover, it would not have helped to lower the cut-off in this case, as the author was not able to find any additional DNA match who had this couple in their family tree even with as low a cut-off as 50 cM. One possible explanation was that the FMFFF/FMFFM couple had fewer living descendants that could test their DNA. In fact, they had six children, of which only three grew up to form their own families, and altogether 19 grandchildren. This was well below all the other ancestors at the same generational distance (see section 3.2).

4. DISCUSSION

The analysis of genealogical junctions proved to be a successful method in the present study. Not only did it lead to the identification of the family of origin of the author's paternal grandfather (the Norberg family) but also to the identification of a person who most probably was the author's FMMFF: Jon Pehrsson (*1795). Admittedly, the analysis failed to identify specifically who among the Norberg brothers was the FF, but this was not due to any weakness of the method but to the fact that three of the FF candidates did not have any known children and therefore no living descendants who could test their DNA.

4.1 Evidence and proof

Genealogists sometimes ask for "proof" in these matters. *Proofs*, however, belong to mathematics and formal logic and not to empirical sciences such as genetic genealogy. What matters in the empirical sciences is *evidence*. Evidence may vary in strength, but never attains the status of proofs in the strict sense of the word, because it is always possible to imagine alternative hypotheses that are logically possible even when they are extremely unlikely. In the present study, the evidence for the FF Norberg hypothesis was quite strong. The Norberg hypothesis was supported by (1) the interconnectedness of three different genealogical junctions (GJ1, GJ2, and GJ3) which covered most of the author's closest unplaced DNA matches and converged in one specific family, the Norberg family, (2) atDNA testing of four of five available Norberg descendants, (3) Y-DNA testing of one of the Norberg descendants, and (4) segment triangulation.

Still, it is possible to imagine alternative hypotheses that are compatible with the findings, although they may seem extremely unlikely. For example, it is logically possible that the mother in the Norberg family, Klara Maria Johansdotter (*1858), had an unknown sister (it must be an *unknown* sister, because according to the records she

had only two brothers, no sister) who for some reason was sent away to be raised in another family. Suppose that the father in the Norberg family, Erik Olof Norberg (*1850), met this unknown sister and they had a child together, and that this child grew up to be a man who was the real FF. This would explain all the available data equally well as the Norberg hypothesis, although it may seem to be an extremely unlikely hypothesis. It is probably possible to construct several other far-fetched logical possibilities. Furthermore, it cannot be completely ruled out that new data might be revealed that would change the picture and make an alternative hypothesis plausible.

In this perspective, it may be worth remembering that the success in this part of the study came after repeated failures to identify the FF in several other ways, based on suggestions from relatives to the foster family and attempts from representatives of the municipality, as well as the author's own search for possible candidates in the FM's vicinity. It needs to be emphasized that the success of the Norberg hypothesis was based *entirely* on genetic-genealogical data, as there was no other evidence even of a meeting between the author's FM and any of the Norberg brothers. No social connections were found between the FM and the Norberg family, and this family could probably never have been identified via any other sources. Yet the Norberg hypothesis was supported both by atDNA testing and a test of Y-DNA, which together represents very strong evidence in support of the hypothesis.

As to the identification of the FMMFF, the evidence is different. Here it is quite easy to find alternative hypotheses that are compatible with the genetic-genealogical data. For example, as already stated in section 3.5.2 on p. 27, the results of the segment triangulations are quite compatible with the possibility that Jon Pehrsson (*1795) was the father of the author's FMMM Susanna Forssén (*1826) rather than being the father of her husband FMMF Carl Johan (*1828). The DNA data from the segment triangulations cannot differentiate between these two hypotheses. *In combination with demographic data*, however, the Carl Johan hypothesis is much more likely to be true than the Susanna hypothesis. Most importantly, (1) Carl Johan's father was unknown, whereas this was not the case with Susanna's father; and (2) Jon Pehrsson was a close neighbour to Carl Johan's mother in Pengsjö at the time when she got pregnant, whereas Susanna was born in another village. These data make it much more *likely* that Jon Pehrsson was the father of Carl Johan than the father of Susanna.

The present results also illustrate the crucial importance of having one's siblings DNA tested. The most conclusive evidence of Jon Pehrsson (*1795) being the FMMFF was found on Brother 2's version of chromosome 16. On this chromosome, large convincing segment triangulations were found between nine descendants of Jon Pehrsson's children and six descendants of the author's FMMF Carl Johan Forssén (*1828). Moreover, these triangulations satisfied the conditions of independent lineages (i.e., going via three of Jon Pehrsson's other children) and the involvement of intermediate MRCAs at the level of 1st, 2nd, and 3rd cousins (cf. Bartlett, 2016; Thomas, 2021). Several triangulations on other chromosomes served to corroborate and strengthen the hypothesis even further.

4.2. The importance of the number of descendants

A more general consideration concerning the analysis of genealogical junctions is that it is clearly sensitive to the number of living descendants of a given ancestor. An illustration of this was found in the last part of the results section, where the method was tested on all the author's ancestors five generations back in time in the paternal branch of his family tree. Of these altogether sixteen ancestors, four (two couples) were not identifiable by the present kind of analysis of genealogical junctions. The method failed with regards to the FFFFF/FFFFM couple Jon Jonsson (*1781) and Magdalena Eriksdotter Vänman (*1786) and with regards to the FMFFF/FMFFM couple

Göran Johansson Ekholm (*1789) and Margareta Larsdotter (*1779). Each of these couples were found in only one family tree of the strongest DNA matches (i.e., those who passed the cut-off of >100 cM shared DNA).

As to the latter couple one part of the explanation most probably was that they had considerably fewer children and grandchildren and therefore fewer living descendants that could test their DNA. The following general principle seems to hold: *The fewer descendants an ancestor has, the fewer DNA matches will probably be found who has this ancestor in their family tree.* It is even quite possible that one shares considerable amounts of atDNA with a certain ancestor five generations back in time without this ever being *possible* to detect via atDNA testing. To see this one may consider the following thought experiment:

Suppose you have an ancestor five generations back in time, Carl Smith, who was born in 1795. Suppose further that this ancestor had several children, but only one of them, Jim Smith (*1828), survived to raise a family. Suppose further that of Jim's children in turn only two of them had children of their own, but only one of these, Carla Smith (*1855), had children of her own, and that only one of them in turn had children: a woman by the name of Anna Smith (*1883). Suppose that Anna Smith is your grandmother, and that she also had only one child: your father. In that case Carl Smith (*1795) would be your FMMFF, but he would have no other living descendants that could possibly test their DNA; you would be his only living descendant. In other words, he could not possibly be identified by any genetic-genealogical method.

Although this thought experiment may describe an extreme case that is probably rarely seen in the real world, such limiting cases may be important to establish general principles. And although such an extreme case may be rare, the important thing is that we may in principle find all kinds of intermediate cases between ancestors who have only one living descendant and ancestors who have thousands of descendants. Further, *the more descendants an ancestor has, the more DNA matches will probably be found who has this ancestor in their family tree.* In other words, if a certain ancestor appears often in the family trees of your atDNA matches, this may in principle be due simply to this ancestor *having many descendants*. A corollary to this is that you cannot conclude that a certain historical person belongs to your ancestors just because you find him or her in the family trees of many of your atDNA matches. An alternative explanation is simply that this person has many living descendants that have tested their atDNA.

This raises the possibility that one reason why Jon Pehrsson (*1795) was found in so *many* family trees of the author's atDNA matches was that he had many now living descendants who had tested their atDNA. In other words, the *number of DNA matches* who had Jon Pehrsson in their family trees cannot be taken as evidence that he is one of the author's ancestors. What counts is the number of *segment triangulations* that were found, and especially the strong segment triangulations on chromosome 16, in combination with demographic data about his being a close neighbour to Carl Johan Forssén's (1828) mother in Pengsjö at the time when she got pregnant.

4.2. A remarkable coincidence?

As to the failure of the genealogical junctions analysis to identify the FFFFF/FFFFM couple Jon Jonsson (*1781) and Magdalena Eriksdotter Vänman (*1786) this could not be due to their having few descendants. As described in the results section they did not have fewer grandchildren (62 grandchildren) than the other ancestors at a similar genealogical distance. In this case, however, it was difficult to ignore another remarkable coincidence that was likely to nourish the imagination: The author's FFFFF Jon Jonsson (*1781) was a farmer at Pengsjö 3 during the same period that the author's FMMFM Greta Stina Olofsdotter (*1800) worked as a maid at Pengsjö 1 and the hypothesized FMMFF Jon Pehrsson (*1795) worked as a farmer at Pengsjö 2. In other words, during the same

time in the 1820s the author's FFFFF/FFFFM as well as his FMMFF and FMMFM all resided in this small village with only five farms. Was this simply a random coincidence?

Some other possibilities easily came to mind. First: could it be that Jon Jonsson (*1781) was the real father of Carl Johan Forssén (*1828)? Like Jon Pehrsson (*1795) he also seemed to be at the right place at the right time. However, a testing of this alternative hypothesis by means of segment triangulation (in the same way as had been done with Jon Pehrsson) did not provide any support for this possibility.

Another question that had to be raised was if Jon Pehrsson (*1795), rather than Jon Jonsson (*1781), could possibly have been the father also of the author's FFFF? Some evidence, however, clearly spoke against this possibility. First, Jon Pehrsson did not move to Pengsjö until 1823 or 1824, whereas the author's FFFF was born already in 1819. Secondly, if Jon Pehrsson (*1795) had been the father of the author's FFFF, he would belong to the same Y-DNA haplo group as the author (R-YP4123); some evidence, however, indicated that Jon Pehrsson (*1795) belonged to another haplo group (Q-BZ4901), which (if true) excluded the possibility that he could be the author' ancestor in the direct paternal line. The information on Jon Pehrsson's haplo group, however, was based on the Y-DNA testing of only one of Jon Pehrsson's descendants as reported on *Geni.com* and should therefore be treated with caution.

A third possibility was that Jon Pehrsson (*1795) and Jon Jonsson (*1781) might be close relatives, and that this explained why they chose to live as neighbours in the 1820s. A comparison of their family trees, however, did not show any genealogical connection between their families until six further generations back in time, in the 16th century. To summarize, the author's FFFFF and FMMFF being neighbours in the small village of Pengsjö in the 1820s might very well be just a remarkable coincidence.

4.3. Limitations and directions for future research

The analysis of genealogical junctions among unplaced DNA matches turned out to be a successful method in the two cases described in the present study. The usefulness of the method, however, needs to be tested also in other studies. For example, it may be of interest to explore different ways of defining the set of unplaced DNA matches that are to be included in the analysis.

In the present study, a cut-off of 100 cM was used for identifying the set of DNA matches, but this was a cut-off for the *combined* DNA shared by the two brothers with their atDNA matches. As can be seen in Table 1, only two of the 16 unplaced DNA matches (*Cesar-128* and *Bianca-102;* both descendants of the hypothesized FMMFF Jon Pehrsson) passed the cut-off of 100 cM for Brother 1. In contrast, six other unplaced DNA matches (*Sofia-150, Maja-132, Willy-124, Igor-124, Clara-114, and Axel-112;* all being related to the Norberg family) passed the cut-off for Brother 2. In other words: if only one of the brothers had tested their DNA the method would not have worked equally well. Furthermore, different sets of unplaced DNA matches would have resulted, depending on which brother did the testing. This suggests that the analysis of genealogical junctions may work best when at least two siblings are used to define the set of unplaced DNA matches.

Another important issue for further research concerns the confounding factor of the *number* of descendants of a given ancestor. Ideally, it would be a good thing if this confounder could be controlled for in some way when evaluating the strength of a given genealogical junction. For example, it might be that a genealogical junction which involves only two close DNA matches should be considered equally important as a genealogical junction

which involves four close DNA matches if the number of descendants for the couple in the former genealogical junction is only half the number of descendants for the couple in the latter genealogical junction.

Again, it should be noted that the cut-off of 100 cM in the present study was quite arbitrary. The possibly most important thing is to set this cut-off so that it produces a sufficient number of unplaced DNA matches. In the present study the cut-off of 100 cM produced nineteen unplaced DNA matches. In some cases it may probably more relevant to set a higher cut-off, whereas in other cases it may probably be more relevant to set a lower cut-off, depending on the number of unplaced DNA matches that are available.

Finally, more research should be done on segment triangulation to clarify the potentials and limitations of this methodology. Just as Bartlett (2016) argued for the importance of identifying *intermediate* MRCAs among DNA matches who share a given DNA segment when searching for the evidence of establishing ancestry, it is possible that there is potential for a similar search for more *remote* MRCAs beyond an established ancestor to explore that ancestor's ancestry. For example, Figures 4-9 do not only illustrate triangulations with DNA matches who had Jon Pehrsson (*1795) in their family trees but also triangulations with DNA matches who had Jon Pehrsson's parents, maternal grandparents, and great maternal grandparents as their MRCAs, thereby adding evidence not only that these DNA segments came from Jon Pehrsson (*1795), but also possible evidence of where he had had received these DNA segments from.

Further, Figure 6 suggests that it *might* be possible to trace DNA segments even further back in time, at least in some cases. When a systematic search was made for DNA matches who shared more than 15 cM of the specific segment on chromosome 1 (see section 3.5.3, pages 30-32 above), this did not only lead to the identification of four matches who had Jon Pehrsson (*1795) in their pedigree, one additional match who had Jon Pehrsson's parents in his pedigree, yet two matches who had Jon's maternal grandparents (MM/MF) in their pedigree, and two additional ones who had Jon's mother's grandparents (MMM/MMF) in their pedigrees. Quite surprisingly, it also led to the finding of yet another 32 DNA matches who had Jon Pehrsson's MMMM/MMMF Märeta Mattsdotter (*1678) and Lars Olofsson (*1675) in their pedigrees. Also quite surprisingly, several of these overlappings of DNA were quite large; twelve of these matches shared even more than 30 cM of the DNA segment.

What is to make of this kind of finding, where the number of DNA matches with a more *remote* MRCA sharing a given DNA segment *increases* in this way (as compared with the number of matches with less remote MRCAs)? A possible explanation would be in terms of pedigree collapse. Such a hypothesis was suggested by the fact that three additional DNA matches (i.e., who did not seem to have the Märeta/Lars couple in their pedigree), and who shared 37 cM, 31 cM, and 30 cM respectively of the segment, had a closer MRCA: the author's FMMFMMF Hans Jonsson Tiger (*1742) and FMMFMMM Magdalena Eriksdotter (around *1742). The father of Hans Jonsson Tiger is described in the genealogical sources as unknown, as is also the parents of his wife. This suggests the hypothesis that the Märeta/Lars couple might have a place somewhere in Hans' and/or Magdalena's pedigrees. If so, this would also mean that the Märeta/Lars couple would have more than one place in the author's pedigree. Maybe a pedigree collapse of this kind could help to explain the multiplication of DNA matches with the Märeta/Lars couple as MRCA who shared DNA segments on chromosome 1. It is a question for further research if it is even possible to answer such questions with segment triangulation methodology. It remains to be seen how far back in time this kind of procedure can be realistically pursued in a way that may result in trustworthy knowledge about ancestry.

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