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AI (MS Copilot Pro with DALL-E 3) Imagining A Genetic Genealogist As A Painter

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Journal of Genetic Genealogy

EDITOR'S CORNER

By J. David Vance

Are we tired of AI-generated images yet? The picture on the front cover is deliberate since AI in many forms has captured attention recently in many fields including genealogy. In some ways it's a solution looking for problems, but it's fun to see all the different ways that it IS solving problems – already in genealogy it is being used for colorizing photographs of our ancestors and estimating when they were taken, transcribing census records and old handwritten documents, and a host of other uses that would have seemed science fiction even just a year ago.

But as far as examples of creativity and ingenuity are concerned, our Spring 2024 issue is much more a showcase of the human variety. Besides Whit Athey and Kathryn Johnston's scientific look at recombination, this issue is otherwise entirely filled with case studies of approaches for solving genealogical puzzles using varied combinations of autosomal DNA, Y-DNA, and mtDNA. I hope these showcase not only the ingenuity of the authors, but also the many creative ways that we can approach these puzzles with DNA – there is in truth no single "right" way to combine DNA analysis with traditional genealogy and our methods need to adapt to the available evidence, both traditional and genetic, and to the testing pool that is available to us.

So while I am certainly excited about the prospects of AI-driven tools lending more and more support to our genetic genealogy efforts in future, I'm not particularly worried about them rising any time soon to the levels of creativity and ingenuity displayed in our regular JoGG articles!

On a more mundane note, I am also very happy to report that with the publication of this Spring 2024 issue of the JoGG, we have finally achieved a goal of mine for the journal to be quarterly! Two issues in two consecutive quarters isn't really a trend of course, but hey, I'll take it. But just so I'm not accused of idle bragging, you'll have to help me keep up this trend – we have a few more articles in queue for another 2024 issue but we need more! What examples of creativity and ingenuity in genetic genealogy do YOU have that we can turn into an article for another issue?

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Journal of Genetic Genealogy

RECOMBINATION AND PHASING FOR A GROUP OF THREE OR FOUR (OR MORE) SIBLINGS--TWO PRACTICAL APPROACHES

By T. Whit Athey, PhD and Kathryn Johnston, MD

Abstract

A method is presented for determining the recombination patterns and phasing in a group of siblings. Two versions of the same basic method are described, one more numerical in nature and the other more visual or graphic. The method requires at least three siblings, preferably four or more, each with an autosomal SNP dataset available, such as those from companies such as Family Tree DNA, 23andMe, or Ancestry. The approach requires for each chromosome, the complete set of matching segments for each sibling pair--the endpoints of the segments along with the type of match (identical on one chromosome of a pair, or identical on both chromosomes of a pair, designated as a "single" or "double" match), plus matching segments for confirmed paternal and maternal second or third cousins. Some examples of recombination in real families will be described, and some general observations on recombination will be summarized.

Introduction

When a parent passes a set of 22 autosomal chromosomes to a child via a sperm cell or egg cell, each parent derives each chromosome from cutting and pasting together an amalgam of the two corresponding parental chromosomes. This process is known as *recombination*, and it brings with it almost unlimited possibilities for producing new and unique chromosomes. The points on the chromosome passed to the child where the DNA has been cut and pasted from the parental chromosome pair are called *crossovers*.

The term "recombination" technically applies to just one point on the chromosome where a crossover has occurred. In this article we also use the term to apply to the collection of crossovers that has occurred in a group of siblings. The term "phasing" technically applies to the separation of the bases of a chromosome into its paternal and maternal copies. In this article we also use the term to apply to the schematic separation of the regions of a chromosome pair into the constituent regions inherited from each grandparent, without regard to the underlying sequence of bases. Thus, we will use the term "visual phasing" to apply to the visual/graphical approach to phasing since that term has already been in general usage.

Determining just how recombination has occurred in a family group of siblings is difficult, but not impossible if the family group is sufficiently large--at least three siblings, preferably four or more, each with an autosomal SNP dataset available, such as those from the companies Family Tree DNA, 23andMe, or Ancestry. The same basic method can be implemented in two versions or approaches, one more numerical or computational in nature [Athey, 2010a] and the other more visual or graphic.

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The approach may yield more than one solution for each chromosome pair, and it is important to have autosomal match data from known cousins to eliminate all but the one correct solution. Having in addition, the data from one parent can also be very helpful, but in this case it would be possible to completely phase the data, and this would result in determining the recombination patterns as a by-product of the phasing analysis [Athey, 2010b]. Therefore, the present approach will normally be most useful when compatible autosomal SNP datasets on three or more siblings are available, but no dataset from a parent is available. Our present approach also avoids the need to examine or use the raw data directly.

Intuitively, we normally expect that recombination will produce two new sets of chromosomes in a child such that all four grandparents contribute DNA approximately equally. However, this is not necessarily the case, even when averaged over all chromosomes. When considering a single chromosome pair, it is even possible, though unusual, to see only two of the four grandparents contributing DNA.

A few principles are very important in regard to the analysis of recombination in a particular chromosome pair in a group of siblings:

1. In any particular region of a chromosome pair, two siblings can (a) match each other exactly on both chromosomes of the pair--said to be "fully identical," (b) match each other on just one of the pair of chromosomes--said to be "half identical", or (c) not match on either one of the pair.

2. Each crossover point in a family group is unique to one sibling and unique to just one of the chromosomes of the pair. We will say that this sibling "owns" that crossover. In practice, some of the crossover points in different siblings may be fairly close to the same location, but it is assumed in the present approach that crossover locations can be determined and are all different.

3. As our focus moves along a chromosome and passes over a crossover, the nature of the matches between the sibling who owns the crossover and the other siblings will change, while the nature of the matches between the siblings not owning the crossover will remain the same.

In the first part of the present article, we will first present the numerical approach to the analysis, while the second part will present the visual or graphical approach. For those who may be averse to numerical methods, it may be preferable to skip directly to the visual approach in the second section, because the visual approach is perhaps more intuitive and understandable. The disadvantage of only considering the visual approach is that there is a particular difficulty that often occurs in the analysis that prevents a unique solution from being possible. This difficulty appears random and unexplainable if only the visual approach is used, but the basis of this difficulty is readily explained in the numerical approach. Therefore, we have elected to present the numerical approach first.

Numerical Method--Case of Four Siblings

In Figure 1 consider an example of recombination in a group of four siblings where the recombination patterns, i.e. the inheritance pattern from the four grandparents, have already been determined. We begin this way, with the “solution” already in hand, in order to define several terms. The chromosomes shaded light blue and pink came from the paternal grandfather and paternal grandmother respectively (through the father), while the dark blue and the

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green chromosomes came from the maternal grandfather and the maternal grandmother (through the mother). In Figure 1 the vertical lines represent the boundaries of two sliding windows--not crossover points--but in subsequent figures, vertical lines *will* denote crossovers. In the region just to the left of the crossover at 27 million, the types of matches between the pairs of siblings are shown at the bottom of Figure 1. After our sliding window passes the crossover at 27 million (located on the maternal side of Sib2), the types of matches in the window change, but only in the three match types involving Sib2, who "owns" that crossover. The match types between Sib1 and Sib3, Sib1 and Sib4, and Sib3 and Sib4 remain the same as single, double, and none respectively.

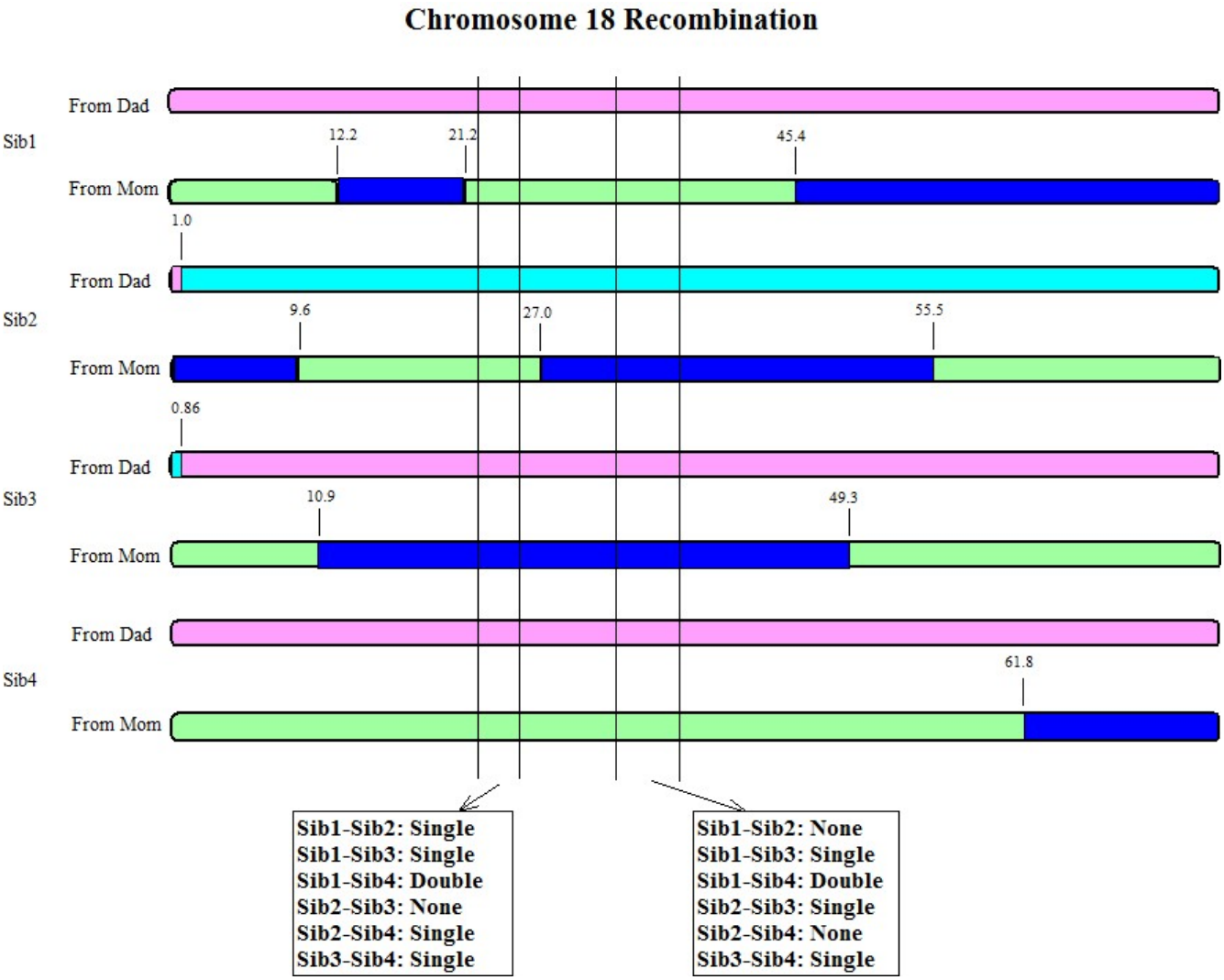

Figure 1. An Example of Four Siblings Where the DNA Inheritance is Already Known

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In Figure 1 we also see that sometimes, especially in the small chromosomes such as 18, a father may pass along a chromosome whole with no recombination. Rarely, the mother may do the same. In general, more recombination will be found in the chromosomes passed down by the mother than those passed by the father, and this phenomenon may sometimes be useful in distinguishing the paternal and maternal chromosomes when no other information is available. Note also in the above example, there is nothing in the matching types alone that would indicate that the crossover at 27 million occurred on the maternal chromosome 18 of Sib2. We have independently confirmed through cousin matches that it did not occur on the paternal side.

In Figure 2 we see for the same example, the match types determined for every region of chromosome 18, and in this figure the vertical lines do represent crossover points. For simplicity in presenting this example, we consider the origin of our analysis to be just to the right of the crossover at 1 million. We ignore for the present the beginning of the chromosome where two crossovers lie very close together and begin our analysis at 2 million. We represent the match types with numerals: 2 means a double match (fully identical), 1 means a single match (half-identical), and 0 means no match. Note that the set of matching codes does not change in the region between crossover points (indicated by the vertical lines).

We will discuss two types of *patterns* in this article, and the patterns of codes shown at the bottom of Figure 2 will be called "segment matching patterns." Again, note that on either side of a crossover, only the code involving the sibling to whom that crossover belongs, will be different--the other three codes must remain the same.

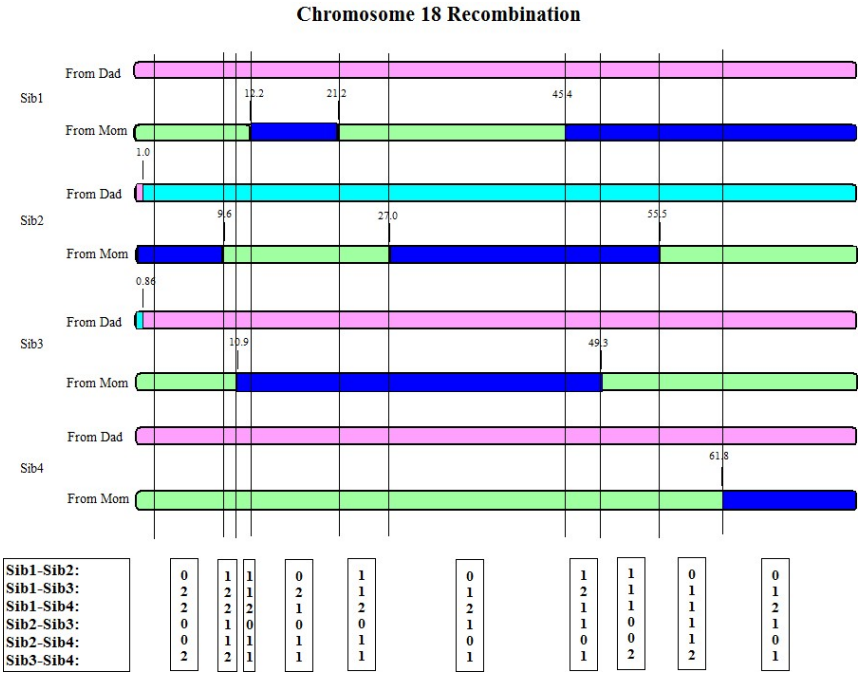

Figure 2. Matching Codes Shown for All the Regions of the Chromosome (except the beginning).

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A second kind of *pattern* used in this presentation will be called "chromosome inheritance patterns." For example, in a particular region between crossovers, if Sib1 and Sib3 received DNA from one paternal grandparent and Sib2 and Sib4 received their DNA from the other paternal grandparent, then the chromosome inheritance pattern for the four siblings would be designated as "ABAB". The A's may sometimes represent DNA from the grandfather and sometimes from the grandmother--we will not know which it is before the analysis is complete. The chromosome inheritance patterns for the paternal and maternal sides will usually be different. Note that the pattern BABA is the same as ABAB, but we will, by convention, require that each of these patterns begin with an "A", and we take the complement of the pattern, if necessary, in order to begin it with an "A". For four siblings there are eight possible patterns for the four siblings' paternal chromosomes and eight for the four siblings' maternal chromosomes. These eight patterns are AAAA, AAAB, AABA, AABB, ABAA, ABAB, ABBA, and ABBB. In the actual case for the example above, in every segment the paternal chromosome inheritance pattern would be the same (ABAA), because Sib1, Sib3, and Sib4 received all of their paternal DNA from the pink chromosome of the paternal grandmother, whereas Sib2 received DNA from the light blue chromosome, and there were no crossovers anywhere on the paternal side (at least in the region beyond 0.2 million). The eight possible chromosome inheritance patterns (for the four-sibling case) are collected in Table 1.

Table 1. The Eight Chromosome Inheritance Patterns for Four Siblings

Pattern Number	Chromosome Inheritance Pattern			
	Sib1	Sib2	Sib3	Sib4
1	A	A	A	A
2	A	A	A	B
3	A	A	B	A
4	A	A	B	B
5	A	B	A	A
6	A	B	A	B
7	A	B	B	A
8	A	B	B	B

Note that there will be a chromosome inheritance pattern for the four siblings' four paternal chromosomes, and another, generally different, for the four siblings' maternal chromosomes. For example, in Figure 2 in the region between 27 million and 45.4 million, the paternal chromosome inheritance pattern, as already noted, is ABAA, while the maternal pattern is ABBA. In the latter case of the maternal chromosomes, the A represents the green chromosome and the B represents the dark blue chromosome, at least in this one segment. In general, for a group of siblings where the recombination has not yet been determined, we will not know which chromosome the A or B represents (paternal or maternal), and we may switch them anyway if we always start a pattern with an A. And, while we will know which sibling owns each crossover, we will not know whether the crossover has occurred on his/her paternal or maternal chromosome.

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It is important to note that there is a relationship between the two kinds of patterns that we have introduced. For each pair of *chromosome inheritance patterns*, regardless of which pattern is from the paternal side and which is from the maternal side, the pair taken together has one and only one corresponding *segment matching pattern*. However, looked at from the point of view of what we would actually know in the beginning from the sibling match comparisons, for each segment matching pattern, we would have just one pair of possible chromosome inheritance patterns, but we wouldn't know which chromosome matching pattern was from the paternal or maternal side. It is the task of this approach to resolve this ambiguity, and if successful, the chromosomes will be resolved into their component grandparent contributions. See Table S1 and Table S2 for a listing of all of the possible segment matching patterns for four siblings, plus the corresponding pair of chromosome inheritance patterns. Due to the length of these tables, they appear at the end of the article.

Table 2. The Two Types of Patterns and Their Relationship

Paternal Chromosome Inheritance Pattern				Maternal Chromosome Inheritance Pattern				Corresponding Segment Matching Pattern					
Sib1	Sib2	Sib3	Sib4	Sib1	Sib2	Sib3	Sib4	Sib1-Sib2	Sib1-Sib3	Sib1-Sib4	Sib2-Sib3	Sib2-Sib4	Sib3 Sib4
A	B	A	A	A	B **X**	A	A	0	2	2	0	0	2
A	B	A	A	A	A	A **X**	A	1	2	2	1	1	2
A	B	A	A	A **X**	A	B	A	1	1	2	0	1	1
A	B	A	A	A **X**	B	A	B	0	2	1	0	1	1
A	B	A	A	A	A **X**	B	A	1	1	2	0	1	1
A	B	A	A	A **X**	B	B	A	0	1	2	1	0	1
A	B	A	A	A	A	A **X**	B	1	2	1	1	0	1
A	B	A	A	A	A **X**	B	B	1	1	1	0	0	2
A	B	A	A	A	B	B	B **X**	0	1	1	1	1	2
A	B	A	A	A	B	B	A	0	1	2	1	0	1

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We will be able to determine the segment matching pattern in each segment by using the chromosome browser tools at the company originating the data, and this set of segment matching patterns becomes the input for our analysis. We can then look up each pattern in Table S1 to find the unique pair of chromosome inheritance patterns. This will be explained in the following development.

In Table 2 we illustrate the relationship between the two types of patterns using the actual patterns from Figure 2. Note that the chromosome inheritance patterns are actually what we would be trying to determine in carrying out a recombination analysis, while the match types would be derived from the empirical segment matching information--the former represents the solution to our problem, while the latter is the input to the problem. Again, the important characteristic of the two kinds of patterns is that there is almost a one-to-one unique correspondence between them. For any given pair of chromosome inheritance patterns, there is just one segment matching pattern, but the two chromosome inheritance patterns may be switched between the paternal and maternal sides without affecting the segment matching pattern. Our task will be to determine the chromosome inheritance patterns from the segment matching patterns, while finding a way to resolve the ambiguity.

In Table 2 an "X" has been placed between the rows of patterns to indicate in which sibling that the crossover has occurred. That is, the "X" shows which sibling "owns" that crossover. In the line following the "X", note that only the segment match type (i.e., double, single, or none) involving that particular sibling will have changed. For example, in the last line of the table, since the crossover starting the last segment occurred in Sib4, only the third, fifth, and sixth match types have changed because those three positions correspond to the Sib1-Sib4, Sib2-Sib4, and Sib3-Sib4 comparisons. This example has crossovers only on the maternal side, but in general we would not know on which side a crossover has occurred.

A second important principle for the analysis is that in passing over a crossover, only one of the pair of chromosome inheritance patterns will change, either the one for the paternal side or the one for the maternal side. Also, only one of the letters in the chromosome inheritance pattern will change, as can be seen from the first to the second segment of the example (Table 2). However, in the case of the transition from the third to the fourth segments on the maternal side, the pattern AABA changes to BABA, but our convention requires that the pattern begin with an "A". Therefore, we write the pattern for the fourth segment as ABAB.

The chromosome inheritance patterns can only change from one to the next at a crossover in a restricted manner because of the constraints discussed in the last paragraph. Table 3 shows the permitted and prohibited transitions for chromosome inheritance patterns, with a "Y" in the right-hand part of the table indicating "permitted" and an "N" indicating prohibited.

Table 3 shows, for example, that a transition from Pattern 1 (AAAA) to Pattern 4 (AABB) is not permitted since it involves two changes.

Our starting point in a recombination analysis is to completely determine the matching segments between each pair of siblings. In the example above, we would obtain graphically, the segments shown in Table 4, with the blue color bar under each segment indicating a match, either half-identical match or a fully identical match, with the green color above the bar indicating fully identical matches. This is an example of the graphical output from the

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comparison tool at GEDmatch, but similar tools are available at Family Tree DNA and 23andMe.

For our computational approach to recombination analysis, we need to have the endpoints of each of the matching segments, which are also the crossovers. These can be obtained, for example by using the utilities of David Pike, or by using GEDmatch. For the four siblings in our example, these segments are shown in Table 5. In practice, the segment boundaries obtained by any matching algorithm will be only approximate, and the same crossover point in two different comparisons may appear to be slightly different. In Table 5 the segment boundaries have been harmonized so that the same physical crossover is assigned the same location in all three segments affected by the crossover. These boundaries do not need to be precisely known, but the locations assigned must be consistent and properly ordered.

In Table 5, for a segment where there is a double match, it is considered by default also to be a single match. In the chromosome diagram from GEDmatch, the fully identical segments are indicated by those segments that are continuously colored green. Note again that we have chosen the starting point of the analysis at location 2 million for simplicity, even though we have information from the beginning of the chromosome. Note also that every segment boundary in Table 5, except for the start and end locations, represents a crossover point and appears three times in the table.

Table 3. Permitted and Prohibited Transitions from one Chromosome Inheritance Pattern to Another

FROM Pattern Number	Chromosome Inheritance Pattern for that FROM Pattern				Permitted or Prohibited Transitions TO Pattern Number							
					1	2	3	4	5	6	7	8
1	**A**	**A**	**A**	**A**	-	**Y**	**Y**	**N**	**Y**	**N**	**N**	**Y**
2	**A**	**A**	**A**	**B**	**Y**	-	**N**	**Y**	**N**	**Y**	**Y**	**N**
3	**A**	**A**	**B**	**A**	**Y**	**N**	-	**Y**	**N**	**Y**	**Y**	**N**
4	**A**	**A**	**B**	**B**	**N**	**Y**	**Y**	-	**Y**	**N**	**N**	**Y**
5	**A**	**B**	**A**	**A**	**Y**	**N**	**N**	**Y**	-	**Y**	**Y**	**N**
6	**A**	**B**	**A**	**B**	**N**	**Y**	**Y**	**N**	**Y**	-	**N**	**Y**
7	**A**	**B**	**B**	**A**	**N**	**Y**	**Y**	**N**	**Y**	**N**	-	**Y**
8	A	**B**	**B**	**B**	**Y**	**N**	**N**	**Y**	**N**	**Y**	**Y**	-

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Table 4. Graphical Illustration of the Matching Segments

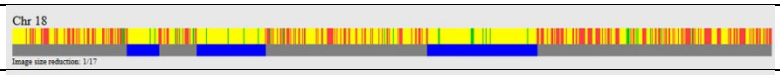
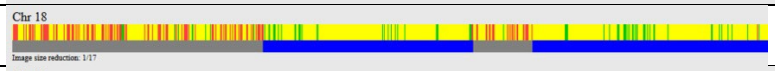
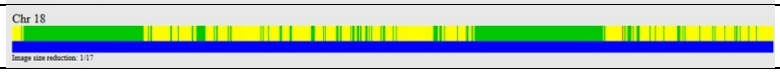
Comparison	
Sib1 to Sib2	
Sib1 to Sib3	
Sib1 to Sib4	
Sib2 to Sib3	
Sib2 to Sib4	
Sib3 to Sib4	

Table 5. Harmonized Matching Segments Between the Four Siblings

Chr	MatchType	#SNPs	Start	Stop	Length	Comparison	
18	Single	708	9.64	12.86	3.02	Sib1	Sib2
18	Single	1523	20.20	27.00	6.82	Sib1	Sib2
18	Single	2459	45.50	55.40	10.73	Sib1	Sib2
18	Double	2690	2	10.89	10.03	Sib1	Sib3
18	Double	1208	12.86	20.20	9.08	Sib1	Sib3
18	Double	924	45.50	49.40	3.92	Sib1	Sib3
18	Single	17010	2	76.12	58.24	Sib1	Sib3
18	Double	3193	2	12.86	12.09	Sib1	Sib4
18	Double	5369	20.20	45.50	25.32	Sib1	Sib4
18	Single	17012	2	76.12	76.06	Sib1	Sib4
18	Double	3821	61.80	76.12	14.31	Sib1	Sib4
18	Single	500	9.64	10.89	1.25	Sib2	Sib3
18	Single	4735	27.00	49.40	22.44	Sib2	Sib3
18	Single	5079	55.40	76.12	19.43	Sib2	Sib3
18	Single	3076	9.64	27.00	17.39	Sib2	Sib4
18	Single	1512	55.40	61.80	6.48	Sib2	Sib4
18	Double	2690	2	10.89	10.03	Sib3	Sib4
18	Double	2873	49.40	61.80	12.49	Sib3	Sib4
18	Single	17011	2	76.12	76.05	Sib3	Sib4

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Table 6. Segment Boundaries, Crossovers, and Match Types

Segment Boundaries			Segment Matching Patterns					
Start (millions)	Stop (millions)	Sib who Owns the Crossover at Stop	Sib1-Sib2	Sig1-Sib3	Sib1-Sib4	Sib2-Sib3	Sib2-Sib4	Sib3-Sib4
2.00	9.64	Sib2	0	2	2	0	0	2
9.64	10.89	Sib3	1	2	2	1	1	2
10.89	12.86	Sib1	1	1	2	0	1	1
12.86	20.20	Sib1	0	2	1	0	1	1
20.20	27.00	Sib2	1	1	2	0	1	1
27.00	45.50	Sib1	0	1	2	1	0	1
45.50	49.40	Sib3	1	2	1	1	0	1
49.40	55.40	Sib2	1	1	1	0	0	2
55.40	61.80	Sib4	0	1	1	1	1	2
61.80	76.12	Sib4	0	1	2	1	0	1

The first step in the analysis is to determine the set of unique crossovers and order the segments, resulting in the following segment definitions as shown in Table 6 (and illustrated in Figure 2). We then add the matching types for each sibling-pair comparison.

Corresponding to each segment matching pattern is just one pair of chromosome inheritance patterns. We have set up a look-up table to determine the pair of chromosome inheritance patterns corresponding to each segment matching pattern (see Table S1). We will not know which of the pair of chromosome inheritance patterns belong to the paternal and maternal sides, but we will have the possible patterns (Pattern numbers as in Table 3). These are shown in Table 7, with the pairs of Chromosome Inheritance Patterns just ordered numerically with the smaller value on the left.

For the first segment from 2.0 million to 9.64 million, the patterns are the same (pattern 5) for both the paternal and maternal sides, so there is no decision to be made regarding which pattern is on the paternal side and which is on the maternal side. However, we do not know if the crossover at 9.64 million is on the paternal or maternal side. Coming out of any segment where the chromosome inheritance patterns are the same on both sides, we will not know on which side the next crossover occurs. We must depend on the existence of a cousin match in the next region to make this determination. Alternatively, a cousin match further down the chromosome may be worked backward to this segment, or a guess may be made that any given crossover has a somewhat greater probability of being on the maternal side. In this example we will assume that we have information that shows that the first crossover at 9.64 million has occurred on the maternal side. If we have the wrong initial assignment of the crossover, we can simply switch the results at the end.

Another important principle needed for making the determination of which side the chromosome inheritance patterns belong on, is that only one of

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the patterns, either that from the paternal chromosome or that from the maternal chromosome, will change at each crossover. Therefore, if we assume that the crossover at 9.64 million is on the maternal side, then the ordered set of pattern numbers in the second segment is 5-1. One of these patterns, either the 5 (ABAA) or the 1 (AAAA), will continue into the next segment since the crossover must be on either the paternal or the maternal chromosome. Therefore, since the pattern 5 appears again in the third segment, it must be on the same side as in the second segment--the paternal side. That leaves pattern 1, changing to pattern 3, to describe the maternal sides in the second and third segments. We can continue to step through the segments, assigning the pattern numbers as above. In this particular case, the pattern on the paternal side continues the same (pattern 5) through all of the segments, but this will not be the case in general. As long as we do not encounter a segment where the Inheritance pattern is the same on both paternal and maternal sides, we will have the rest of the chromosome determined. The final solution to the patterns will be as shown in Table 8, and we will have all the information required to construct a schematic recombination diagram. In fact, the last six columns of Table 8 represent such a schematic diagram.

Table 7. Segment Boundaries and Chromosome Inheritance Patterns

Start (millions)	Stop (millions)	Segment Matching Pattern	Only possible paternal/maternal Chromosome Inheritance Patterns	
2.00	9.64	022002	5	5
9.64	10.89	122112	1	5
10.89	12.86	112011	3	5
12.86	20.20	021011	5	6
20.20	27.00	112011	3	5
27.00	45.50	012101	5	7
45.50	49.40	121101	2	5
49.40	55.40	111002	4	5
55.40	61.80	011112	5	8
61.80	76.12	012101	5	7

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Table 8. Segment Boundaries and Resolved Chromosome Inheritance Patterns

Start (millions)	Stop (millions)		Only Possible Paternal/ Maternal Inheritance Patterns			Schematic Recombination Diagram (In the first segment, both paternal and maternal sides have a Chromosome Inheritance Pattern of 5 (ABAA), so we fill in the same colors for Sib1, Sib3, and Sib4, and a different color for Sib2. Then, if we assume that the first crossover is on the maternal side, then the rest of the diagram is specified by the Chromosome Inheritance Patterns and can be filled in)							
						Sib1		Sib2		Sib3		Sib4	
						Pat	Mat	Pat	Mat	Pat	Mat	Pat	Mat
2.00	9.64		5	5									
9.64	10.89		5	1									
10.89	12.86		5	3									
12.86	20.20		5	6									
20.20	27.00		5	3									
27.00	45.50		5	7									
45.50	49.40		5	2									
49.40	55.40		5	4									
55.40	61.80		5	8									
61.80	76.12		5	7									

As noted in the table heading, we cannot determine from just the paternal/maternal inheritance patterns, which of the four grandparents contributed each color in the schematic recombination diagram. That is, another valid recombination diagram can be made by interchanging the pink and blue along with the blue and green. The (tentative) paternal and maternal chromosomes could also be interchanged. The correct choice must usually be determined from second cousin matches. First cousin matches will not work because first cousins would have DNA from both of your common grandparents, just like you, though first cousin matches can help distinguish the paternal chromosomes from the maternal, and if the first cousin matching segments extend across one or more of the sibling crossovers, they may help extend the analysis and resolve ambiguities. Second cousins, on the other hand, would share DNA with only one of your grandparents. If data from a parent is available, this could correctly distinguish the paternal-maternal chromosome assignments. Obviously, third (or more distant) cousin matches would work also if you have any for whom the exact relationship is known, but usually a third cousin would match with you on only a small number of chromosomes. Any matches you have with known third (or more distant) cousins would still be useful in analyzing that small set of chromosomes where such matches occur.

Now we must look for some second cousin matches to complete the analysis. To illustrate this process, we will assume that we find the following matches:

> A match from 44 million to 74 million between Sib1, Sib3, and Sib4 (but not Sib2) and a second cousin who is related to the four siblings

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through their paternal grandmother. This serves to identify the pink color with the paternal grandmother and confirms that we have made the correct initial assignment of the paternal and maternal sides. This also serves to identify the light blue color with the other paternal grandparent, the paternal grandfather.

A match from 2.2 million to 8 million between Sib1, Sib3 and Sib4 (but not Sib2) with a second cousin who is related to the four siblings through their maternal grandmother. This serves to identify the light green color with the maternal grandmother, and therefore the dark blue color would then be assigned to the maternal grandfather.

The resulting complete schematic diagram can be shown in Table 9.

Table 9. Segment Boundaries and Resolved Chromosome Inheritance Patterns

Start (millions)	Stop (millions)		Only Possible Paternal/ Maternal Inheritance Patterns			Schematic Recombination Diagram							
						Sib1		Sib2		Sib3		Sib4	
						Pat	Mat	Pat	Mat	Pat	Mat	Pat	Mat
2.00	9.64		5	5		PGM	MGM	PGF	MGF	PGM	MGM	PGM	MGM
9.64	10.89		5	1		PGM	MGM	PGF	MGM	PGM	MGM	PGM	MGM
10.89	12.86		5	3		PGM	MGM	PGF	MGM	PGM	MGF	PGM	MGM
12.86	20.20		5	6		PGM	MGF	PGF	MGM	PGM	MGF	PGM	MGM
20.20	27.00		5	3		PGM	MGM	PGF	MGM	PGM	MGF	PGM	MGM
27.00	45.50		5	7		PGM	MGM	PGF	MGF	PGM	MGF	PGM	MGM
45.50	49.40		5	2		PGM	MGF	PGF	MGF	PGM	MGF	PGM	MGM
49.40	55.40		5	4		PGM	MGF	PGF	MGF	PGM	MGM	PGM	MGM
55.40	61.80		5	8		PGM	MGF	PGF	MGM	PGM	MGM	PGM	MGM
61.80	76.12		5	7		PGM	MGF	PGF	MGM	PGM	MGM	PGM	MGF

PGF=paternal grandfather, PGM=paternal grandmother, MGF=maternal grandfather, MGM=maternal grandfather.

Note that the shaded columns represent a schematic set of chromosome diagrams that are identical to those shown in Figures 1 and 2, the only difference in the two tables being the chromosome orientations--horizontal in the figures and vertical in the table.

It is important to note that it is normally not necessary to have a second cousin match for every segment shown in the table. The matches with the two second cousins in our example serve not only to identify the segments where the matches occur, but also the remainder of the chromosome diagram since it is already fixed schematically from Table 9, so all the segments colored the same would be from that same grandparent.

However, the extension of the grandparent assignment throughout a chromosome, based upon just one second cousin matching segment, often runs into a fundamental difficulty. When a segment in the middle of a chromosome has the same

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chromosome inheritance pattern on both the paternal and maternal sides, which we term an "ambiguous segment," then a second cousin match either downstream or upstream from this ambiguous segment cannot be extended through to the other side. Then it is necessary to have an additional second cousin match on the other side of the ambiguous segment to resolve the difficulty. Sometimes there may be more than one ambiguous segment in an analysis, and each one requires an additional cousin match on that chromosome.

At the end of this article under "Web Resources," a link is provided for downloading an Excel spreadsheet that will automatically do all of the pattern determinations and conversions discussed above for the four-sibling problem, with the schematic recombination diagram as final output. There is also a link to instructions for use with this spreadsheet.

There are a number of practical complications to using the approach described above (and any other approach).

1. When there are crossover points very close together, the segment boundaries being only approximate may cause difficulties in defining the unique segments--particularly in regard to which of two closely located crossovers comes first. Sometimes, approaching the crossovers from different directions, along with use of the rules on permitted and prohibited transitions, can help resolve which crossover comes first. It is also possible for cousin matches to aid in location of close crossovers.

2. As discussed above, whenever the chromosome inheritance patterns are the same within a segment on both the paternal and maternal chromosomes--an ambiguous segment, then the next crossover cannot immediately be assigned to the paternal or maternal side, and two possible solutions issue from that point. This equality of the chromosome matching patterns may occur more than once along the chromosome, each time doubling the number of possible solutions. Usually, by carefully examining cousin matches, the difficulty can be resolved. Even matches with distant cousins that are known to be on the paternal or maternal sides, if the match extends across the crossover in question, can serve to assign the crossover to the proper side. This problem also applies to the visual/graphical approach that is described next--there is no way around the difficulty except to resolve the ambiguity with cousin matches.

One advantage of using four or more siblings is that the more siblings in the analysis, the more possible inheritance patterns exist and the probability of finding inheritance patterns the same on both paternal and maternal sides becomes smaller. The probability of finding both sides with the same inheritance pattern in any given segment is approximately 1/4 for 3 siblings, 1/8 for 4 siblings, 1/16 for 5 siblings, etc. Adding more siblings complicates the analysis, but a complete (unique) solution becomes more probable.

3. in order to use the referenced Excel spreadsheet for the recombination analysis, the endpoints of the matching segments between siblings must be harmonized manually. The program will not work if the same crossover has slightly different locations in different matching segments. It is often the case that the most important part of the analysis is coming up with a clean set of sibling matching segments with the crossovers harmonized for use as input.

4. Sometimes a matching segment will be too small to be reported by the standard comparison

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algorithms using the default match parameters. Since we know that siblings are definitely related, false positives are less of a concern and the match criteria can be significantly relaxed. But, it may sometimes be necessary just to infer that a segment is missing and then construct a suitable matching segment to complete the set. For example, in Table 5 the segment from 9.64 to 10.85 was not reported by the matching algorithm, so it was artificially constructed to complete the segment set.

5. The same method may be applied in the case of five or more siblings with data, but the number of possible patterns becomes rapidly much larger--the number doubles with each added sibling. It will be easier in general to just analyze four of the five (or six, etc) siblings, then analyze four more including those left out of the first analysis, though the choice of which siblings to include in the analysis should be made in a way that minimizes the number of ambiguous segments.

Numerical Method--Case of Three Siblings

The minimum number of siblings that can be analyzed using the approach described above is three. We present an example of a different set of three siblings, but also using data from their chromosomes 18. We begin with the match segments for the three siblings. The match segment endpoints must have been harmonized so that each crossover has a uniquely assigned location. The short double match from .1 to .96 has been inferred, so no number of SNPs has been entered into Table 10.

As in the four-sibling example, we determine the unique segments, each delineated by a crossover, as we "scroll" through the chromosome.

Similar to the four-sibling case, with three siblings we have four possible chromosome inheritance patterns and there are restrictions on the transitions from one to another. Table 12 shows the permitted transitions (indicated by a Y) and prohibited transitions (indicated by an N) for the four patterns.

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Table 10. Segment Match Data for Three Siblings

Chr	MatchType	#SNPs	Start	Stop	Length	Comparison	
18	Single	1018	0.10	6.00	5.90	Sib1	Sib2
18	Double		0.10	0.96	0.86	Sib1	Sib2
18	Single	4013	47.00	76.09	29.09	Sib1	Sib2
18	Single	12550	6.00	76.09	70.09	Sib1	Sib3
18	Double	4559	52.81	76.09	23.28	Sib1	Sib3
18	Single	5470	0.96	47.00	46.04	Sib2	Sib3
18	Single	4878	52.81	76.09	23.28	Sib2	Sib3

Table 11. Segment Boundaries and Match Types

Start (millions)	Stop (millions)		Sib1-Sib2	Sig1-Sib3	Sib2-Sib3
0	1		2	0	0
1	6		1	0	1
6	47		0	1	1
47	53		1	1	0
53	76 (end)		1	2	1

Table 12 . Permitted or Prohibited Transitions From One Inheritance Pattern to Another

FROM Pattern Number	Chromosome Inheritance Pattern for that FROM Pattern			Transitions TO Pattern Number 1	2	3	4
1	**A**	**A**	**A**	-	**Y**	**Y**	**N**
2	**A**	**A**	**B**	**Y**	-	**N**	**Y**
3	**A**	B	A	**Y**	**N**	-	**Y**
4	**A**	**B**	**B**	**N**	**Y**	**Y**	-

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Also similar to the four-sibling case, we have a one-to-one correspondence between the segment matching pattern and the pair of chromosome inheritance patterns. The four-chromosome inheritance patterns are shown again by their number as a part of the complete correspondence table as follows.

Table 13. Look-Up Table--Converting Segment Matching Patterns to Pairs of Chromosome Inheritance Patterns

Segment Matching Patterns				Chromosome Inheritance Pattern	
Sib1-Sib2	Sib1-Sib3	Sib2-Sib3		(either order)	
2	2	2		1	1
2	1	1		1	2
1	2	1		1	3
1	1	2		1	4
2	1	1		2	1
2	0	0		2	2
1	1	0		2	3
1	0	1		2	4
1	2	1		3	1
1	1	0		3	2
0	2	0		3	3
0	1	1		3	4
1	1	2		4	1
1	0	1		4	2
0	1	1		4	3
0	0	2		4	4

Note: Some Segment Matching Patterns do not occur. For example, the pattern 2-1-2 does not occur, because if siblings 1 and 3 are fully matching, and sibling 2 and 3 are fully matching, it is impossible for the sibling1-sibling3 comparison to be anything other than fully matching.

Returning to our example, in each unique segment we can take the segment matching pattern and look it up in Table 13 to obtain the corresponding pair of chromosome inheritance patterns. This pair of chromosome inheritance patterns will initially be unordered--we will not know which of each pair is paternal and which is maternal. However, we can either (1) arbitrarily guess the assignment in the first segment and then propagate that assignment throughout the chromosome (subject to later correction), or (2) use a cousin match to make the initial assignment in one of the segments, and propagate that assignment to either side of the cousin-matching segment.

In Table 14 we make an initial guess that the first crossover takes place on the maternal side. If this turns out to be incorrect on the basis of cousin

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matches, then we would simply switch the assignments. Even with the paternal-maternal assignments determined, we would still not know which grandparent should be assigned to each color.

Table 14. The Segment Matching Patterns Transformed Into a Schematic Recombination Diagram

Start	Stop		Segment Matching Pattern (from Table 10)				Only possible Paternal/ Maternal Chromo-some Inheri-tance patterns			Ordered Chromo-some Inheritance Patterns			Schematic Recombination Diagram (In the first segment, both paternal and maternal sides have a Chromosome Inheritance Pattern of 2 (AAB), so we fill in the same colors for Sib1 and Sib2, and different colors for Sib3. Then, if we assume that the first crossover is on the maternal side, then the rest of the diagram is specified by the Chromosome Inheritance Patterns and can be filled in)					
			1-2	1-3	2-3		Unordered			Pater-nal	Mater-nal		Sib1		Sib2		Sib3	
													Pat	Mat	Pat	Mat	Pat	Mat
0	1		2	0	0		2	2		2 (AAB)	2 (AAB)		. . .	. . .	. . .	. . .	. . .	. . .
1	6		1	0	1		2	4		2 (AAB)	4 (ABB)		. . .	. . .	. . .	. . .	. . .	. . .
6	47		0	1	1		3	4		3 (ABA)	4 (ABB)		. . .	. . .	. . .	. . .	. . .	. . .
47	53		1	1	0		2	3		3 (ABA)	2 (AAB)		. . .	. . .	. . .	. . .	. . .	. . .
53	76		1	2	1		1	3		3 (ABA)	1 (AAA)		. . .	. . .	. . .	. . .	. . .	. . .

Now we must look for cousin matches to complete the analysis. To illustrate this process, we will assume that we find the following cousin matches:

> A match from 40 million to 50 million between both Sib1 and Sib3 (but not Sib2) and a second cousin who is related to the three siblings through their paternal grandmother. This serves to identify the blue color with the paternal grandmother and confirms that we have made the correct initial assignment of the paternal and maternal sides. This also serves to identify the green color with the other paternal grandparent, the paternal grandfather.
>
> A match from 20 million to 40 million between both Sib2 and Sib3 (but not Sib1) with a second cousin who is related to the three siblings through their maternal grandfather. This serves to identify the yellow color with the maternal grandfather, and therefore the purple color would then be assigned to the maternal grandmother.

The resulting complete schematic diagram can be shown in Table 15.

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Table 15. The Segment Matching Patterns Transformed Into a Schematic Recombination Diagram

Start	Stop		Segment Matching Pattern (from Table 10)				Only possible Paternal/ Maternal Chromo-some Inheri-tance (CI) patterns			Order-ed CI Pat-terns			Schematic Recombination Diagram (The grandparent assignment has been filled in here, with PGF = Paternal Grandfather, PGM = Paternal Grandmother, etc.)					
			1-2	1-3	2-3		Unordered			PAT	MAT		Sib1		Sib2		Sib3	
													Pat	Mat	Pat	Mat	Pat	Mat
0	1		2	0	0		2	2		2	2		PGF	MGM	PGF	MGM	PGM	MGF
1	6		1	0	1		2	4		2	4		PGF	MGM	PGF	MGF	PGM	MGF
6	47		0	1	1		3	4		3	4		PGM	MGM	PGF	MGF	PGM	MGF
47	53		1	1	0		2	3		3	2		PGM	MGM	PGF	MGM	PGM	MGF
53	76		1	2	1		1	3		3	1		PGM	MGM	PGF	MGM	PGM	MGM

Since we did not have any ambiguous segments in the middle of this chromosome, we could propagate our cousin matches throughout the chromosome. However, we will not usually be so lucky as will be illustrated in an example from a different family, but which is also from chromosome 18. Consider the following Table 16 that is similar to Table 10:

Table 16. Segment Boundaries and Match Types

Start (millions)	Stop (millions)		Sib1-Sib2	Sig1-Sib3	Sib2-Sib3
0.0	1.0		1	1	2
1.0	12		2	1	1
12	23		2	0	0
23	34		1	0	1
34	44		1	1	0
44	56		2	0	0
56	71		1	0	1
71	72		0	0	2
72	END		1	1	2

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Table 17. The Segment Matching Patterns Transformed Into a Schematic Recombination Diagram

Start	Stop		Segment Matching Segment Matching Pattern (from Table 15)				Only possible Paternal/ Maternal Chromosome Inheritance (CI) patterns	
			1-2	1-3	2-3		Unordered	
0.0	1.0		1	1	2		1	4
1.0	12		2	1	1		1	2
12	23		2	0	0		2	2
23	34		1	0	1		2	4
34	44		1	1	0		2	3
44	56		2	0	0		2	2
56	71		1	0	1		2	4
71	72		0	0	2		4	4
72	79 End		1	1	2		1	4

These segment matching patterns can be looked up in Table 13 and the corresponding pairs of chromosome inheritance patterns can be determined as shown in Table 17.

In this example we now see that we have three ambiguous segments (highlighted in pink) in the chromosome. It will be necessary to have cousin matches in all four of the regions outside of the ambiguous segments, and this makes the analysis more difficult. However, it is not impossible because in this example from an actual case, the necessary cousin matches were found and the solution could be completed. That solution will be illustrated in the following section which uses the visual approach. It is important to note that the progress of the solution, using either the numerical approach or the visual approach, is temporarily stymied by the presence of the ambiguous segments. However, the nature of the problem would not be so obvious when using the visual approach alone if one did not understand how ambiguous segments arise. If there are no ambiguous segments to deal with, both the numerical approach and the visual approach can proceed in a straightforward manner to the final solution. If ambiguous segments are present, both approaches will depend on extra cousin matches to complete the analysis.

For the case of three siblings, we can see from Table 13 that the four segment matching patterns that produce ambiguous segments are: 222, 200, 020, 002, two of which are present in Table 17. It will usually be worthwhile when using the visual approach to use at least this much of the numerical approach--checking the segment matching patterns in each segment--to determine if the ambiguous segment problem will be present in a proposed analysis.

As was the case for the four-sibling problem, a link to an Excel spreadsheet that can do all of the analysis automatically for the three-sibling problem is included under "Web Resources." A link to instructions is also provided.

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Visual/Graphical Method or *Visual Phasing*

We now start over with the last three-sibling example discussed above in Tables 16-17, but this time we take a more intuitive and visual approach, which is often termed "visual phasing" (Johnston 2015). We use GEDmatch for this example because of the chromosome diagrams that can be obtained along with the matching segment determinations. GEDmatch also has the advantage that fully identical matches may be identified in the diagrams. Microsoft PowerPoint was used in this example solution and it is recommended for this purpose, but other software (e.g., Excel) could potentially be used if it has similar functionality, or even paper and pencil could be used.

Because we already know that there are three ambiguous segments involved in the analysis of this example, we can anticipate that the analysis is going to stall and that more cousin matches than usual will be necessary to complete the analysis.

Following is a step-by-step approach to the visual phasing analysis based on recombination.

1. The goal is to use crossover lines among siblings in PowerPoint to phase the parents' chromosomes, then determine segment mapping to grandparents when no parents or grandparents are available for testing. Although this is an intuitive method geared toward genealogists, an understanding of recombination is required.

2. Choose a single chromosome to compare at GEDmatch in the one-to-one comparison between full siblings. The same version from the same company is recommended for the best alignment. The unique graphic that GEDmatch provides helps to distinguish the fully identical, half identical and non-identical segments which aids in the identification of crossover borders made during recombination. A half-identical "single match" is determined when one out of every two alleles over a segment are matching and a fully identical "double match" is determined when both pairs of alleles match for a minimum distance of 7 cM. The raw data includes selected single nucleotide variants and the matching segment measurement is not representative of an exact distance in the traditional sense. You can expect some indistinct borders in the match process even though the crossover border created by a parent is at a distinct physical site. It is therefore advisable to round off to the nearest million base pairs when identifying crosssover points.

3. In our example, Chromosome 18 data from 23andMe is used to compare siblings at GEDmatch, using the one-to-one comparison feature. The present version of match tools at 23andMe also identifies full- and half-identical segments, which can be quite useful. We use the initials B, K and W to label each sibling, and we use the standard default match settings. In GEDmatch, take a screenshot of the graphical match diagram, then adjust the size (under Format) after copying it to PowerPoint. It should be emphasized that screenshots should be exactly cropped at the beginning and end. The image can also be resized by dragging its edge or corner. Stack each comparison between the three siblings as shown below.

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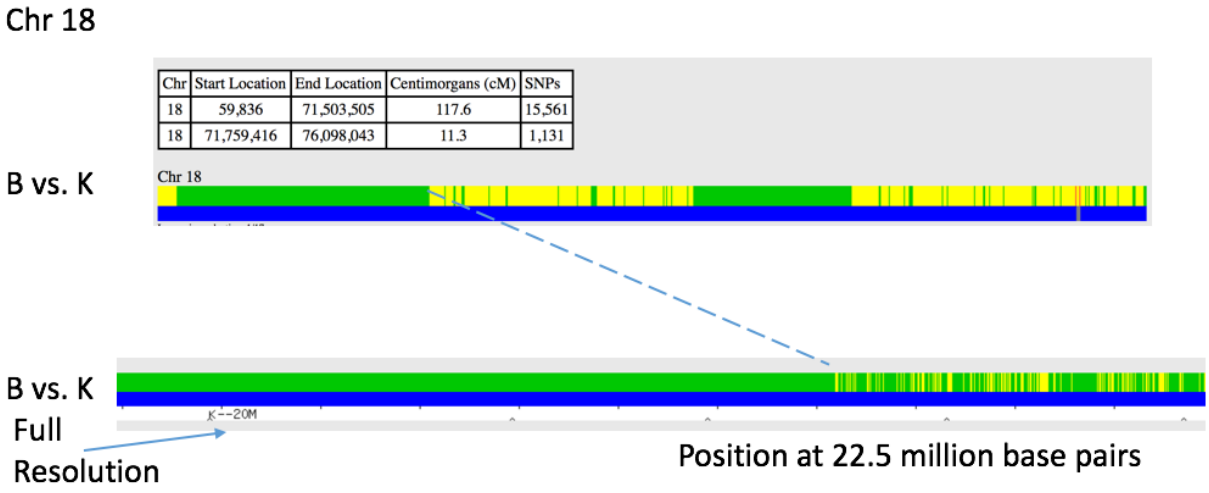
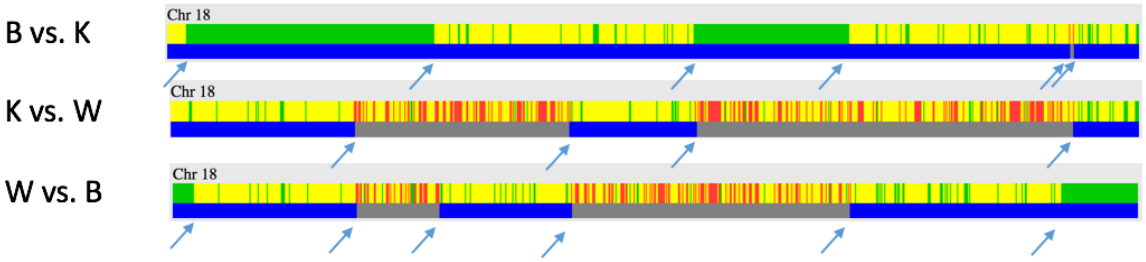
4. Line up the segments according to location:



5. Identify the borders to the single matching and double matching segments. Skip the arrows if you already know how to do this.



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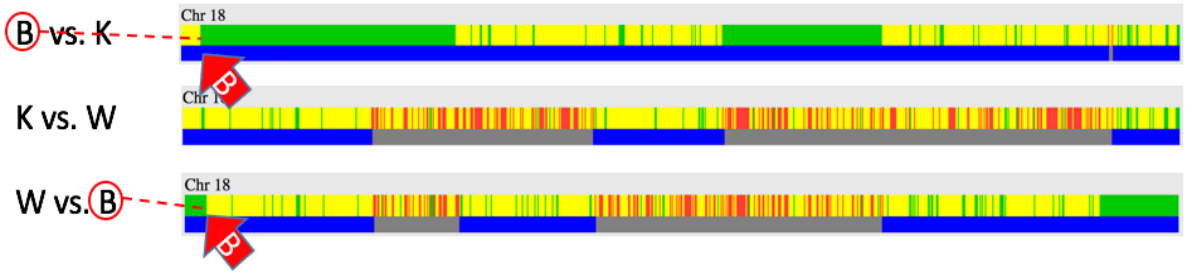
6. Any particular crossover point will occur in only one sibling; identify that sibling. The owner of the crossover is the one who is in-common with that point for two comparisons. For example, the first one belongs to B because the first and third comparisons both involve B. The second comparison (K vs. W) does not show any breakage or borders at this initial transition so therefore by process of elimination, K and W are not likely to own this crossover. There are exceptions to be discussed later.



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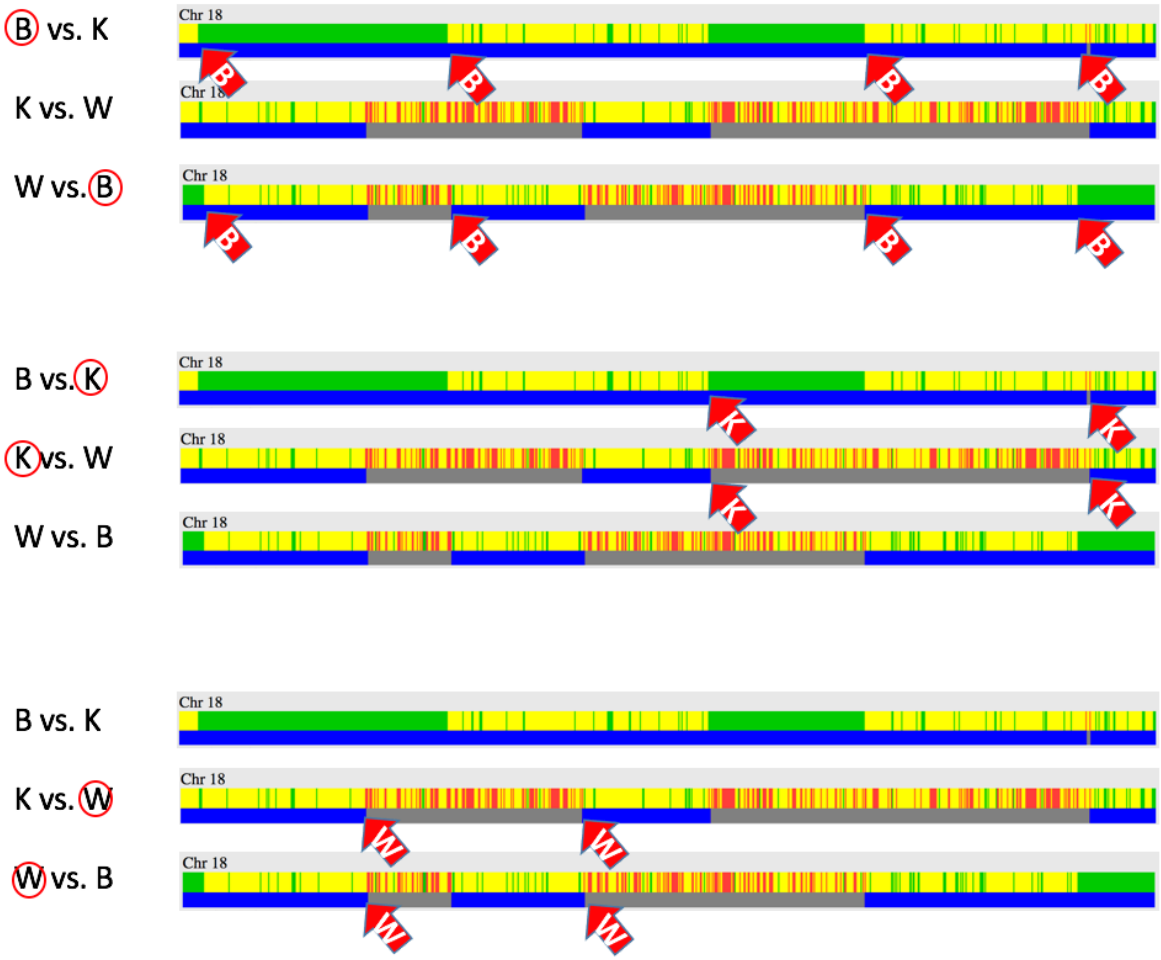
7. The following shows how to quickly identify each crossover with the most likely sibling.



A common challenge is the occurrence of two crossover points that are located very close as seen in the last crossover site. The last two crossovers may have looked like a single one made for W but on closer inspection, there was instead an interruption in the top blue B vs. K segment match indicative of nearby crossovers for B and K. Unless crossovers are made by the same parent for the same child there is no rule of thumb on how close the crossovers can be. Crossovers can be hidden from sight when parents use the same location for a crossover for two children or when two parents use the same location for one child. This author has seen crossovers as close as 6 cM made by the same parent on the same chromosome for the same child, but not closer than that. If the final configuration

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shows that the same parent made very close crossovers for the same child, that can be an indication that the identification of crossover ownership was incorrect. Interference makes this an unlikely event. More research needs to be done in real life situations to explore interference.

When each chromosome can be identified as either maternal or paternal, that is called phasing. When the segments on each phased chromosome can be identified from the crossover lines, that is what we are calling grandparent mapping. Through crossover recombination, each parent slices and splices two chromosomes together and passes a single one on to each offspring independently. A parent's two homologous chromosomes originated from the pair of chromosomes coming from his or her side of the family, the grandparent spouses. Ultimately this method will be used to map those alternating segments back to the grandparents' pairs and to fill in all the gaps through cousin matches. This is a first step in the DNA reconstruction of your ancestors from living descendants. Note that only the chromosomes coming from the parents will end up being phased, not the pairs coming from the grandparents.

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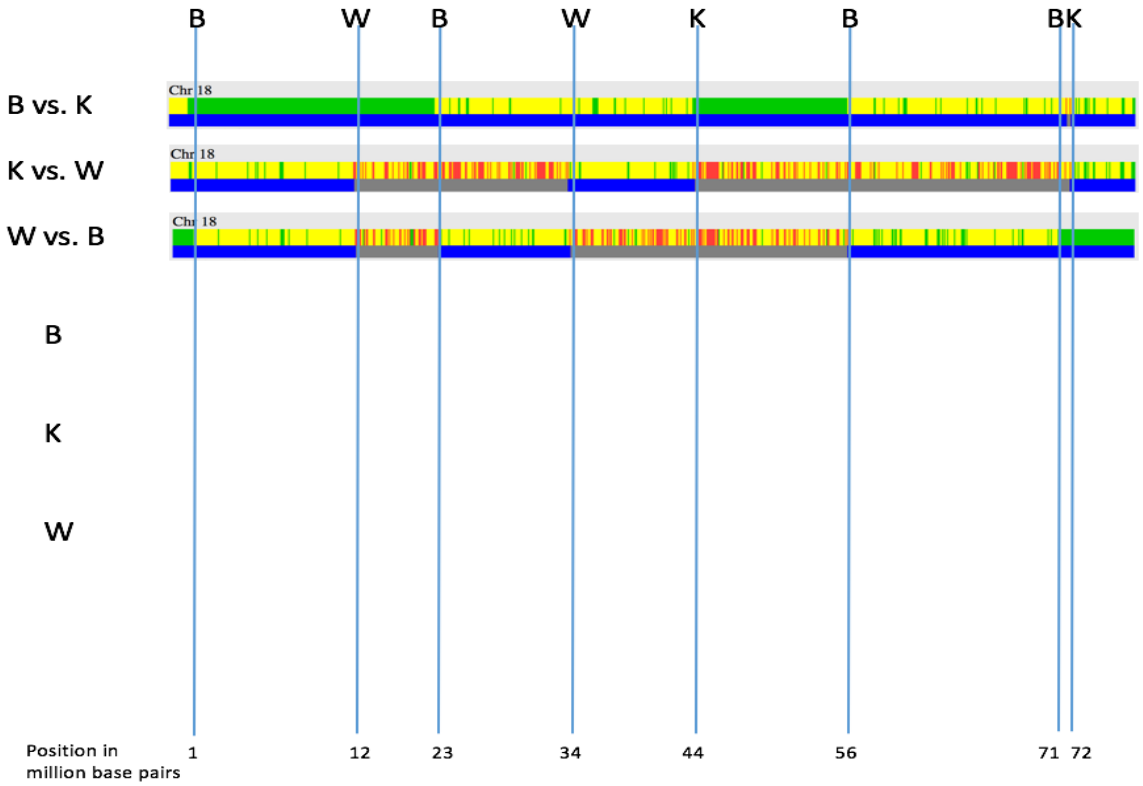
8. Click on “Insert” then “Shape” to add the crossover lines. Make sure the crossover lines are perpendicular to the comparisons. Move the crossover lines to run through approximate borders. Label each crossover line with the owner of that crossover. The parent who provided that crossover is still unknown. Later on that parent will be determined.



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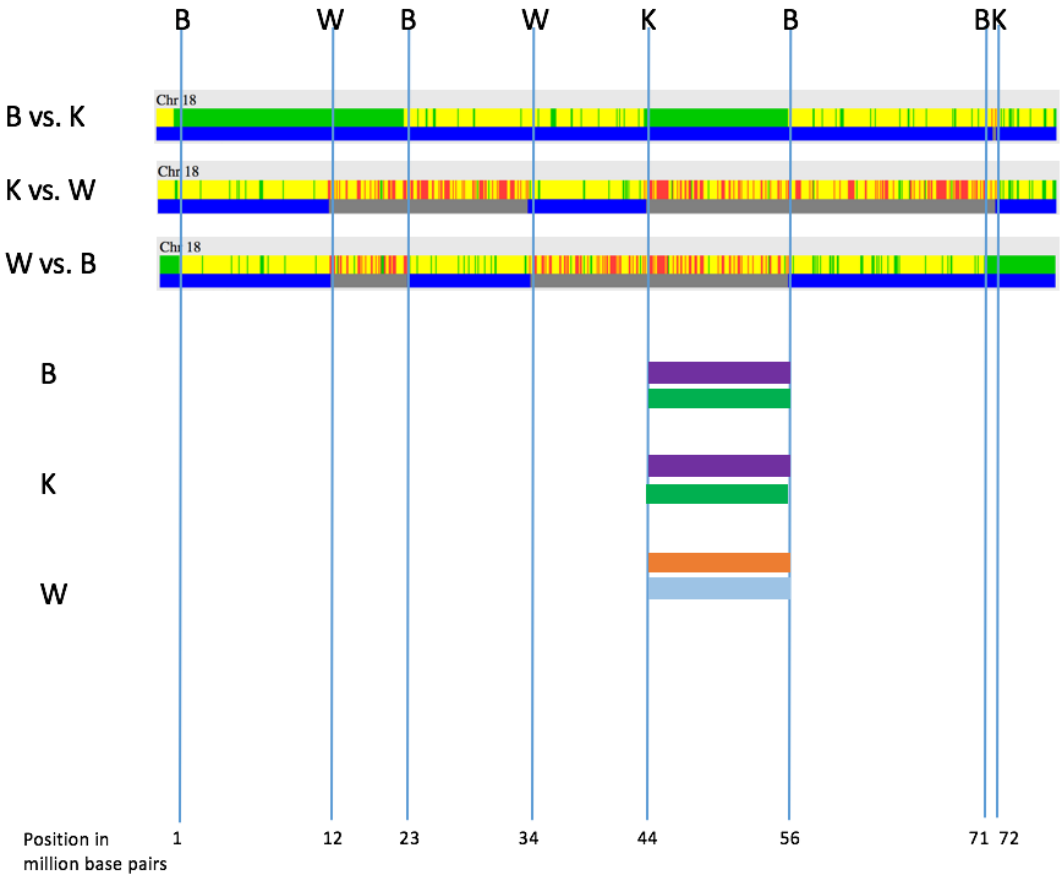
9. In PowerPoint, start with this skeleton of crossover lines. These will be the borders to the segments (these locations are also shown in Table 15). Leave room for three pairs of chromosome diagrams belonging to siblings B, K and W. Use a text box that can be filled in with four colors representing four grandparents. Double matching will show the same two colors. Single matching will show only one matched color. Non-identical regions will have four different colors, i.e. zero matching. Note how the number of color matches correlates to the numbers 2,1,0 used in the computational method. Pick any four colors but try not to add any extensions to segments that are not certain until you reach a point where you can map no further. To fill in the region with color, click on "Insert" then "Text Box" then click on "Format", "Shape" and "Fill". Click on the border of the segment until you see a solid cross, then move the colored chromosome segment to the crossover border line. Always refer back to the original stacked chromosome comparisons with the crossover lines. You may instead want to use colored pencils and skip the computer program for your comparisons or use another program such as Excel. Double matched, fully identical areas are a good place to start as shown below. B and K show an exact match between 44 and 56 but W does not share with the others in this location. We picked warm colors, purple and orange for the top set of grandparents and cool colors blue and green for the bottom set of grandparents.



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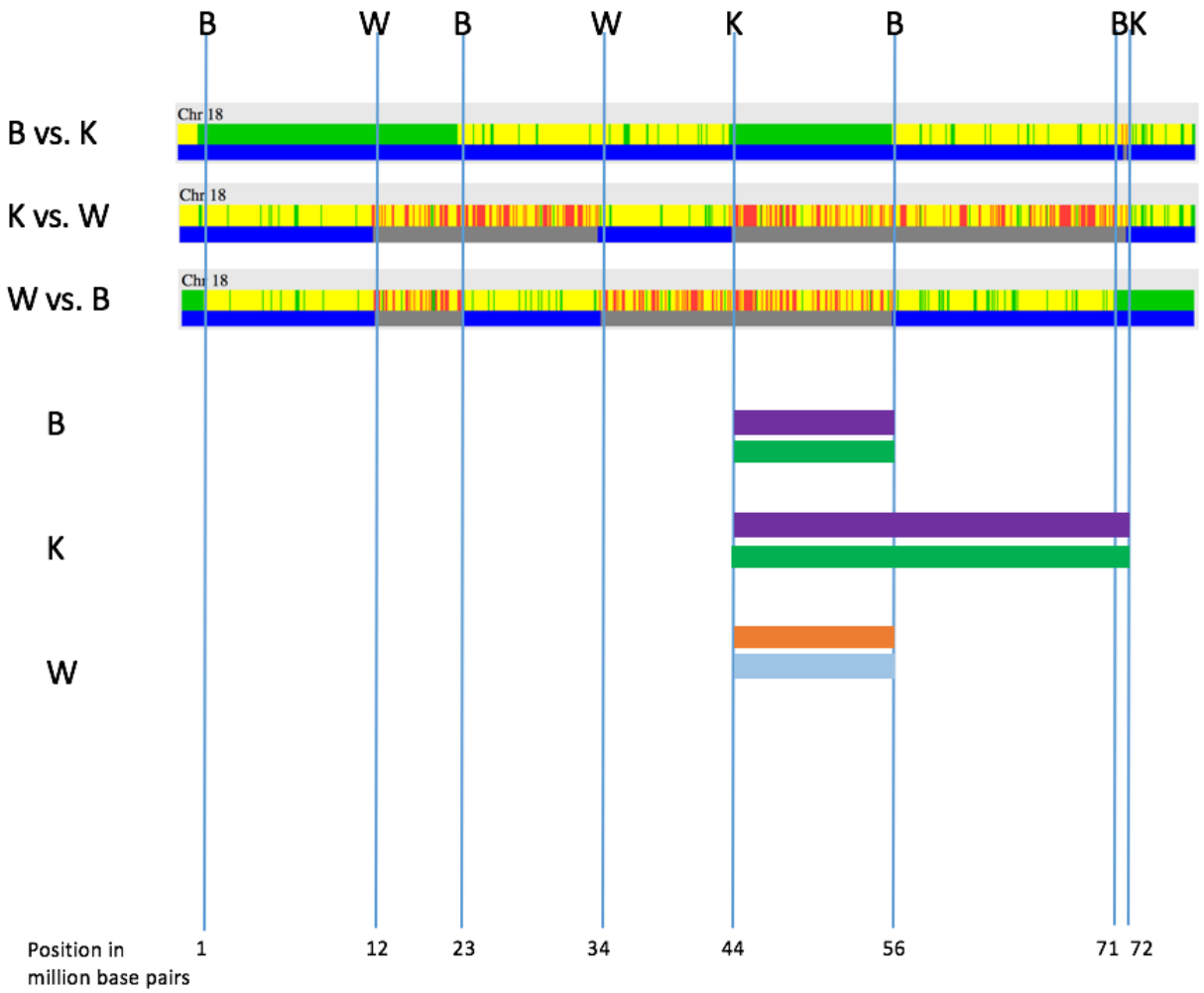
10. Extend the chromosome colors for K to the right to the crossover line K. Since K did not have any crossovers in the next two segments, then K maps to these same grandparents for the entire length until a K line signals a stop or until the chromosome ends. The top chromosome in the pair could come from either parent, but if the top chromosome is maternal, then the bottom chromosome has to be paternal and vice versa.



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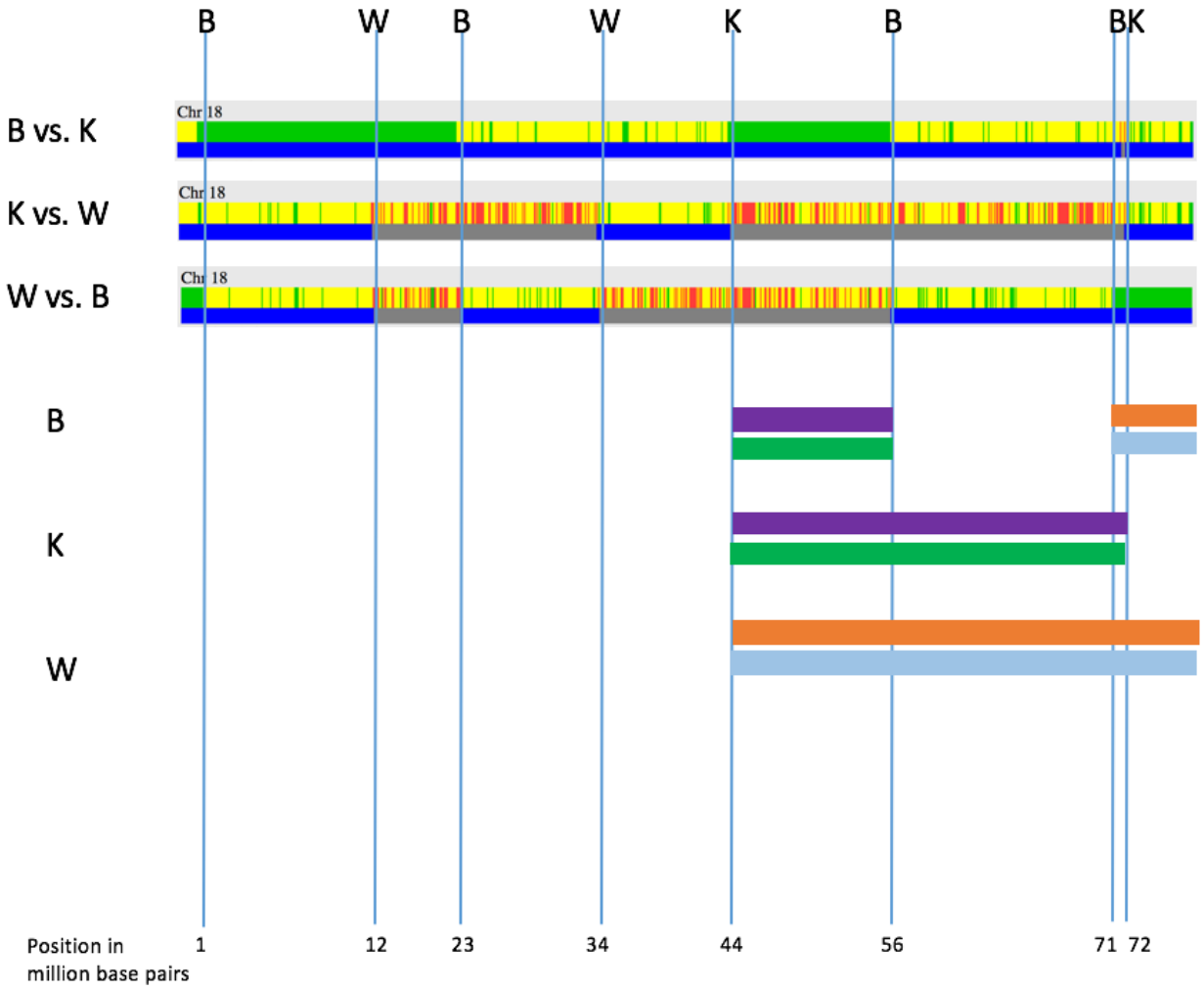
11. The two segments for W can be extended out to the end since no more W crossovers are encountered in this region. In the last segment before the end, W completely matches B, so we can color B's chromosomes in this last section to be the same as W's. Note that these are just the preliminary assignments, and we will be able to extend all of the colored regions farther as we go along.



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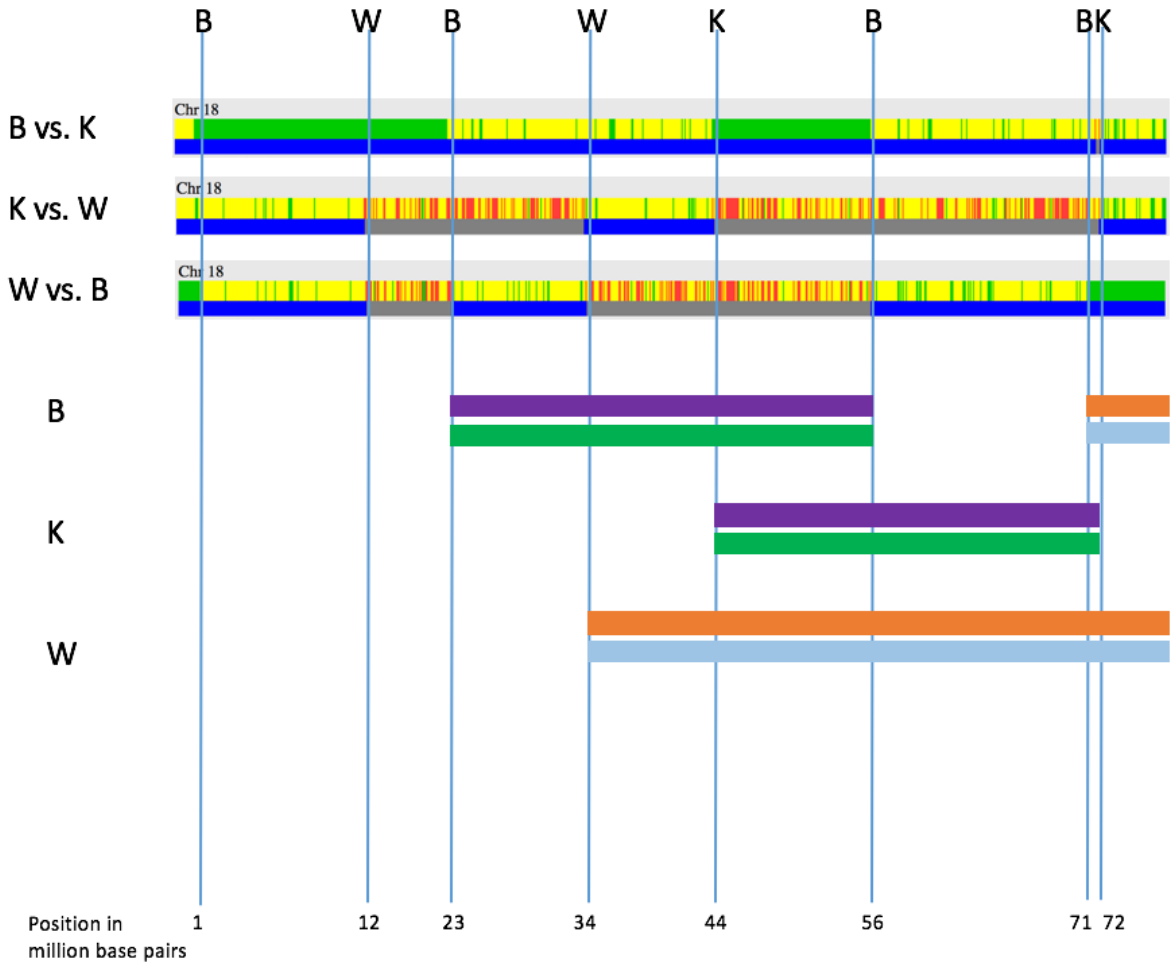
12. Extend both segments for W to the left to the crossover W at position 34 where W and B no longer match. Extend both B chromosomes to the left until the B crossover line at position 23 signals a preliminary stopping point.



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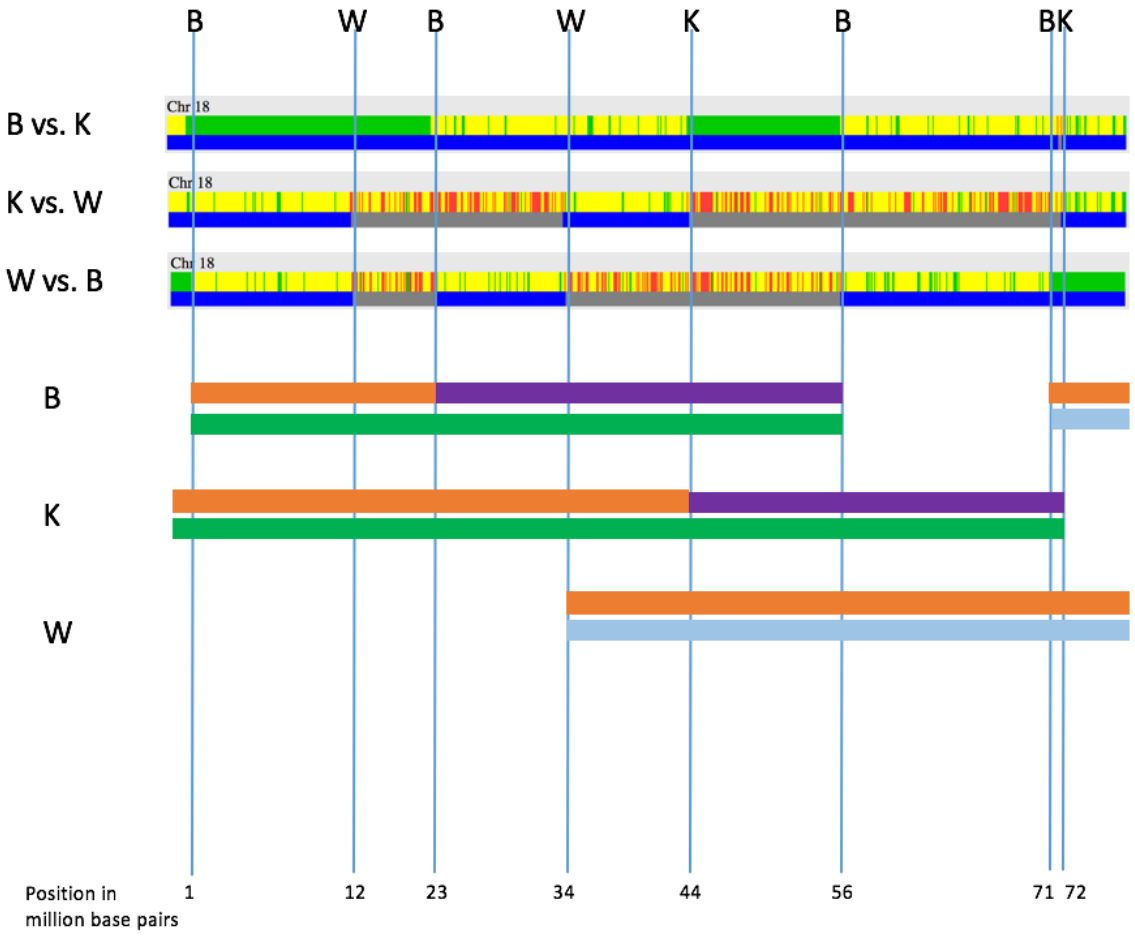
13. Up until now the filled-in regions of the chromosomes on the top and bottom have been the same size i.e. symmetrical, covering the same locations on both chromosomes. At this point a decision must be made to break this symmetry. No other color matches are certain. One chromosome color can be arbitrarily chosen for K that extends all the way to the beginning. That means that the other chromosome for K would have to change colors at the border. As a general rule only one segment can change at a crossover line within a pair. Try not to make any more arbitrary decisions after the first one. You get one guess during the entire process. If the first guess does not go as far as you wish, you can return to this point, delete (or save elsewhere) your original extension and try another guess. We choose the upper chromosome for B to make the change at B's crossover at 23 million (from purple to orange). It is now obvious that the chromosomes for B and K chromosomes can be filled in between the B crossover at 23 million and the B crossover at 1 million because B matches K exactly between positions 1 and 23. Then we can fill in the gap in K's chromosome pair between 23 and 44 million so that the same colors match at 44 million.



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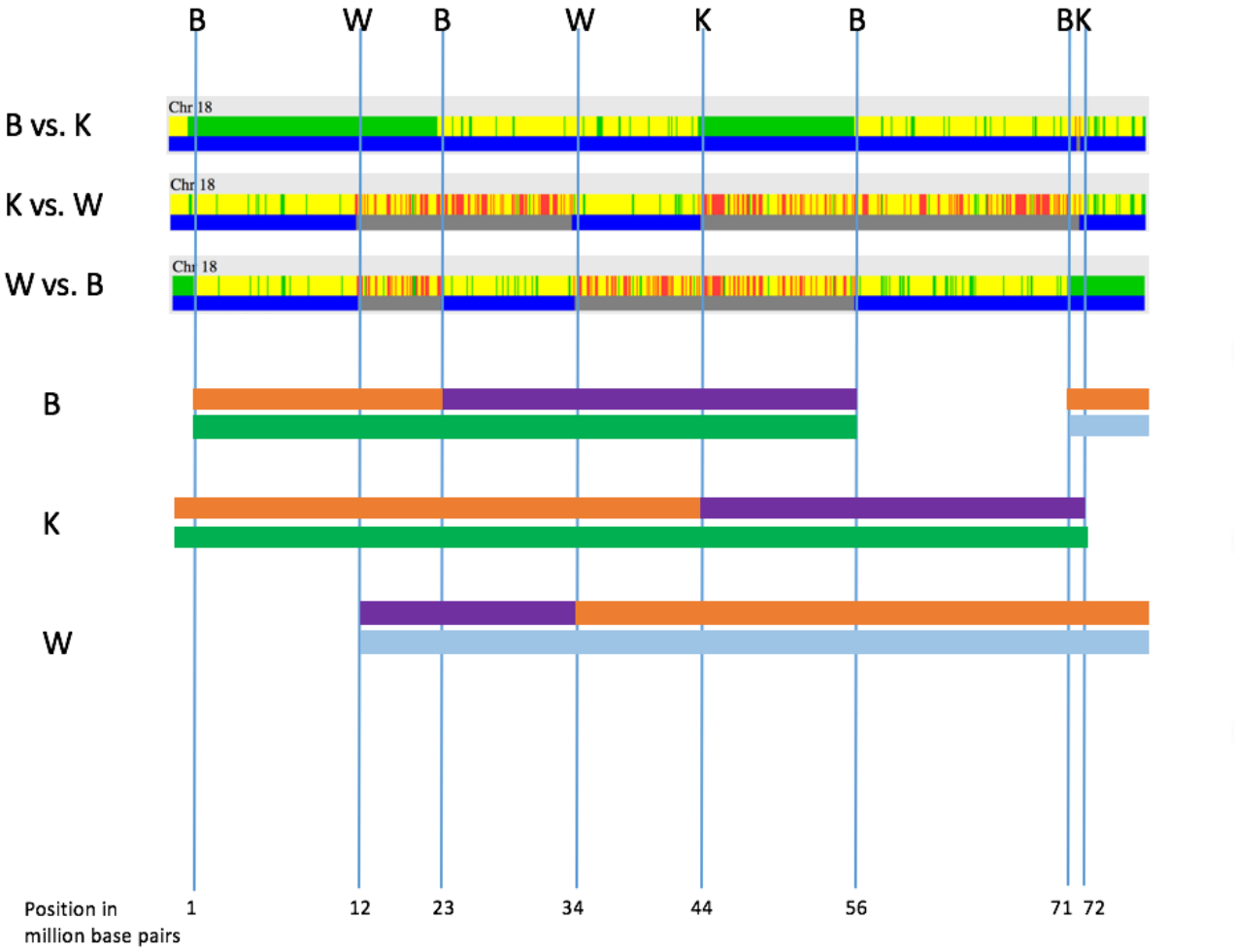
14. The remaining colors are now ambiguous for B and K where more than one color could be chosen as a single match. It is the single matching areas for two comparisons that often cause this uncertainty. For example, between positions 56 and 71, B's purple could be extended from56 to 71, or orange could be extended to the left from 71 to 56. It is best not to continue if the configuration is unknown until other relatives are found to confirm the matching colors.

    However, we do know that the orange segment for W cannot be extended between 34 and 23 because K and W do not match between 12 and 34, so there is no uncertainty there. We can fit the W vs K matching by filling in the upper chromosome of W with the purple color while extending W's lower blue color from 34 down to 12.

    At this point we have taken the sibling matching data as far as we can without resorting to cousin matches. This reason for this roadblock is discussed above in the Numerical Approach. Without cousin matches we also can't assign the four colors to a specific grandparent, or even which of the colors are paternal or maternal. Four or five siblings are always preferred over three to minimize the ambiguities, but the demand has become great among genealogists to find a way to solve these puzzles with fewer siblings and more cousin matches.



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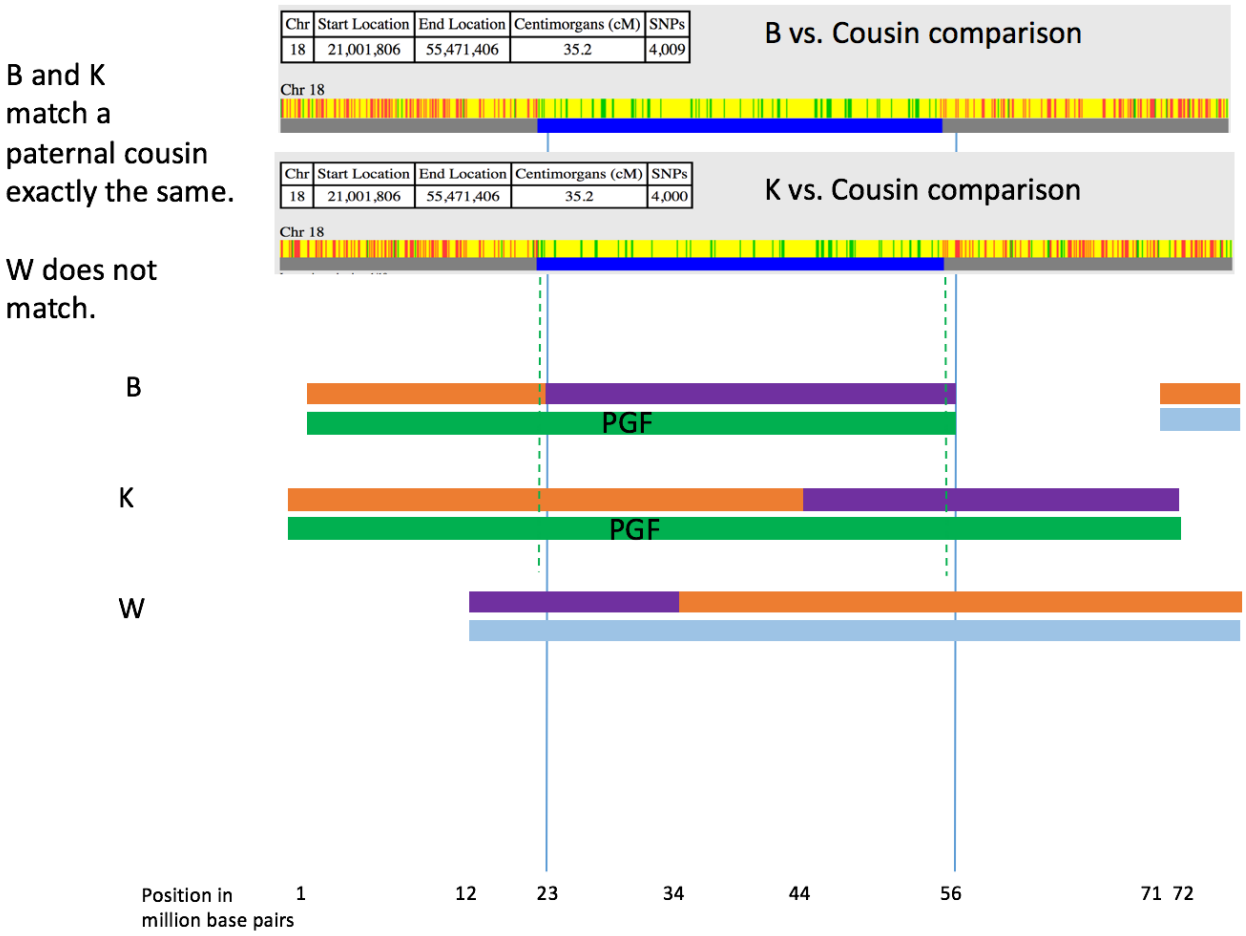
15. At GEDmatch, a paternal third cousin appeared who only matched B and K associated with the chromosome colored green above. The green single matching region can be labeled PGF (Paternal Grandfather) because out of the four grandparents, this cousin is only related to the PGF. This segment must fit within the borders passed down from the father. Each step is based on logic. The parents are not related to each other according to another GEDmatch tool, so only one parent can transmit the entire matching segment which must fit within the chromosome template. Think of a segment match with a cousin like a puzzle piece that must either be the same size or smaller than the match with a single color on a chromosome as shown below. The green regions can now be assigned to the PGF as shown below.



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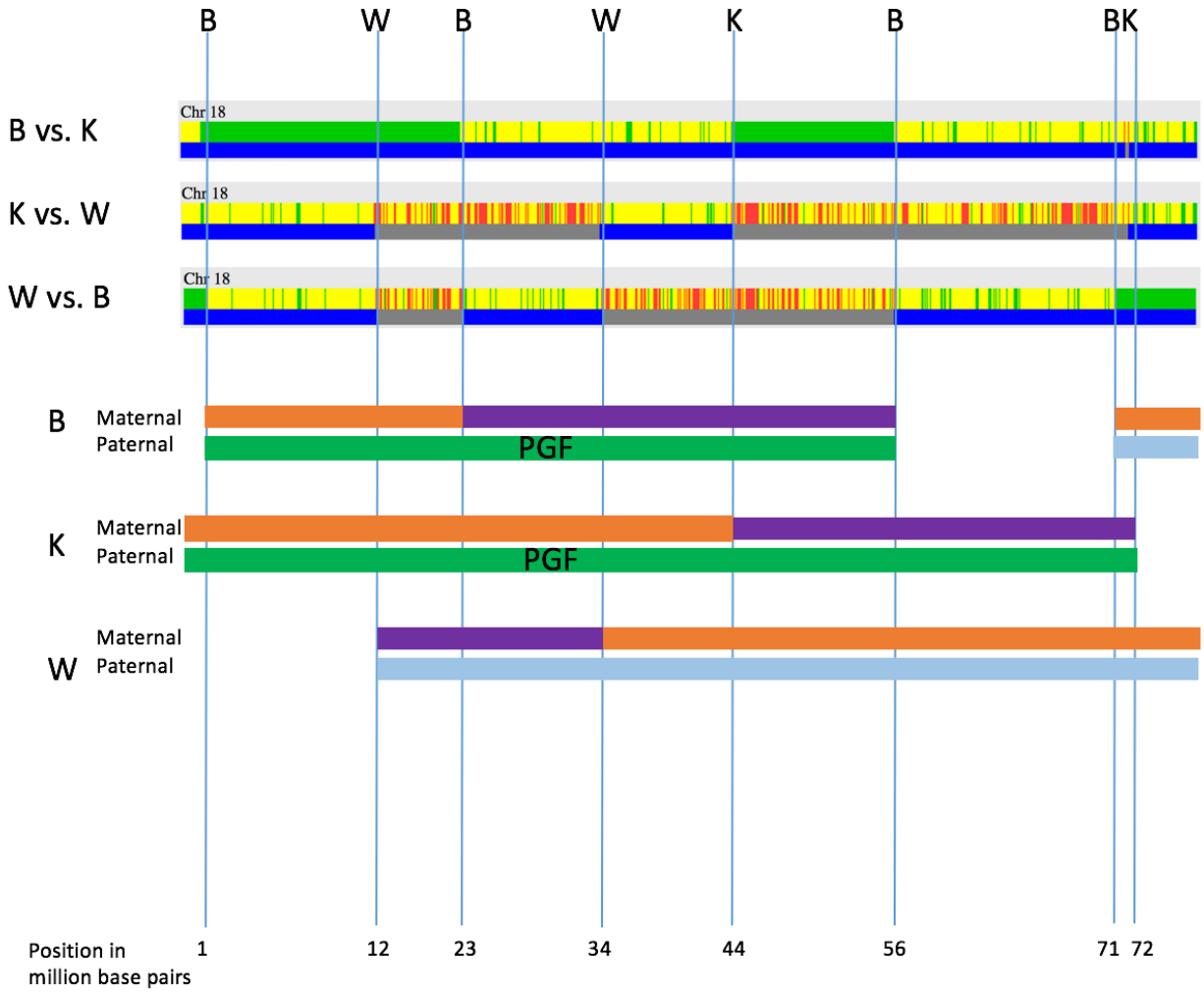
16. We also now know that the green-blue colors are paternal, while the orange-purple colors must be maternal as shown below:



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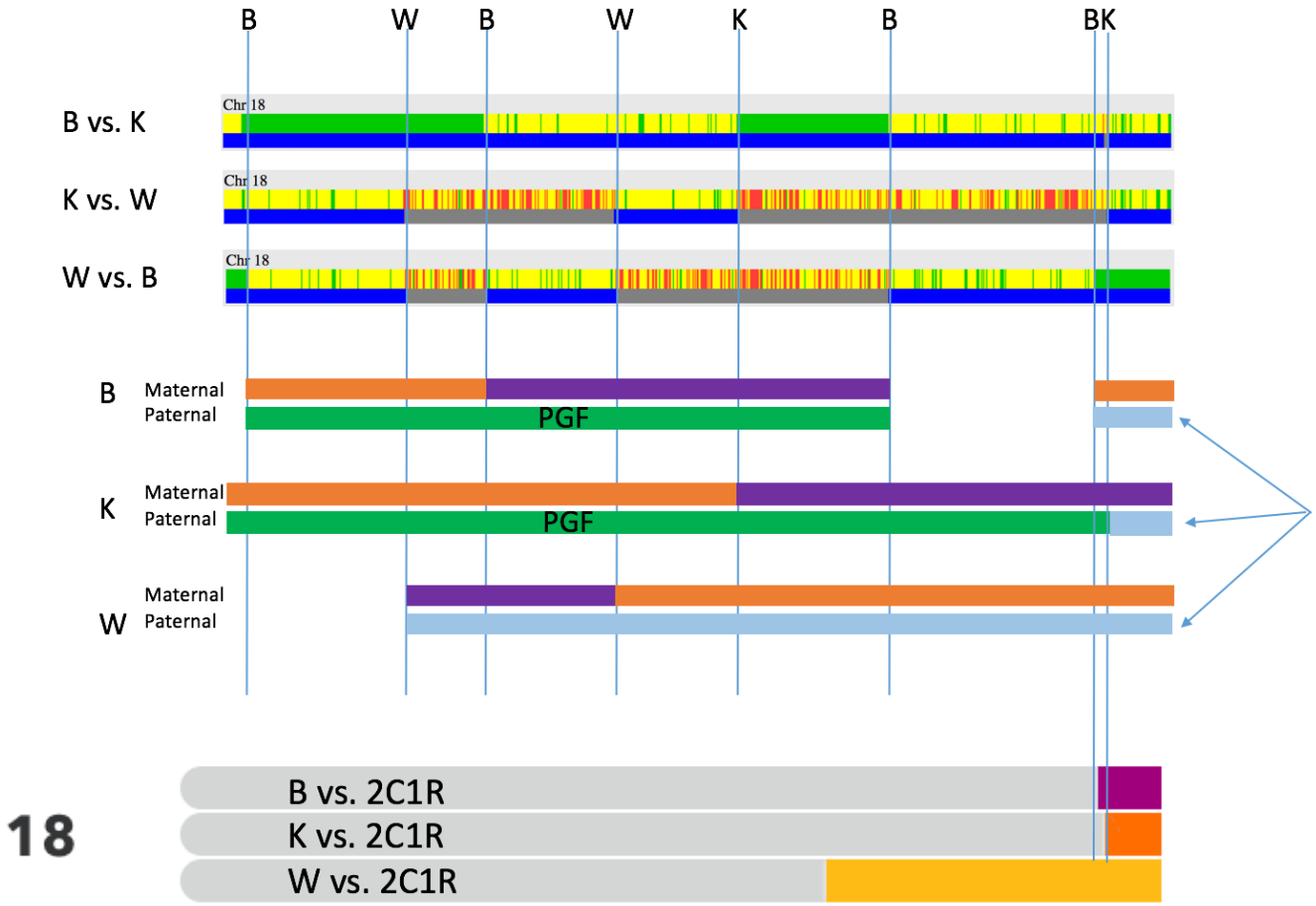
17. A second cousin once removed related to the PGM (Paternal Grandmother) provided the needed proof for the rest of the paternal assignments. The start borders in the 23andMe comparison showed differences between the siblings that indicated B and K received close crossovers at 71-72 million, but not exactly in the same location.



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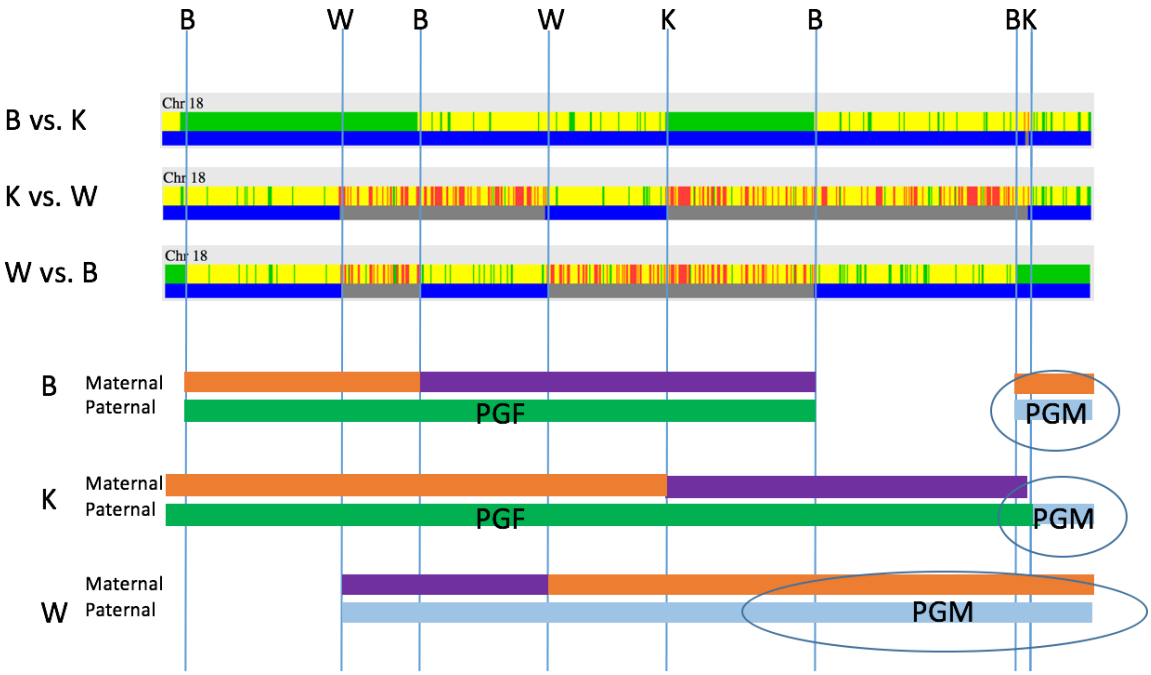
18. Assign blue PGM to the last segment for K because the cousin not only relates to the paternal grandmother but also because the borders and segments must match within the paternal chromosome. Through process of elimination, the maternal line has no crossover point for K at the end and a maternal relative later confirmed the configuration. The last crossover for B also only involves the paternal blue chromosome and not the orange. Note that the Build 36 position numbers were no longer available at 23andMe so conversions may be necessary to match the GEDmatch start points. Currently the different builds are usually within a million base pairs of each other.



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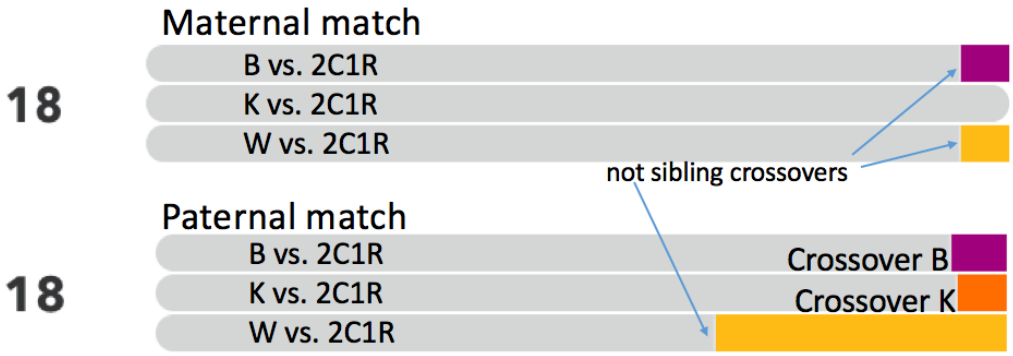
19. Another cousin was identified who was only related to the MGF's side of the family and as expected did not match the cousin above. One group of chromosome segments fits with maternal orange and the other group fits with paternal blue. It is always helpful when cousins match your family on the same chromosome location but they do not match each other proving the maternal and paternal identity of the segments.



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20. A paternal uncle confirmed the first crossover at position 1 for B. All remaining maternal and paternal crossovers could be identified by either the process of elimination or by testing known relatives. Reconstruction of most of the grandparent contributions (represented by all four colors covering most of the chromosomes) was possible using no more than three siblings despite the fact that no direct line ancestors were still living.

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Conclusions

Knowing the recombination patterns for a family group can be very useful in researching matches with unknown persons in the company and third-party databases. Using the approach described herein, we can map every part of the chromosomes of a group of siblings back to particular grandparents. A comparison of just one sibling with an unknown person will not tell us exactly which grandparent we are matching through, but by examining the pattern of matches of each sibling with the unknown person, and comparing with the phased chromosome diagrams, we can determine just which grandparent that the matching segment came through to the siblings.

The methods described here can be applied to each of the 22 autosomal chromosomes, and usually the X chromosome as well, to completely determine the way that recombination has occurred in a family group. Two approaches to recombination analysis, one more computational in nature, and the other more visual, have been described and illustrated.

Since these methods were developed, several third-party tools have appeared that make the process easier. For example, see below under Web Resources, Steven Fox. Also, the DNAPainter tool has gained popularity as an aid to chromosome mapping to more distant ancestors.

It has been somewhat surprising to us in analyzing several family groups that over several generations, the contributions, by great-great-grandparents for example, may vary widely, from 3% to 9% in one case, when an average of 6.25% would be expected. In the case of one particular small chromosome in the family of one of us (Athey), I received my father's maternal chromosome copy whole (which he got from his mother), and I passed it whole to my daughter, and she passed it whole to her son, all without any detectable recombination in four generational passages. There was another interesting finding in a grandson's recombination diagrams--there were many chromosomes where only three or four of my daughter's eight great-grandparents, contributed anything to the copy that she passed to her son.

In the analysis of several family groups using our method, we have confirmed the previous suggestions that males produce fewer crossovers than females in putting together the composite chromosome that is passed to offspring (Coop 2008). For example, in the four-sibling analysis presented above, there were two crossovers (total, in all four siblings) on the paternal side and nine crossovers on the maternal side. In the 22 pairs of chromosomes of these same four siblings, there was only one chromosome pair where there were more crossovers on the paternal side than the maternal side, and the excess was only one crossover. In the example of the visual approach, there were three crossovers on the paternal side and five on the maternal side.

Males also tend to put in crossovers near the beginning of chromosomes, say a location under 5 million, whereas females usually do not.

In summary, recombination is not a very regular or even process on any given chromosome in terms of the relative contributions of grandparents and great-grandparents. It only approximately approaches normality in the average of contributions of ancestors over all chromosomes.

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Web Resources

Four-Sibling Excel Spreadsheet http://www.hprg.com/storage/Recomb-4-Siblings.xlsx

Instructions for using the 4-sibling spreadsheet http://www.hprg.com/storage/Instructions-4-Sib.docx

Three-Sibling Excel Spreadsheet http://www.hprg.com/storage/Recomb-3-Siblings.xlsx

Instructions for using the 3-sibling spreadsheet http://www.hprg.com/storage/Instructions-3-Sib.docx

GEDmatch http://www.gedmatch.com

David Pike's Utilities http://www.math.mun.ca/~dapike/FF23utils/

Blaine Bettinger's blog, The Genetic Genealogist, has a five-part series exploring the visual phasing technique, and this has been instrumental in bringing the technique to a wider audience. See: http://thegeneticgenealogist.com/2016/11/21/visual-phasing-an-example-part-1-of-5/

Steven Fox has developed an Excel-based program to do much of the time-consuming parts of the visual phasing process. A video presentation may be found at: https://vimeo.com/224877731/6ba212fa67. To access the Excel program you must join the Visual Phasing Working Group on Facebook and download it from that site. The Visual Phasing Working Group site provides many helpful suggestions, and feedback may be obtained on any problems that arise.

Conflicts of Interest

The author(s) declare no conflicts of interest and no commercial interests in the subjects covered by this study.

References

Athey TW (2010a) The numerical method was first presented by one of us (Athey) in September 2010 at the monthly meeting of the Northern Virginia Genetics Interest Group of the National Genealogical Society. A more developed and formalized version of this work was again presented to the same group in the Spring of 2016.

Athey TW (2010b) Phasing the chromosomes of a family group when one parent is missing. *Journal of Genetic Genealogy*, **6**(1).

Coop G, Wen X, Ober C, Pritchard JK, Przeworski M (2008) High-Resolution Mapping of Crossovers Reveals Extensive Variation in Fine-Scale Recombination Patterns Among Humans. *Science*, **319**:1395-1398. DOI: 10.1126/science.1151851 (http://science.sciencemag.org/content/319/5868/1395.full)

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Johnston K (2015) "Visual Phasing of a Single Chromosome -- the Use of Crossover Lines." Presented on the Family Tree DNA Forum, "Family Finder Advanced Topics," 23 Jan 2015.

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Table S1. Look-Up Table--Converting Segment Matching Patterns to Pairs of Chromosome Inheritance Patterns

Segment Matching Patterns							Chromosome Inheritance Patterns	
Sib1-Sib2	Sib1-Sib3	Sib1-Sib4	Sib2-Sib3	Sib2-Sib4	Sib3-Sib4		(either order)	
2	2	2	2	2	2		1	1
2	2	1	2	1	1		1	2
2	1	2	1	2	1		1	3
2	1	1	1	1	2		1	4
1	2	2	1	1	2		1	5
1	2	1	1	2	1		1	6
1	1	2	2	1	1		1	7
1	1	1	2	2	2		1	8
2	2	2	2	2	2		2	1
2	2	0	2	0	0		2	2
2	1	1	1	1	0		2	3
2	1	0	1	0	1		2	4
1	2	1	1	0	1		2	5
1	2	0	1	1	0		2	6
1	1	1	2	0	0		2	7
1	1	0	2	1	1		2	8
2	1	2	1	2	1		3	1
2	1	1	1	1	0		3	2
2	0	2	0	2	0		3	3
2	0	1	0	1	1		3	4
1	1	2	0	1	1		3	5
1	1	1	0	2	0		3	6
1	0	2	1	1	0		3	7
1	0	1	1	2	1		3	8
2	1	1	1	1	2		4	1
2	1	0	1	0	1		4	2
2	0	1	0	1	1		4	3
2	0	0	0	0	2		4	4
1	1	1	0	0	2		4	5
1	1	0	0	1	1		4	6
1	0	1	1	0	1		4	7
1	0	0	1	1	2		4	8
1	2	2	1	1	2		5	1
1	2	1	1	0	1		5	2
1	1	2	0	1	1		5	3
1	1	1	0	0	2		5	4
0	2	2	0	0	2		5	5
0	2	1	0	1	1		5	6
0	1	2	1	0	1		5	7

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0	1	1	1	1	2		5	8
1	2	1	1	2	1		6	1
1	2	0	1	1	0		6	2
1	1	1	0	2	0		6	3
1	1	0	0	1	1		6	4
0	2	1	0	1	1		6	5
0	2	0	0	2	0		6	6
0	1	1	1	1	0		6	7
0	1	0	1	2	1		6	8
1	1	2	2	1	1		7	1
1	1	1	2	0	0		7	2
1	0	2	1	1	0		7	3
1	0	1	1	0	1		7	4
0	1	2	1	0	1		7	5
0	1	1	1	1	0		7	6
0	0	2	2	0	0		7	7
0	0	1	2	1	1		7	8
1	1	1	2	2	2		8	1
1	1	0	2	1	1		8	2
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0	1	0	1	2	1		8	6
0	0	1	2	1	1		8	7
0	0	0	2	2	2		8	8

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Table S2. Same as Table S1, but Sorted on Segment Matching Patterns for Ease of Look-Up

Segment Matching Patterns							Chromosome Inheritance Patterns	
Sib1-Sib2	Sib1-Sib3	Sib1-Sib4	Sib2-Sib3	Sib2-Sib4	Sib3-Sib4		(either order)	
0	0	0	2	2	2		8	8
0	0	1	2	1	1		7	8
0	0	1	2	1	1		8	7
0	0	2	2	0	0		7	7
0	1	0	1	2	1		6	8
0	1	0	1	2	1		8	6
0	1	1	1	1	0		6	7
0	1	1	1	1	0		7	6
0	1	1	1	1	2		5	8
0	1	1	1	1	2		8	5
0	1	2	1	0	1		5	7
0	1	2	1	0	1		7	5
0	2	0	0	2	0		6	6
0	2	1	0	1	1		5	6
0	2	1	0	1	1		6	5
0	2	2	0	0	2		5	5
1	0	0	1	1	2		4	8
1	0	0	1	1	2		8	4
1	0	1	1	0	1		4	7
1	0	1	1	0	1		7	4
1	0	1	1	2	1		3	8
1	0	1	1	2	1		8	3
1	0	2	1	1	0		3	7
1	0	2	1	1	0		7	3
1	1	0	0	1	1		4	6
1	1	0	0	1	1		6	4
1	1	0	2	1	1		2	8
1	1	0	2	1	1		8	2
1	1	1	0	0	2		4	5
1	1	1	0	0	2		5	4
1	1	1	0	2	0		3	6
1	1	1	0	2	0		6	3
1	1	1	2	0	0		2	7
1	1	1	2	0	0		7	2
1	1	1	2	2	2		1	8
1	1	1	2	2	2		8	1
1	1	2	0	1	1		3	5
1	1	2	0	1	1		5	3

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1	1	2	2	1	1		1	7
1	1	2	2	1	1		7	1
1	2	0	1	1	0		2	6
1	2	0	1	1	0		6	2
1	2	1	1	0	1		2	5
1	2	1	1	0	1		5	2
1	2	1	1	2	1		1	6
1	2	1	1	2	1		6	1
1	2	2	1	1	2		1	5
1	2	2	1	1	2		5	1
2	0	0	0	0	2		4	4
2	0	1	0	1	1		3	4
2	0	1	0	1	1		4	3
2	0	2	0	2	0		3	3
2	1	0	1	0	1		2	4
2	1	0	1	0	1		4	2
2	1	1	1	1	0		2	3
2	1	1	1	1	0		3	2
2	1	1	1	1	2		1	4
2	1	1	1	1	2		4	1
2	1	2	1	2	1		1	3
2	1	2	1	2	1		3	1
2	2	0	2	0	0		2	2
2	2	1	2	1	1		1	2
2	2	2	2	2	2		1	1

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Journal of Genetic Genealogy

A CARPENTER, A BAKER, … A CAROTHERS? - A MULTIPLE MPE CASE STUDY

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Abstract

There are multiple instances where DNA testing, either autosomal DNA (atDNA) or Y-DNA, has uncovered a misattributed parentage event (MPE) whereby a biological parent is not the person expected. This article describes how a search for a paternal great-great grandfather of the author using DNA analysis led to the discovery of an MPE that negated one-fourth of the author's family tree and that his true surname should be BAKER … or should it? Building a BAKER family tree based on DNA matches identified James Alton Baker (1912-1996) as the author's biological grandfather instead of Oliver Ballard Carpenter (1914-1988) of record. The Baker line can be traced back to Hiram Baker (1806-?) and his wife Anna Marie Kellogg (1811-1881). Shared DNA matching and the What are the Odds? tool are used to place two different subgroups of Baker matches into the family tree. A Big Y-700 match who shares the same confirmed haplogroup (I-FT336746) as the author and is a direct descendant of John Carothers (d. 1796) is evidence of another MPE. Numerous atDNA matches of the author's father also descend from John Carothers. How or when Hiram Baker fits in with the Carothers line is unknown. Y-DNA results also demonstrate that Hiram Baker does not descend from Francis Baker of Yarmouth, Massachusetts, as some researchers have indicated.

Introduction

Before the use of genetic genealogy, the author's paternal family tree is shown in Figure 1. Charles and Rose are children of Emma May Keyes from her first marriage. She remarried about 1890 to William Leslie Carpenter. William's obituary, along with Charles' death certificate, indicate Emma's first husband's surname was Thompson (first name unknown). Charles and Emma are listed with the Thompson surname and as step-children of Warren in the 1900 federal census for Galeton, Potter Co., PA. Charles is listed with the Carpenter surname in the 1910 census for Wharton Twp., Potter Co., PA. Although the author had no experience with genetic genealogy, it was thought it might open doors to help find the biological father of Charles and Rose.

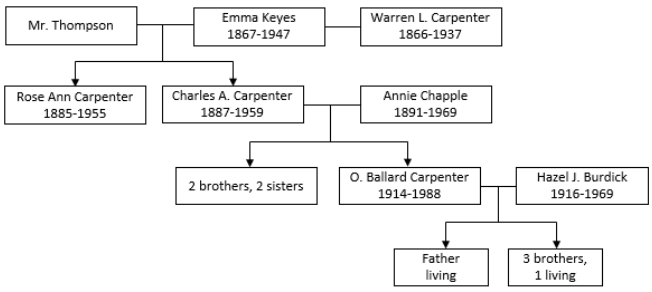

Figure 1. Author's Paternal Lineage Pre-DNA Testing

The author started DNA testing in 2018, first with AncestryDNA and eventually with the other four major companies. At the top of Ancestry's match list were two females that were unknown to the author.

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The amount of shared DNA for each is 557 cM and 462 cM respectively. According to the Shared cM Project, version 3.0[1], these individuals are close relatives, most likely half-first cousins, half-great nieces or first cousins, once removed. Due to the age of the author (67), half great aunts or great-great aunts were ruled out.

Determining how these two matches are related led to a totally unexpected surprise – the misattributed parental event (MPE). The following report will demonstrate three instances of MPE. The first case had an immediate impact since it negated one-fourth of the author's family tree. Building out the new tree uncovered a case of adoption at birth and the last case was discovered using Y-DNA. A possible fourth case involves a cluster of DNA matches that descend from a single person that will be shown to belong in the new tree, but genealogical records cannot place him.

Methods and Data

Uncovering the Pivotal MPE

This report utilizes only AncestryDNA match data. For privacy concerns, initials will be used for the unknown DNA matches. The first unknown match, BS, actually made things easy by contacting the author for help, indicating that she was an adopted child and her birth father was Sidney Clark Baker (1927-2000). She also indicated that the next closest unknown DNA match (SY) was her half-sister, also a child of Sidney. Sidney was a traveling musician and managed to have at least 17 children with at least four different spouses/partners.

The author manually generated shared matching clusters in an Excel spreadsheet for BS and SY. All shared matches were unknown and many of them indicated relatively close relationships. It became necessary to determine if this unknown branch belonged to the author's paternal or maternal line. Two brothers and two sisters had also tested with Ancestry, along with author's father. One of the sisters is a half-sister and is not a biological daughter of the author's father. BS and SY were found as DNA matches for both brothers and the full sister as well as the author's father, thus establishing a paternal linkage. When presented with this knowledge, the author's father discussed a hunch that he had always felt he was not Oliver's son, mainly from how he was treated growing up. With this revelation, the only surviving brother of the author's father was tested with Ancestry. His results came back as a half-brother, and he had the expected matches along Charles Arthur Carpenter's maternal line. The first pivotal MPE had been uncovered.

The Baker Family Tree

By knowing the father of the matches, traditional genealogical practices were used to build a Baker family tree as shown in Figure 2.

Sydney Baker's parents were James Alton Baker and his first wife, Catherine Jane Clark, daughter of Otto Clark and Edith Pfaff. They also had a daughter

[1] Version 3.0 has been superceded by Version 4.0 in March 2020. The average cM values and ranges changed slightly as a result of sampling a larger data base. The likely relationship of the two DNA matches will not change.

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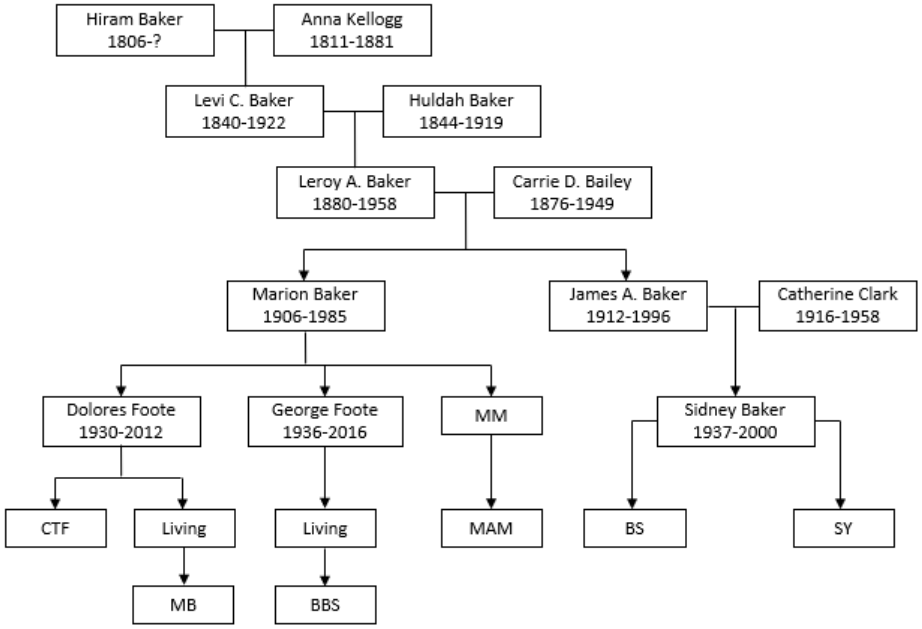

Figure 2. Abbreviated Baker Family Tree Connecting Close Family DNA Matches

that is still living. James is the fourth child of Leroy Alexander Baker and his first wife, Carrie Dell Bailey, daughter of Bradley Perry and Lenora Warner. Leroy and Carrie had four other children: 1) Marion Frances who married Adrian Foote, 2) Lawrence Wellington (1907-1933), 3) Edna Mae (1909-1999) who married Anthony Fabroni, and 4) Russell Bailey (1920-1985) who was unmarried. Leroy is the only son of Levi Carver Baker and his second wife, Huldah Baker, daughter of Almond Baker and Hannah Roblyer. Leroy also had a sister, Anna V., who was married three times. Levi is the third child of Hiram Baker and Anna Marie Kellogg, daughter of Amasa Kellogg and Eunice Chadwick. Hiram and Anna had two other children – Lyman (1834-1925), who married Elizabeth Gravely, and Elvira (1838-1862), who married James Warren. Little is known about Hiram. According to the Kellogg genealogy (Hopkins [1903]), he was born 7 Aug 1806 in Rochester, NY to Josiah and Mary Baker. He was a farmer and mechanic, living in Columbia, Bradford and Sullivan Counties in Pennsylvania. He was last heard from in 1860 while visiting his sister.

Unless stated otherwise, discussions of DNA matches are relative to the author's father. As of this writing, there are five confirmed DNA matches in Ancestry that are descendants of Leroy and Carrie Baker's daughter Marion. Based on the amount of shared DNA with these matches, James Alton Baker is believed to be the paternal grandfather of the author. The brothers of James were ruled out as the grandfather since Lawrence died over a year before the author's father was born and Russell would have only been 14. The relationship seems plausible in that James and Hazel Burdick were both living in the Nunda, NY area between 1930 and 1940 and there is a four-year age difference between them. Table 1 shows how the author arrived at this conclusion based on values from the Shared cM Project, Version 3.0. These relationships were also confirmed by trees that the DNA matches provided.

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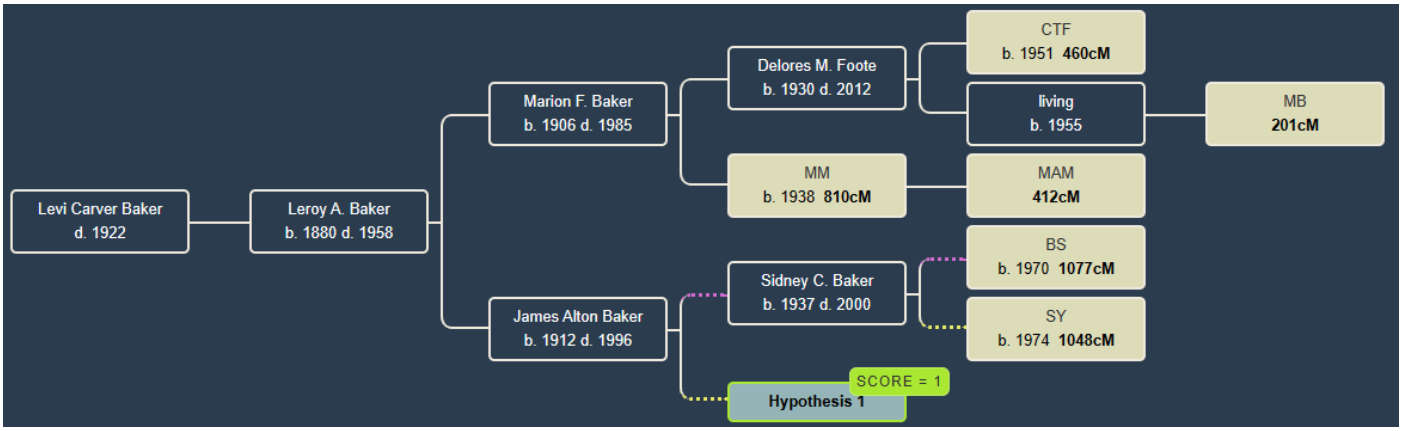
Table 1. DNA Matches Descended from Leroy Baker

Match	Assumed Relationship	actual	estimated average	estimated range
BS	half-niece	1077	891	500 - 1446
SY	half-niece	1048		
MM	1C	810	874	553 - 1225
CTF	1C1R	460	439	141 - 851
MAM	1C1R	412		
MB	1C2R	201	229	43 - 531
BBS	1C2R	109		

Recently, the What Are the Odds? (WATO) tool in DNA Painter was used to check this hypothesis. Figure 3 shows that the WATO tool predicts only one hypothesis with a positive probability, the one the author assumed.



Match name & Shared cM		Hyp. 1
BS	1077	Half Aunt / Uncle 99.02%
SY	1048	Half Aunt / Uncle 100.00%
MM	810	1C 95.02%
CTF	460	1C1R 87.08%
MB	201	1C2R 45.41%
Combined odds ratio		**1.00**

Figure 3. Where Does The Author's Father Fit In the Baker Tree?

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Connecting Descendants of an Adoptee

DNA match HEH shares 533 cM with the author's father. He supplied his family tree, identifying himself as a child of Doris L. Smith (1923–1998). When the author researched Doris, it was discovered that the indicated parents in the tree were for a different Doris Smith. After contacting HEH in November of 2019, the author was told that Doris was adopted by David P. and Marion Smith and passed on without telling whom her real parents were. Based on the amount of shared DNA, Doris was initially placed as an undocumented sister of James Alton Baker. In November 2021, the author was in contact with MM and was told that Doris was believed to be a half-sister that was given up for adoption since their mother was only 17.

The WATO tool was used to check this hypothesis using amounts of shared DNA from HEH (HEH was kind enough to share his DNA match list with the author). As shown in Figure 4, the initial assumption was not a very good one while the half-sister of MM is the best.

Table 2 identifies the DNA matches that are descendants of Doris Smith. She had two husbands. HEH is from her first marriage; SL and HH are his children. The estimated values reflect Version 4.0 of the Shared cM Project. MB and AB are descendants from Doris' second marriage.

The author asked MM and HEH if they would be willing to do mitochondrial DNA tests which would prove the half-sibling assumption, but HEH is satisfied with these results and sees no reason for the test.

Table 2. DNA Matches Descended from Doris Smith

Match	Relationship	actual	estimated average	estimated range
HEH	1C1R	433	433	102 - 980
SL	1C2R	273	221	33 - 471
HH	1C2R	262		
MB	1C2R	263		
AB	1C3R	237	117	25 - 238

Extended Family Connections

The next batch of DNA matches are descendants of Lyman Baker, brother to Levi Carver Baker and son of Hiram Baker. As such, the author expected shared DNA amounts associated with 3rd cousins, their children and grandchildren. Again, these relationships have been verified with supplied trees and genealogical records.

Table 3. DNA Matches Descended Lyman Baker

Match	Relationship	actual	estimated average	Estimated range
JB	3C	70	73	0 - 234
RBJ	3C	51		
FC	3C	49		
PA	3C1R	65	48	0 - 192
DMB	3C1R	52		
MG	3C1R	49		
RG	3C1R	43		
BG	3C1R	38		
DA	3C1R	26		
DK	3C1R	26		
PJ	3C1R	25		
DGS	3C1R	21		
KF	3C1R	15		
RG2	3C2R	35	36	0 - 166
JR	3C2R	23		
NH	3C2R	16		
AI	3C2R	7		

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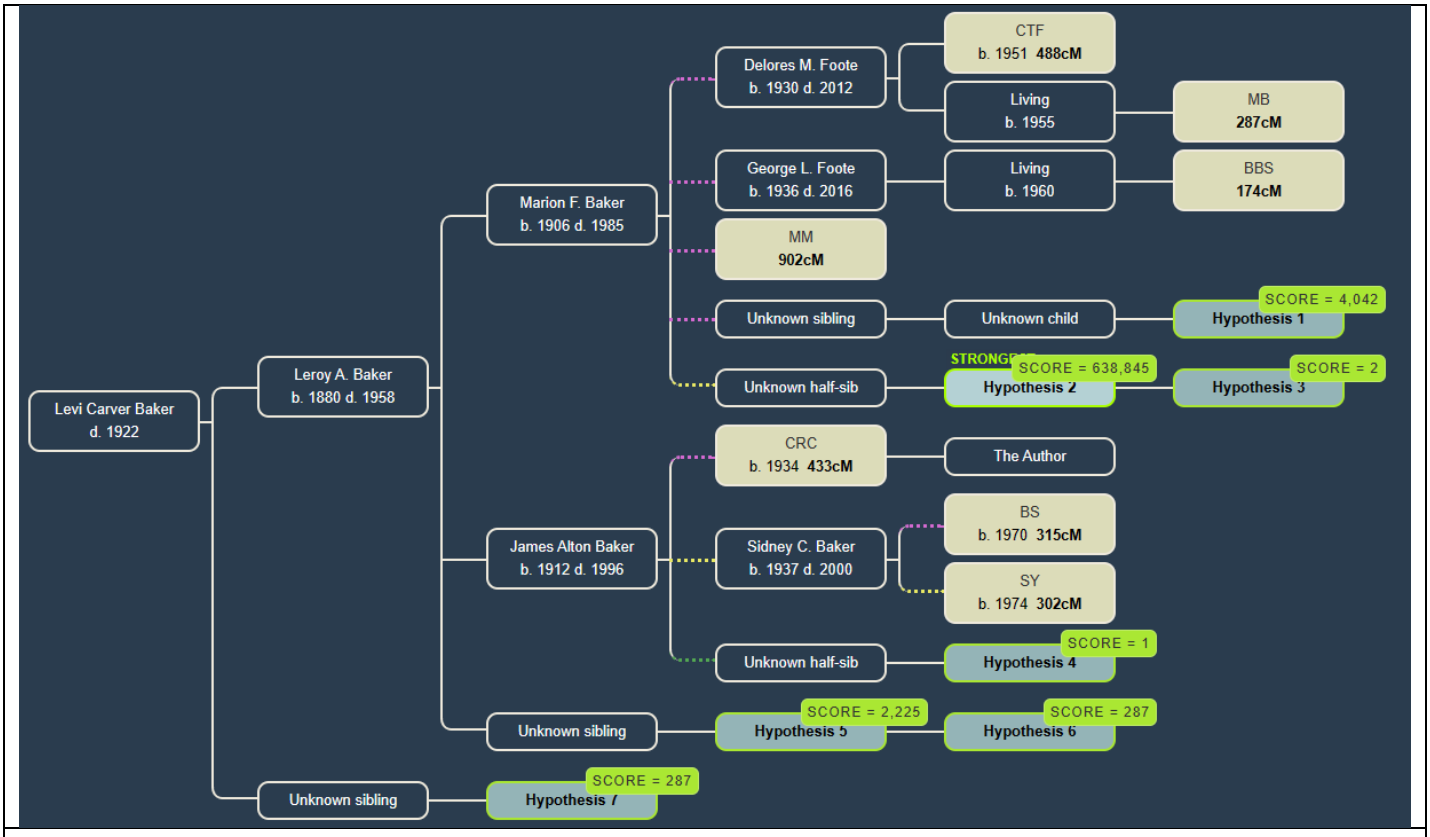

Match name & Shared cM		Hyp. 1	Hyp. 2	Hyp. 3	Hyp. 4	Hyp. 5	Hyp. 6	Hyp. 7
MM	902	Great-Niece / Nephew 98.33%	Half Niece / Nephew 98.33%	Half Great-Niece / Nephew 1.67%	1C1R 1.67%	1C 98.33%	1C1R 1.67%	1C1R 1.67%
CTF	488	1C1R 89.25%	Half 1C 89.25%	Half 1C1R 6.42%	2C 6.42%	1C1R 89.25%	2C 6.42%	1C2R 6.42%
CRC	433	1C2R 17.31%	1C1R 82.05%	1C2R 17.31%	Half Niece / Nephew 0.63%	1C 0.63%	1C1R 82.05%	1C1R 82.05%
BS	315	2C1R 8.49%	2C 52.08%	2C1R 8.49%	Half 1C 39.43%	1C1R 39.43%	2C 52.08%	1C2R 52.08%
SY	302	2C1R 10.33%	2C 56.19%	2C1R 10.33%	Half 1C 33.48%	1C1R 33.48%	2C 56.19%	1C2R 56.19%
MB	287	2C 59.15%	Half 1C1R 59.15%	Half 2C 14.23%	2C1R 14.23%	1C2R 59.15%	2C1R 14.23%	1C3R 14.23%
BBS	174	2C 33.45%	Half 1C1R 33.45%	Half 2C 51.20%	2C1R 51.20%	1C2R 33.45%	2C1R 51.20%	1C3R 51.20%
Combined odds ratio		**4041.77**	**638844.83**	**1.82**	**1.00**	**2224.66**	**287.17**	**287.17**

Figure 4. Where Does HEH Fit In the Baker Tree?

Where Do These Matches Belong?

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The last batch of DNA matches poses a problem. These individuals descend from William J. Baker, born 28 Aug 1872 and died 9 Feb 1963. To date, the author has not been able to determine who his parents are. A Shared DNA cluster diagram (Figure 5) was generated manually in an Excel spreadsheet. The tight coupling demonstrates that these individuals do descend from Hiram and Anna Baker as they share DNA from all three previous groups. The open question is how.

The assumption is to place William J. Baker as a son of Levi Carver Baker with a mother to be determined. This is based on the magnitude of the DNA matches – 426 cM (LB), 261 cM (SM), and 253 cM (JH). All three are grandchildren of William. These values, along with their birth years, suggest second cousins or their children.

The issue with this placement in the family tree is William's birthdate. He was born after Levi's first wife died and before he married his second wife. There is no paper trail to indicate another wife.

Using WATO, the real question that would like to be asked is where William J. fits into the Baker tree. Instead, one must test the grandchildren individually. Unfortunately, there is no capability to create a sub-tree and test all three assumptions at once.

Figure 6 asks where LB could fit. Hypothesis 1, 2, 3 and 4 are automatically eliminated, even though hypothesis 2 was deemed the strongest. William Baker cannot be the son of James or Leroy Baker. Hypothesis 6 could work if the test was for William, not his grandchild. Hypothesis 5 is the only one that works when the age of William is factored in and knowing the target subjects are his grandchildren. The same conclusion is reached when SM and JH are tested (See Figures 7 and 8).

We are still stuck with the problem of William's birth date. The date comes from the Social Security Death Index. How reliable is it? Could it have been transcribed incorrectly? Ancestry does not show the original document. The 1900 Federal Census lists a William J. Baker born in August 1872 living as a servant in the household of the Sidney Disinger family living in Fayette Township, Seneca County, New York. Our William does live in Seneca Falls by 1910. Unfortunately, the birth state of his parents is inconsistent from census to census so that cannot be used as a check.

Another analysis was tried by starting with William's sub-tree and asking how the author's father would fit in. This does not work either. The problem is that there is additional information that must be factored in, such as known relationships of the target subject and birth dates of all people involved.

Perhaps with the judicious use of X, Y and mtDNA analysis, one could prove the true relationship of William to Levi, provided the correct combination of male and female descendants are available to test.

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	CTF	MB	BBS	HH	AB	MB	BS	SY	HEH	SL	MAM	MM	Me	JH	LB	SM	NB	JB	PA	DA	DMB	RBJ	MG	RG	DK	FC	PJ	DGS	BG	RG2	JR
CTF		X	X	X	X	X	X	X	X	X	X	X	X		X						X										
MB	X		X	X		X	X	X	X	X	X	X	X																		
BBS	X	X		X	X	X	X	X	X	X	X	X			X																
HH	X	X	X		X	X	X	X	X	X	X	X	X	X																	
AB	X		X	X		X	X	X	X	X	X	X	X	X					X												
MB	X	X	X	X	X		X	X	X	X	X	X	X	X	X																
BS	X	X	X	X	X	X		X	X	X	X	X	X					X	X												
SY	X	X	X	X	X	X	X		X	X	X	X	X	X	X		X	X	X		X			X							
HEH	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X	X		X	X											
SL	X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X		X	X											
MAM	X	X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X		X	X	X									
MM	X	X	X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X	X	X	X									
Me	X	X		X	X	X	X	X	X	X	X	X		X	X	X	X	X	X	X	X	X	X	X							
JH				X	X	X		X	X	X	X	X	X		X	X	X	X	X	X			X	X	X	X					
LB	X		X			X		X	X	X	X	X	X	X		X	X		X	X		X	X	X			X	X			
SM									X	X	X	X	X	X	X		X	X	X	X	X		X	X			X	X			
NB								X	X	X	X	X	X	X	X	X				X	X		X	X			X				
JB							X	X			X	X	X		X					X	X	X	X	X	X	X	X	X	X	X	
PA					X		X	X	X	X		X	X	X	X	X	X	X			X		X	X	X	X	X	X	X	X	X
DA									X	X	X		X	X	X	X	X	X	X		X	X	X		X	X	X		X		X
DMB	X							X			X	X	X			X		X		X		X	X		X	X	X				
RBJ											X	X	X	X	X		X	X	X	X	X		X	X	X	X	X	X	X	X	X
MG													X	X	X	X	X	X	X	X	X	X				X			X		
RG								X					X	X	X	X		X				X			X	X		X	X	X	X
DK														X			X	X	X	X	X		X		X	X	X	X	X	X	X
FC														X				X		X	X	X	X	X		X	X	X	X	X	X
PJ															X	X	X	X	X	X	X				X	X					
DGS															X	X		X	X			X		X	X	X			X	X	X
BG																		X	X	X		X	X	X	X	X		X		X	X
RG2																		X	X			X		X	X	X		X	X		X
JR																			X	X			X	X	X	X		X	X	X	

Descendants of James Alton Baker
Descendants of Leroy Alexander Baker
Descendants of Lyman Baker
Descendants of ?

Figure 5. Shared DNA Cluster Analysis Using Father's DNA Match List

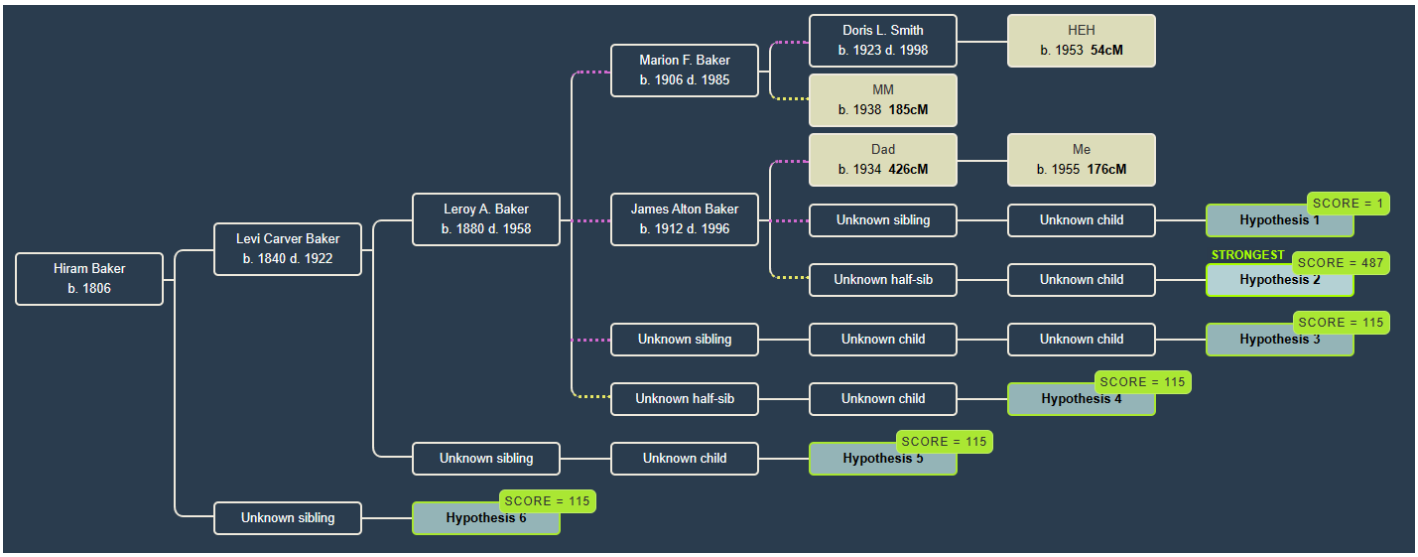

Figure 6. WATO hypothetical placements of LB (b. 1956)

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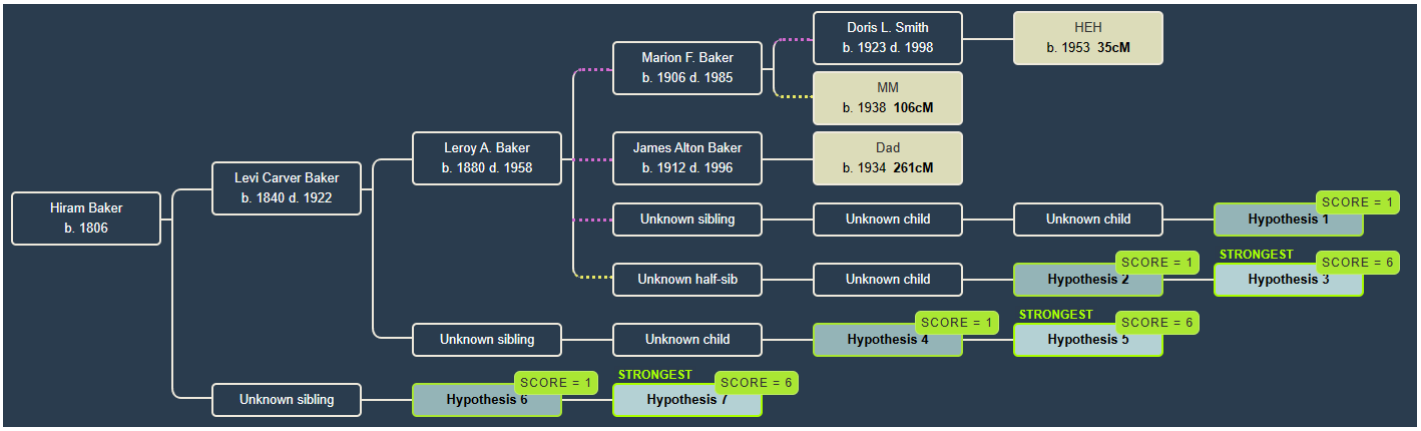

Figure 7. WATO hypothetical placements of SM (b. 1939)

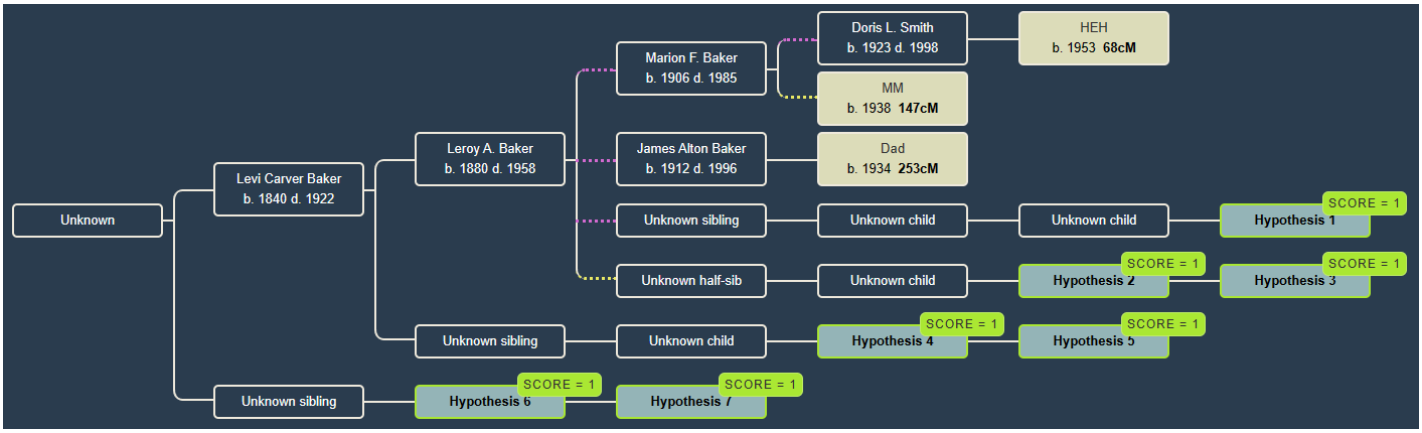

Figure 8. WATO hypothetical placements of JH (b. 1929)

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Using Y-DNA

So far, all analysis has involved atDNA. Y-DNA could also be used to help solidify any conclusions that have been made such as the initial MPE, William J. Baker's paternal parentage, and possibly extending the Baker lineage beyond Hiram Baker. Levi Baker's wife Huldah is also a Baker. Is her line the same as her husband's?

The author initially ordered the Y-111 test which resulted in an estimated haplogroup of I-M253. There were no matches at any STR testing level that had the Baker surname. This doesn't necessarily mean that there is not a Baker ancestor beyond Hiram. A male ancestor from such an individual just has not taken a Y-DNA test yet. Eventually, DNA match DMB had the Y-111 test done at the author's request. As expected, his estimated haplogroup is I-M253.

To see if there are any possible Baker ancestors, the author looked in the Baker group project and extracted all testers that have the estimated haplogroup of I-M253. At the time of this writing, there were 116 testers including the author that fall into this category. The data was arranged in an Excel spreadsheet by the size of the test taken. Similar to what is done in the surname projects, the STR value for each single valued marker was color coded relative to the author's value to visualize a possible close relationship. In the author's opinion, the Y-111 test values are the most useful since it will provide the best estimate of genetic distance. Deviations in STR values were encountered across the board, regardless of what level of testing was done. With the exception of DMB, 70 out of 111 markers showed deviations. DMB has only two markers that deviate by a value of one each.

Upon closer examination of the other testers in the Baker group project, the author found two testers that descend from Josiah Baker (1765-1847), grandfather of Huldah Baker, wife of Levi Carver Baker. Josiah is a son of Josiah Baker (1735-~1820) and Sarah Haynes (1736-1840). The first tester only did the Y-37 STR test and shows an estimated haplogroup of R-M269. The other tester had either the Big Y-500 or Big Y-700 test done and belongs to haplogroup R-BY101963. Since Levi Baker descends from the I-M253 line, he is not related to his wife.

The elder Josiah is consistently shown across the various genealogy websites as a son of Josiah Baker (1704-1795) and Charity Eddy. This Josiah is a descendant of Francis Baker (1611-1696) of Yarmouth, Massachusetts (Baker [1931]). The cited reference does not list a Josiah as a child of Josiah and Charity. However, the Baker group administrator specifically groups the two testers mentioned above in with a group that is labelled as being descendants of Francis Baker. Assuming the lineage is correct, Hiram Baker cannot be a descendant of Francis Baker of Yarmouth.

The Carothers MPE

The purpose of shared DNA clustering is to potentially identify a common ancestor or ancestral couple. Once the clusters of shared DNA have been generated, it is necessary to identify the commonality in the family trees of each member of the cluster if possible, which will lead to identifying the common ancestor or ancestral couple. DNA match clusters were manually generated that specifically targeted the descendants of William J. Baker. From the clusters that were generated, the author was able to trace the ancestry of 11 individuals to John Carothers/Crothers. John was of Scottish descent, coming to America from Northern

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Ireland around 1755. He originally settled in Little Britain, NY, moving to Ballston, NY shortly after the American Revolution, then to Phelps, Ontario Co., NY where he died on 1 Jul 1796. He had seven children – Robert Pegel, John, Elizabeth, Sally, Henry, William and Nancy. Three of the children (Robert Pegel, Henry and William) died in Wayne or Ontario County, NY. These two counties border Monroe County, NY to the East and Southeast. Hiram Baker is reported to have been born in Monroe County.

Using the surname search tool, a total of 29 DNA matches were found that descend from John. Table 4 lists those matches, grouped by the children (generation 2), then by the grandchildren (generation 3). The generation of each match is given along with the amount of shared DNA. The last few columns indicate which people in the Baker tree share matching DNA or have the Carothers descendant in their respective list of DNA matches. The matches highlighted in red indicate two grandchildren that married each other resulting in pedigree collapse. Even if the amount of shared DNA is exaggerated because of the collapse, it still reflects a distant relationship most likely beyond 5th cousin of the author's father. Descendants of Robert Pegel Carothers seem to show the closest relationship.

The fact that all four groups of Hiram Baker descendants share DNA with Carothers descendants implies the Carothers connection is older than Hiram Baker or Anna Kellogg. Anna's lineage is well documented and no Carothers are known as ancestors. This leads to the assumption that the Carothers must be in Hiram Baker's lineage. Y-DNA analysis proved it.

Table 4. DNA Matches of John Carothers Descendants

Generation 2	Generation 3	DNA Match	Generation	cM unweighted	cM longest	cM shared	# segments	BS	SY	MM	HEH	LB	SM	JH	JB	PA
Robert Pegel	John	MEC	8	Y-DNA Match												
		SL	9	32	32	25	1	X	X	X	X					
	William V.	JI	10	15	15	13	1			X	X					
		CM	7	68	68	52	1			X	X	X		X		
		GH	8	25	25	21	1	X	X							
		JP	9	26	26	20	1			X	X					
		BR	7	80	71	73	2	X	X	X	X	X	X	X		X
		DR	8	71	71	51	1	X	X	X	X	X	X	X		X
	J	MH	9	31	31	26	1	X	X		X					X
John	Wm. B	tomiswho1	8	15	15	13	1									
		GB	8	9	9	9	1									
	Austin	BB	7	48	39	31	2					X	X			
		WM	8	22	15	18	2				X	X				X
		DM	8	22	15	17	2				X	X				X
		JM	8	18	11	15	2									
		SM	9	21	15	15	2				X					
	Delora	sdtidwell	9	19	19	16	1			X	X					
		mnpbennet	9	23	23	22	1				X					
	D	DR	8	25	9	24	3			X				X	X	
E		RE	7	9	9	9	1									
Sally	N	AR	8	16	16	14	1				X					
N		DB	7	35	35	30	1	X	X	X	X					X
Henry	Hiram	LK	8	60	39	53	2									
		NS	8	15	15	9	1									
	Samuel W	WL	8	12	12	11	1			X						
		AW	7	30	19	28	2			X		X	X			
		HB	8	27	33	20	2					X				
		MM	6	66	41	61	2					X	X	X		
		mil268	7	16	8	14	2									
		EA	7	19	10	18	2					X		X		
W		MW	7	25	13	18	2									
Nancy	Nancy	BB	7	48	39	31	2					X	X			
		WM	8	22	15	18	2				X	X				X
		DM	8	22	15	17	2				X	X				X
		JM	8	18	11	15	2									
		SM	9	21	15	15	2				X					

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As mentioned previously, the author initially tested with FTDNA at the Y-111 level and later upgraded to the Big Y-700 test which at this time results in a confirmed Haplogroup of I-FT336746. As mentioned previously, there are no Baker surnames found in the lists of Y-DNA matches at any level (except for DNA match DMB who is at the top of the list with a genetic distance of 2). The Carruthers surname is prevalent along with variations such as Carothers and Crothers. Other surnames that appear frequently are Dunning, Akers, Stainback and Colburn.

The project administrator of the Carruthers Group project suggested that the author join his group and for good reason. The administrator grouped the tests as to where they belong on the Y-DNA haplotree. The author is descended from the Mouswald line of the Carruthers.

Eventually, another person, MEC, tested with Big Y-700 and shows up with the same confirmed haplogroup as the author with a genetic distance of 3. His mismatched markers are at DYS444, DYS715 and DYS504. All three are classified as fast mutators. The mismatched markers for DMB are at DYS710 which mutates very fast and DYS587 which mutates medium-slow

What is intriguing about MEC is that he is a direct descendant of Robert Pegel Carothers. As seen in Table 4, this path also exhibits the largest atDNA matches. With a genetic distance of 3, the MPE from Carothers to Baker could have occurred sometime in the 1700s and the author could be a descendant of Robert Pegel Carothers.

Summary

The original goal with DNA testing was to find the father of the author's great grandfather Charles Arthur Carpenter, nee Thompson. This study uncovered several instances of a misattributed parental event (MPE). With a clue given by a close DNA match of unknown relationship, a Baker family tree was generated. DNA testing of some of the author's sisters and brothers, his father and his uncle, showed that the Baker matches belong to the paternal line of the author's father. The first MPE is the discovery of the author's true grandfather, James Alton Baker. In the process of building out the Baker tree through conventional genealogical research, the author was able to link in a group of matches whose ancestor was an adoptee with unknown parentage (MPE 2). The most probable placement of the author's father and this sub-group in the Baker family tree has been confirmed using the What Are the Odds? (WATO) Tool in DNA Painter. Another subgroup of DNA matches can be shown to belong to the Baker tree using shared matching cluster analysis. This is a third MPE in that an unknown person is involved. In yet another twist, Y-DNA testing indicates a fourth MPE and that the author's parental line descends from John Carothers (d. 1796) of Scottish heritage, possibly through his son, Robert Pegel Carothers. The MPE could have occurred within a generation or two previous to the birth of Hiram Baker (1806-?), the author's third great-grandfather. Y-DNA results also demonstrate that Hiram Baker is not a descendant of Francis Baker of Yarmouth, Massachusetts, although Huldah Baker, wife of Hiram's son Levi, is.

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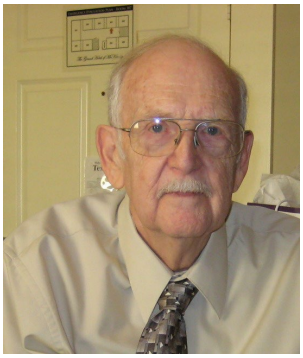
They say a picture is worth a thousand words. Meet the author's father (left)and James Alton Baker. The similarities are striking.



Acknowledgements

The author wishes to thank his father and uncle for taking the Ancestry DNA test which established a half-brother relationship and pointed the paternal line in a different direction. Steve Colburn, a Carruthers Y-DNA group project administrator, must also be acknowledged for guiding the author to the right direction of my paternal lineage. Thanks must also be given to Baker DNA match DMB who agreed to do a Y-111 test from FamilyTreeDNA which has helped to confirm the haplogroup I-FT336746.

Conflicts of Interest

The author declares no conflicts of interest and no commercial interests in the subjects covered by this study.

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Journal of Genetic Genealogy

Genetic Genealogy of Irish Terry lineages

Kevin Terry

Abstract

The focus of this paper will be to gain an insight to the genetic haplogroups or lineages of Irish Terrys; those from counties Cork and Waterford.[1] These are the counties where most Terrys came from in former times. Several testers from the United States, Ireland and Peru have their results on the web. One of the United States participants and the sole participant living in Peru, have Spanish Terry ancestry. The fact that the Spanish Terrys of Cadiz descended from Cork Terrys and in the case of one lineage, Terrile from Italy, is well documented.[2]

New insights to several Cork and Waterford Terry lineages, based on genetic data in combination with traditional genealogy are outlined. It also provides new insight to related lineages who settled in other parts of the world in recent centuries. Genetic time lines show the locational European origins of these lineages. How this information compares with what traditional genealogy said about these lineages is commented on. Some of the shortfalls in this approach in explaining Terry family history is considered.

Keywords: Terry surname, Cork, Waterford, genetic genealogy

Introduction

The surname Terry where it occurs in Ireland is most prevalent in counties Cork and Waterford. Over the centuries ancestors of these Terrys migrated to Continental Europe, Great Britain, the United States and Australia among other places. Their presence is found in Central and South America also, following from their settlement in Spain in the 18th century. Within this surname grouping are a small number of distinct lineages. Paper records can distinguish between these lineages back to about 1750. But for earlier than this time it is difficult to accurately distinguish between the lineages from paper sources. Genetic genealogy has contributed to distinguishing between the Terry lineages.

In this paper I will look at the role genetic genealogy has played in adding to our understanding of Terry lineages with reference to counties Cork and Waterford in Ireland. Also, descendant lineages of these Irish Terrys who settled abroad in former times will be considered. New analytical tools available from the DNA testing Company, FamilyTreeDNA, can show very clearly the outcomes of test results in terms of ancestral origins, genetic time lines and other information.

Six distinct genetic lineages will be examined. In concluding consideration will be given to how genetic information has added to and altered some previously held views on Terry ancestry.

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Origins in Ireland

The surname Terry is not a common name in Ireland. It is most prevalent in counties Waterford and Cork, with clusters of Terrys also to be found in West Clare and Donegal see Fig. 1. which shows the prevalence from the 1901 Census. When they first arrived in Ireland, some 800 years ago possibly to Cork or Waterford, for the most part they were rurally based.[3] However, from the early 15th century some branches of the surname are recorded as living in Cork city. These branches began to play a prominent role in the civic affairs of the city. They became one of the leading merchant families. They maintained this status for a period of about 230 years, until the mid-17th century. Terrys of Cork and Waterford are generally accepted as being an Anglo-Norman family. They are recorded as having settled in Cork from the thirteenth century. Records show that they were a landed family and were royal servants. They acted as jury members and were witnesses to several acquisitions. Some other spellings of the name were Tyrry, Tirry and Therry, as recorded in documents over the centuries. Over the centuries the number of people in Ireland at any given time bearing the surname Terry numbered in the low hundreds. In the 1901 Census of Ireland there were 266 people with this surname. As can be seen from Fig. 1, most were from Waterford and Cork.

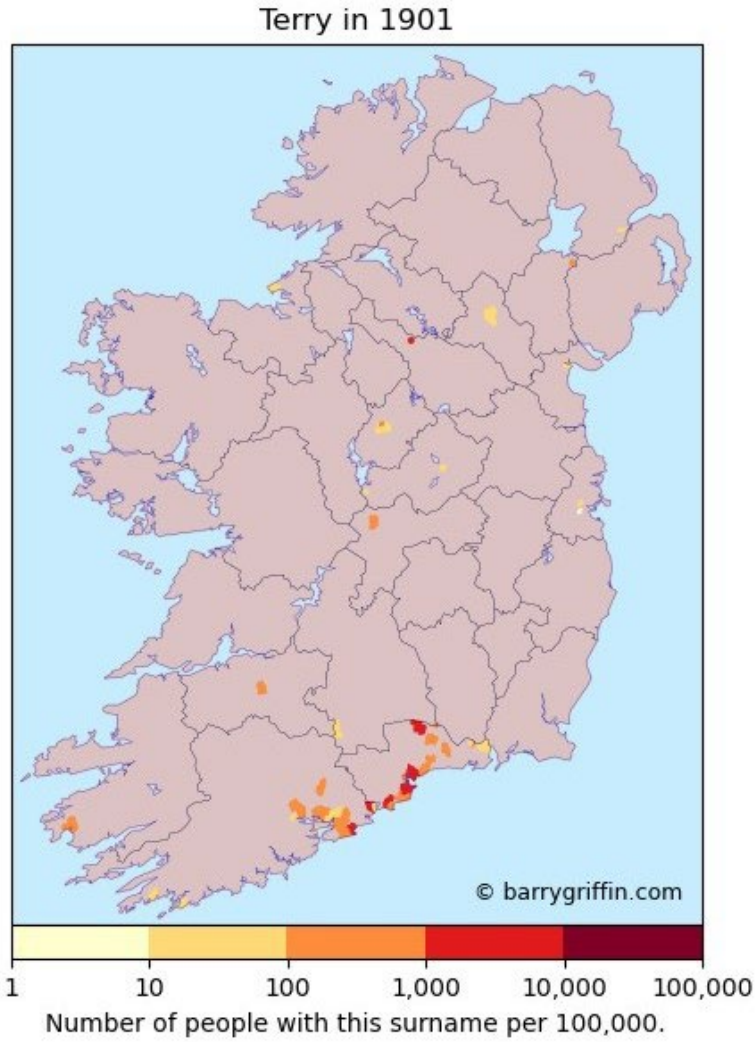

Fig. 1 Terry surname 1901 (©barrygriffin.com)

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It is these and their ancestors who emigrated that will be the focus of this paper.

Terrys; what the paper trail tells us

Generally, in Ireland paper trails go back to the 18th/19th century. In the case of Terrys, there are good paper trails for some Spanish Terry branches, of Cork origin, to the beginning of the 17th century. Where land or property were involved, records can go back much further but it can be difficult to distinguish between families. Civil and church records for mayors and bishops etc provide relevant information as far back as the arrival of the Normans in Ireland. But again, it is not possible generally to link the information from these to specific modern day Terry lineages. Cork Terrys in medieval times were often urban based and were merchants and traders. Records of these are more plentiful than say Waterford Terrys who were more rurally based and associated with agricultural and fishing activities. In the 17th and 18th centuries two genealogical documents were written by professional genealogists at the time providing Terry genealogies going back to origins in France.

The role of genetic genealogy

To add to the understanding of what paper records reveal, data from Y-chromosome DNA Terry testers where publicly available is utilised. Extensive paper records going back several centuries are extant. But often it is not clear who is related to who before 1800 CE. There are several locations in Cork County where Terrys resided in former times, Castleterry, Rathcormack, Carrigtwohill and Cobh to mention a few. They were also prominent in Cork city. In county Waterford clusters of Terrys resided in Dungarvan and Ardmore among other places. Some migrated to Limerick and West Clare in the 17th century. Dublin was also a city that attracted Terrys of Cork origin. Further afield, Cork Terrys migrated to Spain, France the UK, north and south America and Australia.

Genetic genealogy is beginning to help distinguish between different branches of Terrys and those who may have, for example, adopted the surname, Terry.

To-date six distinct lineages have been established from Y chromosome DNA results. Two of these are from Cork, two from Waterford, and two from Spain/Italy and Peru. One of the Cork lineages is connected with one of the Waterford lineages having a common ancestor around 1400 CE. These six lineages will be examined in this paper. The six lineages previously mentioned will now be looked at in turn.

The Rathcormack Terry lineage

Based on currently available data, some 3750 years ago likely in the Czech Republic near Prague, a new SNP FGC13326 was formed.[4] This was towards the end of the Únětice culture. There are several downstream branches from this.

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Fig. 2 Migratory path of R-Y129823 (Source: FamilyTreeDNA)

The migratory path of this lineage is shown in Fig. 2.[5] This shows FGC13326 originating in Kent, England. A different interpretation of its origin is that by Iain McDonald,

We think that R-Z156 and later R-Z304 and R-DF96, arose from the Únětice *Culture around modern Prague in the period 2300-1700 BC. Many of the R-Z156 men migrated from the* Únětice *Culture into the Tumulus Culture, which peaked around 1300 BC in modern southern Germany*
and
R-U106>Z381>Z156>Z306>DF96>FGC13326

Likely MRCA data range: 2200-1600 BC

Likely origin: central Europe?

Culture: Únětice *culture?.*[6]

The three ancient connections to FGC13326 and downstream from this SNP in FamilyTreeDNA Discover, are from Bavaria, Viking Britain and Jutland all living in the first millennium CE.[7] So based on present knowledge it is probable, in my view, that the origin of FGC13326 is Bohemia during the Únětice culture.

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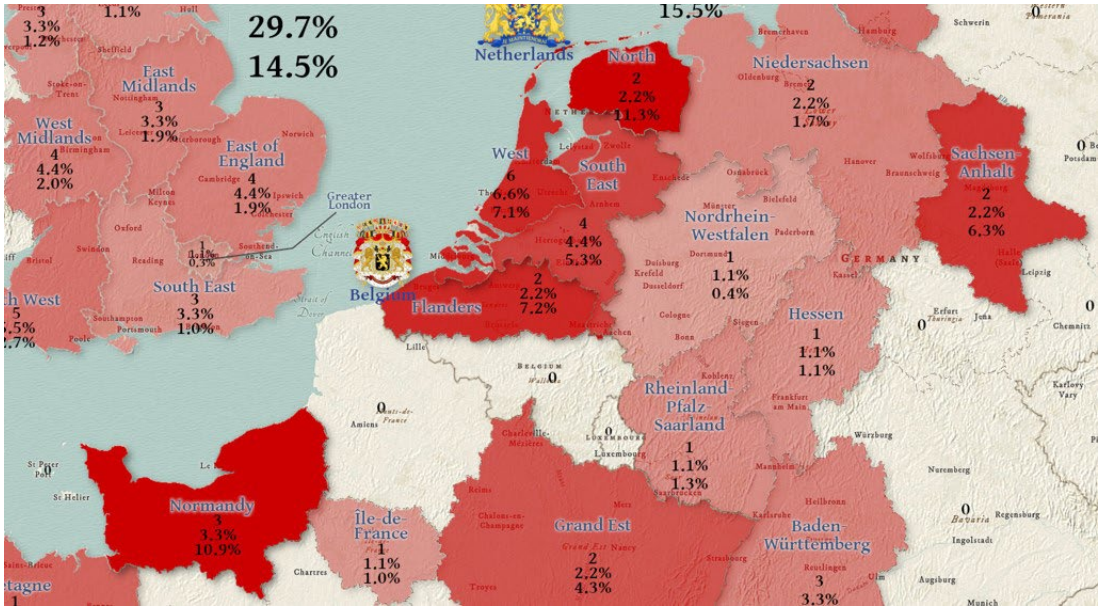

Fig. 3 High concentrations of FGC13326 (Courtesy: Ewenn Gicquel, France)

Fig. 3 shows regions of relatively high concentrations of FGC13326, based on the location of the earliest known ancestors of DNA testers.[8] These are testers mainly from FamilyTreeDNA but also includes some others. The percentages are adjusted to take account of testing biases in the various countries. This map probably reflects the dispersal of a haplogroup around the 18th century.[9] It is not possible to show this map for earlier centuries as the information on the earliest known ancestors does not go back to these times. The map shows the highest concentrations in Normandy, The Netherlands, Belgium, and Sachsen Anhalt.

The downstream branch from FGC13326 associated with Terrys of Cork and Waterford is R-Y128031. This SNP is about 600 years old when branching occurred, differentiating Cork and Waterford Terrys. This branching resulted in two downstream haplogroups, R-BY152948 for the Dungarvan, Waterford Terry lineage and R-Y129823 for the Rathcormack, Cork Terry lineage. No genetic evidence exists on how the man, or his ancestors, who originally had this SNP arrived in Ireland. There is a gap between 1750 BCE and 1400 CE. Why this is so is discussed later in the paper. The distinction between the Dungarvan and Rathcormack lineages is manifested by the lack of extensive paper records for the Dungarvan lineage in the later medieval period. They were dispersed and rurally based. The Rathcormack lineage were linked to early settlement in Cork in the 12th and 13th centuries and strongly associated with Cork city. Extensive paper records of this lineage are extant.[10]

The first lineage, or branch, looked at is the Rathcormack one. This lineage is defined by SNP, R-Y129823. The most recent common ancestor of this lineage occurred about 450 years ago. This lineage is downstream of R-Y128031, see Fig. 4. This shows Cork and Waterford Terrys with branching occurring around 1400 CE.

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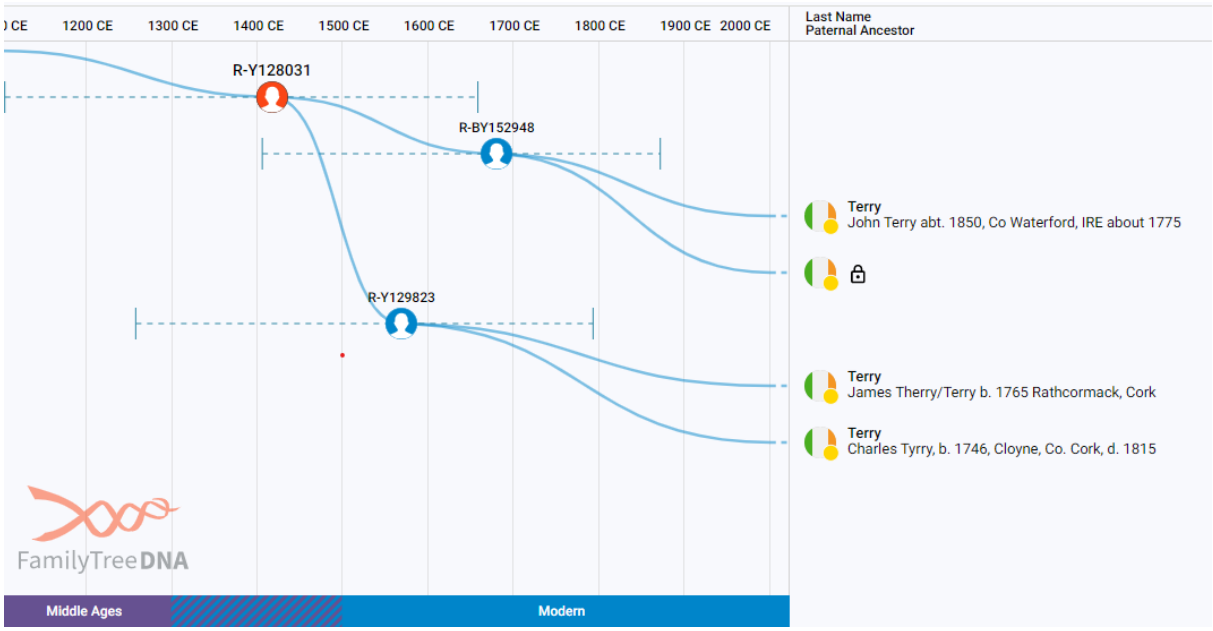

Fig. 4 Genetic Time Tree of Cork and Waterford Terrys (Source: FamilyTreeDNA)

R-Y129823's paternal line was formed when it branched off from the ancestor R-Y128031 around 1400 CE.

So, Cloyne Terrys and Rathcormack Terrys share a common ancestor living around 1550 CE. These also match at the Y-111 str level with an O'Brien whose earliest known ancestor was from Cork city. The O'Brien name arose from probably a non-paternity event (NPE) a few centuries ago.

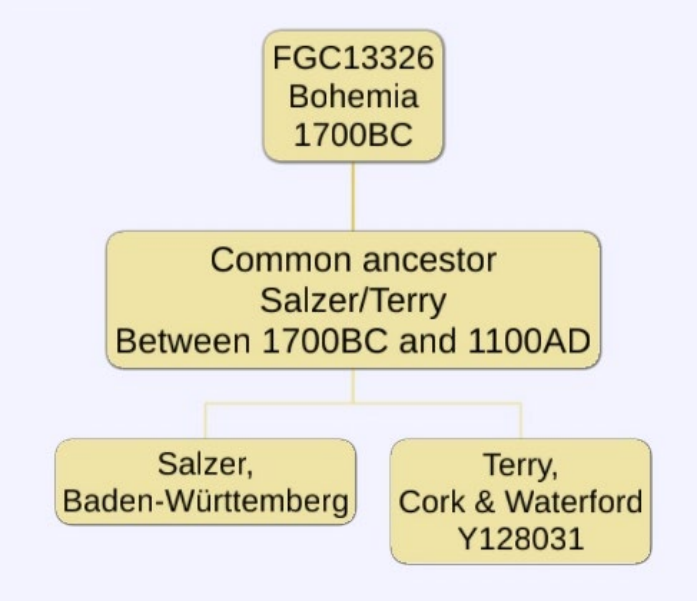

Fig. 5 Common ancestor of two FGC13326 testers (Source: Kevin Terry)

Fig. 5 shows a relationship between a person, Salzer, from Baden-Württemberg and a Terry from Cork and Waterford. Descendants of both these men have tested positive for FGC13326.

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FGC13326 originated in central Europe about 3750 years ago. Another FGC13326 match is with a person, surname Last, from Pomerania, Poland, and this Terry lineage, with a common ancestor about 450 BC has been gleaned from test results on Yfull, a Y DNA analysis service.[11] Still a further match is with Sundermann from Ladbergen, North Rhine Westphalia.
Autosomal DNA identifies additional Terry or Terry related matches with the Cloyne and Rathcormack Terrys separately. For example, the descendant of Charles Tyrry who tested is showing matching a Terry from Australia with a shared DNA of 27.3 cM.

The Castlemartyr Terry lineage

DF19 is a SNP mutation that defines one of the smaller subclades below R-P312, which is the most common Y-haplogroup in Western Europe. The origin of the P312 haplogroup can be situated around 2800 BC, and just like its "brother clade" U106 it was tightly linked to the Bell Beaker culture, which was at that time spreading rapidly throughout central and western Europe. The DF19 mutation most likely happened in a R1b-P312* man who had been born around 2500 BC in a Bell Beaker community, most likely living in – what is nowadays – the coastal region of the Netherlands. He was the common male ancestor of all DF19+ lineages.

Within a few generations (by about 2400 BCE) other SNP mutations occurred in the Y-chromosome: one being the founding father of the DF88 subclade. That this event can be placed in the Netherlands is suggested by the discovery of ancient DNA results. One of these was from Ottoland (Zuid-Holland) was dated to 2500 – 2100 BC, and it carried the DF19 and DF88 mutations.

R-S18811 is downstream from DF88 and is about 1800 years old.

Locations of where haplogroup R-S1881 is most found is shown in Fig. 6.[12] The Netherlands shows the highest concentration.

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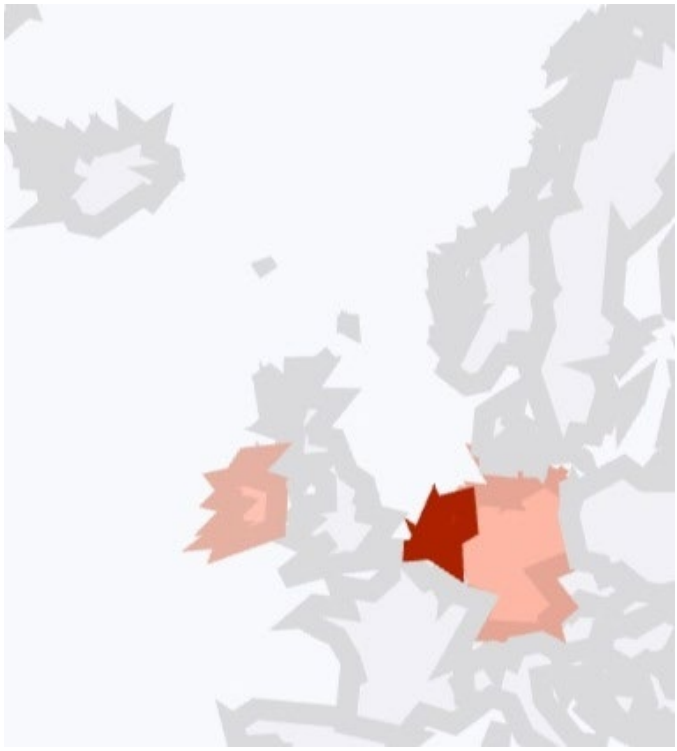

Fig. 6 Map view of where haplogroup R-S1881 is most found (Source: FamilyTreeDNA)

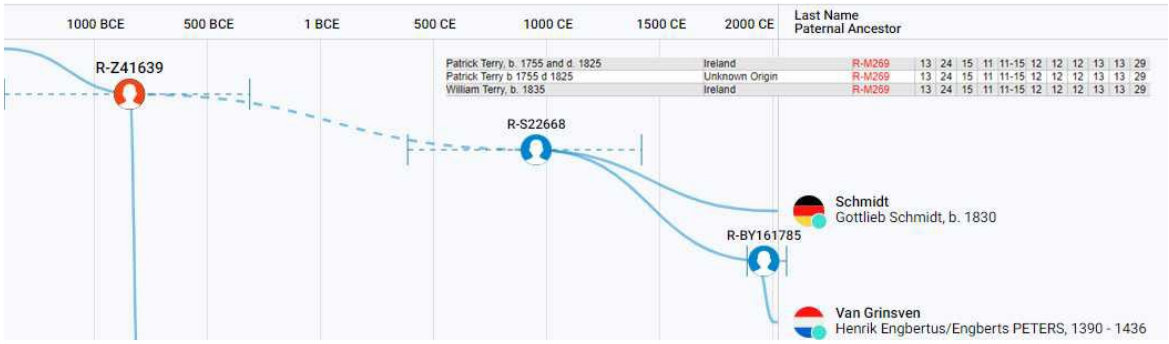

Fig. 7 Time Tree Castlemartyr lineage (Data source FamilyTreeDNA; © Kevin Terry)

Fig. 7 shows the time tree of the Castlemartyr lineage. Three Terry test results for this lineage appear in the Terry DNA surname project.[13] These are shown as an inset; the numbers being the results of the first 12 str markers. One of these has further tested with YSEQ and is DF19+>R-S18811+.[14] R-S18811's paternal line was formed when it branched off from the ancestor R-Z41639, see Fig. 8. This terry lineage tested negative for BY162529; this is in the same block as R-S22668 in the FamilyTreeDNA Block Tree.

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Fig. 8 Time Tree of R-Z41639>R-S18811 (Source: FamilyTreeDNA)

The man who is the most recent common ancestor of this line is estimated to have been born around 150 CE.

Fig. 8 shows four DNA tested descendants, and they specified that their earliest known origins are from Germany, Ireland, and Netherlands with 1 from unknown countries.[15] The Castlemartyr Terry lineage belongs to this branch, the line terminating with the Irish flag.

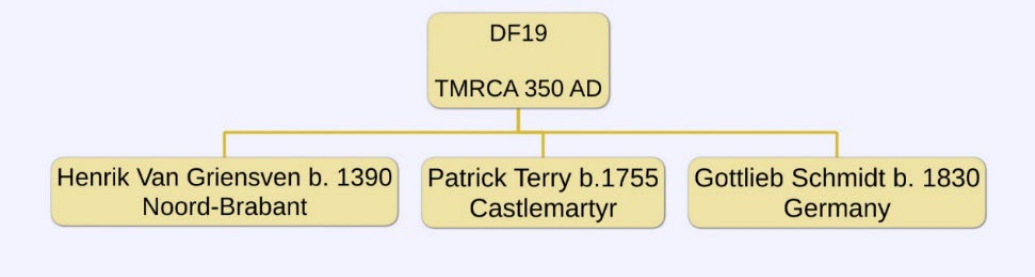

Fig. 9 Common ancestor of three DF19 testers (Source: Kevin Terry)

Fig. 9 shows the relationship between three people, from Noord-Brabant, Netherlands, from Germany and from Castlemartyr, Cork. The TMRCA (time to the most recent common ancestor) is 150 AD.[16]

Using GEDmatch to analyse autosomal DNA it was possible to determine whether some Terry descendants belonged to the Rathcormack or Castlemartyr Terry lineage.

Comparing two GEDmatch kits, A103877 (*12Terry) and A009181 (Sue Nichols), it was possible to determine that they shared a common ancestor 3.7 generations ago, with the common ancestor being a Terry from Knockastruckeen, Cloyne; originally from Castlemartyr.

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The Dungarvan Terry lineage

The Dungarvan Terry lineage is defined by SNP R-BY152498. R-BY152948's paternal line was formed when it branched off from the ancestor R-Y128031 and the rest of mankind around 1400 CE, see Fig. 4. The man who is the most recent common ancestor of this line is estimated to have been born around 1700 CE. He is the most recent paternal line ancestor of all members of this group.

As well as Dungarvan there are several other locations in county Waterford where Terrys from this lineage resided. These are shown in Fig.10. The Rathcormack and Dungarvan lineages split sometime around 1400 CE.

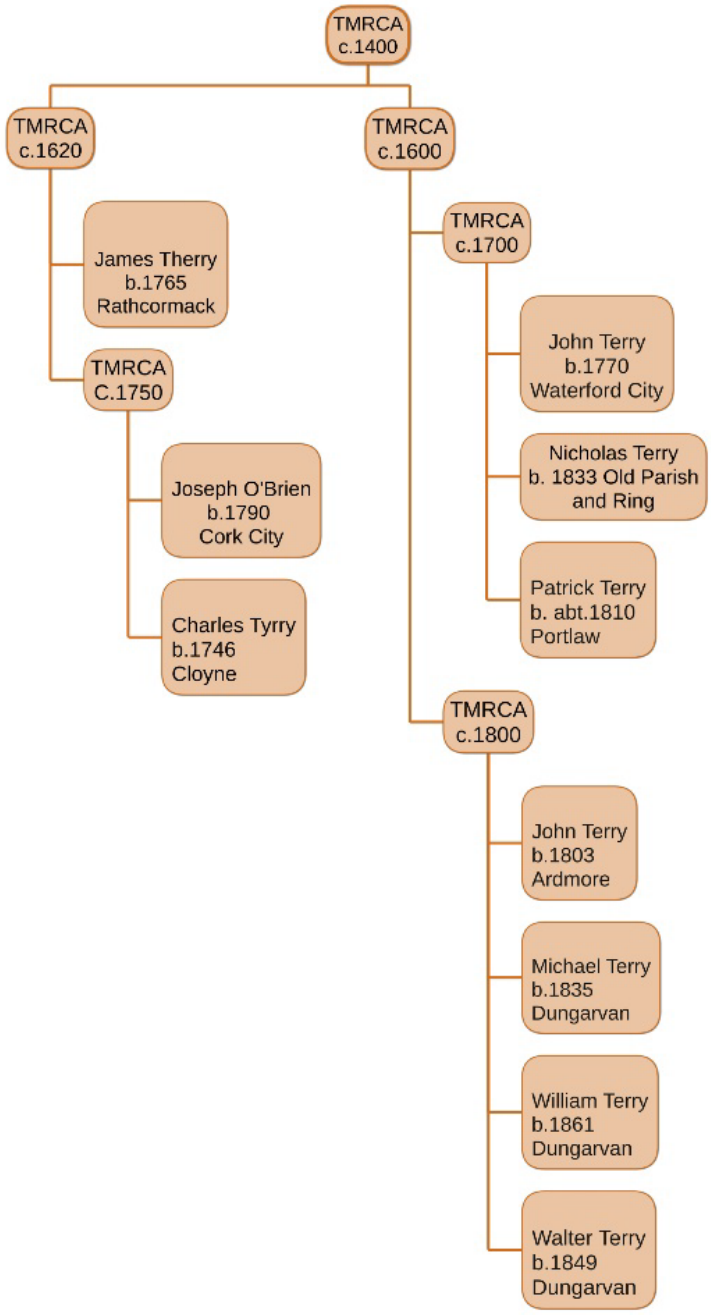

Fig. 10 Rathcormack and Dungarvan Terry lineages (Source: Kevin Terry)

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The four other lineages, Castlemartyr, Newcastle, Genoese and La Libertad are completely distinct from the Rathcormack and Dungarvan lineages.

The Newcastle Terry lineage

This Waterford Terry lineage is I-M253 from Newcastle on the border with Co. Tipperary. This Terry family has several matches with McNeill's from Northern Ireland and Scotland. The lineage is of Viking origin and the Terry name is introduced due to a non-paternity event in the McNeill line several centuries ago. Descendants initially lived in New Brunswick, Canada and later some settled in Minnesota, U.S. The earliest known record for this family is a baptism record for the parish of Newcastle in 1822. Thomas, son of Thomas Terry and Margaret Kealahan.[17]

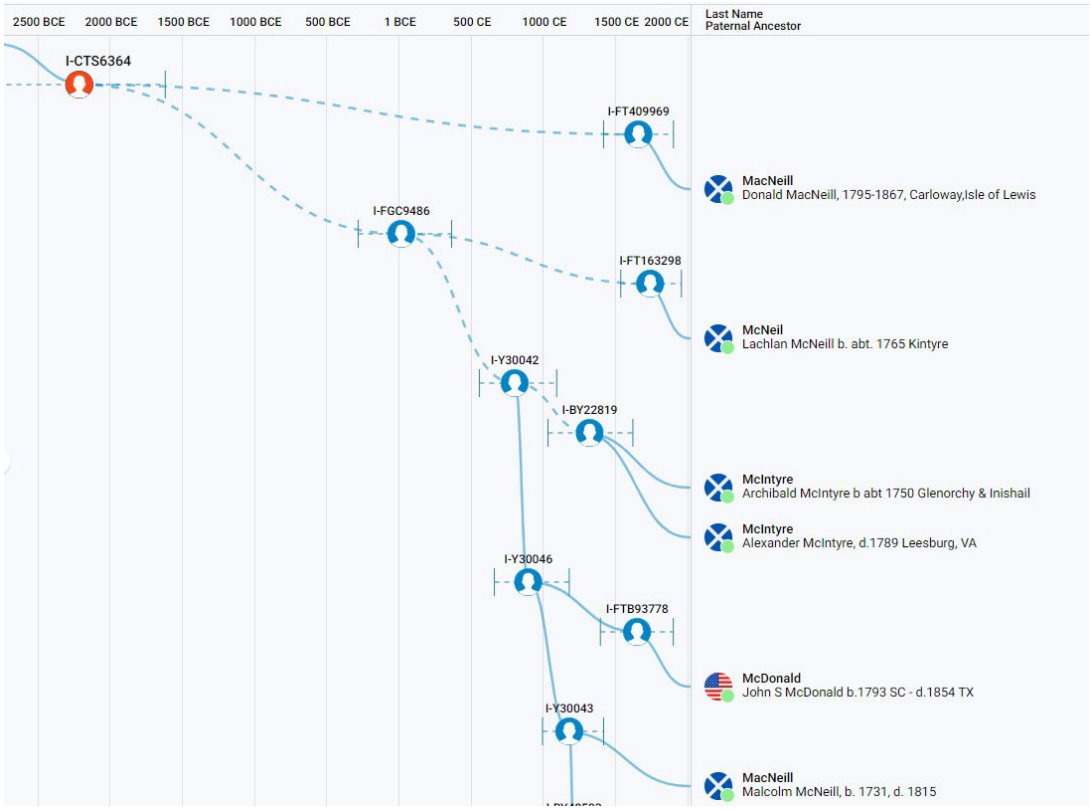

Fig. 11 Genetic time tree of Malcolm MacNeill (Source: FamilytreeDNA)

Based on a Genetic Distance of 1 at the Y-67 test level, the Terry tester, a descendant of Thomas Terry, and the MacNeill, descendant of Malcolm McNeill, are estimated to share a common paternal line ancestor who was, with a 95% probability, born between 1600 and 1900 CE. The most likely year is rounded to 1800 CE. This date is an estimate based on genetic information only. Malcolm's haplogroup is I-Y30043, see Fig.11. This is likely the haplogroup of the Newcastle Terry lineage also.

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A case study on this Terry was carried out by Tyrone Bowes. [18] He found that

this family has a genealogical paper trail that places their recent Irish ancestors in County Waterford on Ireland's south coast. However, the Y-DNA test revealed that Mr Terry is part those males who's Y-DNA does not match their (Terry) surname. His association with the Terry surname is a result of a non-paternal event that occurred at some point in his distant paternal ancestry. Mr Terry's closest DNA matches were overwhelmingly Scottish surnames, and specifically with the MacNeill's and the area around Swin Castle on the Kintyre peninsula in the Western Isles of Scotland. Strikingly his more distant matches included many of clear Scandinavian origin and others with Scandinavian surnames. His paternal ancestors were the Vikings who settled in Scotland, who adopted the Gaelic language and customs, and served in Ireland as mercenaries. They left evidence of their presence in the DNA of the Irish people and their descendants, even those with a paper trail leading back to Waterford.

An upstream SNP, CTS6364, see Fig.11, is closely linked with ancient remains of a man who lived between 41 and 212 CE during the Roman Age and was found in the region now known as Cemetery Weklice, Weklice, Poland. He was associated with the Wielbark cultural group.[19]

The Genoese lineage

One of three Terry lineages, with present day links to Cadiz, can trace their genealogy back to one Don Antonio Maria de Terry and Dona Maria Angela Andreano, originating in Genoa, Italy. In a family tree prepared by Manuel Jose de Terry from Seville it shows a Francis Terry, from Limerick, and his son John emigrating to Finale, Italy around 1631. He is said to be the son of a David Terry from Cork. This Francis is shown on the tree as great grandfather Antonio Maria de Terry. Church records from Finale would suggest that the Genovese branch of Terrys descend from the family of Terrile, an Italian family. A Peruvian patrilineal descendant of Francesco Antonio Terrile born 1726, Italy, did a Big Y test.[20] His terminal SNP is G-Z31423. This Francesco Antonio Terrile was father of Don Antonio Maria de Terry. The genetic time tree of the lineage is shown in Fig. 12.

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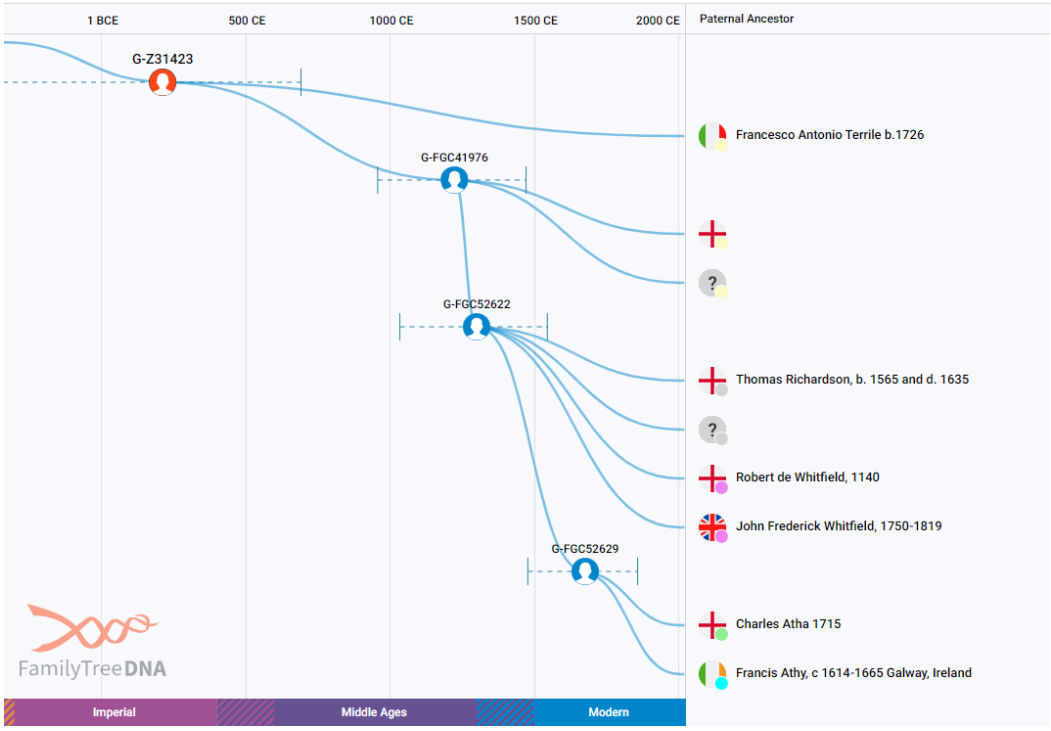

Fig. 12 Genetic time tree of the Genoese Terry lineage (Source: FamilyTreeDNA)

The man who is the most recent common ancestor of Z31423 is estimated to have been born around 200 CE. There are 10 DNA tested descendants, and they specified that their earliest known origins are from England, Ireland, Italy, and one other country with two from unknown countries.[21] Fig. 13 gives a map view of the migratory path of G-Z31423 to Italy.[22] Further genetic testing and analysis would be beneficial to determine the specific origins of the Genoese Terrys.

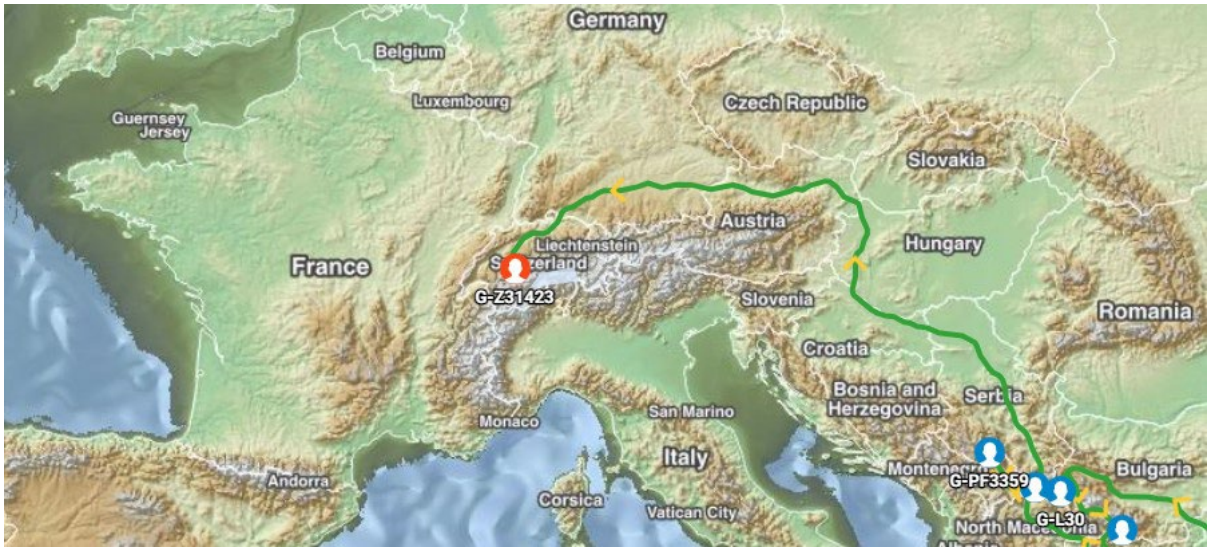

Fig. 13 Map view of migratory path of G-Z31423 to Italy (Source: FamilyTreeDNA)

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The La Libertad Peruvian lineage

Fig. 14 Map view of where haplogroup PH1047 is most found (Source: FamilyTreeDNA)[23]

For this lineage there is one tester who tested to Y 111. Separately he tested positive for R-PH1047 but negative for R-PH28 with YSEQ. This La Libertad lineage is of Spanish origin. It is not, on the patrilineal line, connected to the Cork and Waterford Terry lineages. The tester of this lineage has matches with YBarra, IBarra, a Basque name. The earliest known ancestor Victor Terry Loayza born about 1890 in Peru. Fig. 14 is a map view of where haplogroup PH1047 is most found.

Discussion and conclusions

Aspects of the six genetic time trees

One comparison of the six Terry lineages is to look at where branching took place that has been identified from testers.

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Time	Rathcormack lineage	Castlemartyr lineage	Dungarvan lineage	Newcastle lineage	Genoese lineage	La Libertad lineage
1750-1500 BCE	Branching[24]	Branching	Branching	Branching		Branching
1500-1250 BCE		Branching		Branching		
1250-1000 BCE		Branching				
1000-750 BCE		Branching		Branching		Branching
750-500 BCE				Branching		
500-250 BCE						
250-0 BCE				Branching		Branching
0-250 CE		Branching		Branching	Branching	
250-500 CE						
500-750 CE						
750-1000 CE				Branching		
1000-1250 CE				Branching		
1250-1500 CE	Branching		Branching	Branching		
1500-1750 CE	Branching		Branching	Branching		
1750-2000 CE		Branching	Branching	Branching		

Table 1 Branching of six genetic time trees

Table 1 shows the time periods when branching occurred for the six genetic lineages. For the Rathcormack and Dungarvan time tree branching occurred in the period 1750 BCE to 1500 BCE. No further branching is shown until 1250 CE-1500 CE. This can be because of a few factors. Ancestors of these lineages may have resided in countries where there is limited DNA testing. So possible distant relations would not be identified. For example, in France there is limited DNA testing for genealogical purposes. If the ancestors of the Rathcormack and Dungarvan Terry lineages resided in France in the first millennium CE the very sparse testing would mean that matches are unlikely to be found.

Another reason a line may not branch is that it may have come close to dying out or becoming extinct. This will happen where there is no male-to-male line of descent. There is a high probability that the line from any male ancestor will eventually hit a generation with no sons. The probability depends on the chance of each descendant having zero, one, two, three (and so on) sons who themselves become fathers, and, linked with that, the average population growth. The calculations of the likelihood of extinction first became known through the work of Galton and Watson. The Galton-Watson process predicts that for a single ancestor there is a 91% chance of a surname being extinct by 20 generations if there is no average growth in population, an 86% chance of extinction if there is a 5% growth per generation, and an 80% chance if there is a growth rate of 10% per generation. Where there is perhaps only a single line of descent over several generations then there will be no branching.

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The Castlemartyr Terry lineage shows more branching than the other lineages in Table 1. Before 250 CE there was growth in this lineage. But between 250 CE and 1750 CE there is no branching.

The Newcastle lineage looks to have thrived throughout the period. This lineage is associated with Scots and Vikings. Lack of testing in the countries associated with the Genoese lineage is probably the main reason for no branching in this lineage. The La Libertad lineage shows some branching up to 1 BCE but none since. This is probably due to the low level of testing in Spain and Peru.

Additional considerations, FGC13326

FGC13326 is the next SNP upstream of R-Y128031 where branching has been observed from test results to date. The most common lineages of Cork and Waterford Terrys are part of this branching. So, some further aspects of this SNP, FGC13326, are discussed here. What mutations occurred downstream from this SNP, when it originated around 1750 BCE? Is the population growing or contracting? A small number of SNPs in each haplogroup means the population is growing. A large number means the population has contracted. Is the population migrating? Do haplogroups appear only in places their parent haplogroup does not.

One of the Cork Terry lineages is defined by haplogroup R-Y129823. The man who is the most recent common ancestor of this line is estimated to have been born around 1550 CE. R-Y129823's paternal line was formed when it branched off from the ancestor R-Y128031 around 1400 CE. R-Y128031's paternal line was formed when it branched off from the ancestor R-FGC13326 around 1750 BCE.

Between R-FGC13326 and R-Y128031 are 40 SNPs with no branching from tests carried out and publicly available as of 2023. This represents a new SNP being formed about every 80 years. Now immediately beneath R-FGC13326 are nine branching lines in the first 250 years of its existence. These are R-S25234, R-S22047, R-FGC34162, R-FGC50047, R-Y13174, R-Y128031, R-Y63213, R-FGC79603, and R-BY55641.[25]

Cumulative number of branching lines formed under FGC13326 at intervals of 500 years are shown in Table 2

Up to 1500BCE	13
Up to 1000BCE	38
Up to 500BCE	62
Up to 1BCE	78
Up to 500CE	106
Up to 1000CE	131
Up to 1500CE	190
Up to 2000CE	316

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Table 2 Branching lines under FGC13326, March 2023 (Source: Kevin Terry)

This indicates a rapid expansion of branching lines up to 1000BCE; some expansion in the next 500 years and with no big increase again until after 1500CE. There was a significant increase in the last 500 years. Comparing this in growth terms with European population at similar intervals, Table 3, the population increased up to 0 CE but did not exhibit growth in the 1st millennium CE. Thereafter the European population expanded.

2000BCE	7.19 million
1000BCE	13.13 million
1BCE	32 million
500CE	28.54 million
1000CE	36.34 million
1500CE	58 million

Table 3 European population at intervals 2000BCE to 1500CE

Comparing growth patterns in these two tables suggests that,

-The number of branching lines downstream of marker FGC13326 grew faster than population growth between 1750BCE and 1000BCE.

-From 1000BCE to 1BCE, there is no discernible pattern of growth or decline. From 1BCE to 500CE the population in Europe declined but the branching lines of FGC13326 increased by 28% from the total up to 1BCE. Again, after 500CE to the present there is no discernible pattern.

- From 500 CE to the present, branch nodes of downstream of marker doubles ever 500 years, whereas European population did not grow by the same rate until after 1000CE.

So, there were two periods of greater growth of FGC13326 and its downstream branches, the first in the couple of hundred years after it was formed and the second in the latter half of the 1st millennium CE.

The Galton-Watson process helps explain why only a handful of males in the deep past of humanity now have any surviving male-line descendants, reflected in a rather small number of distinctive human Y-chromosome DNA haplogroups.

A corollary of high extinction probabilities is that if a lineage has survived, it is likely to have experienced, purely by chance, an unusually high growth rate in its early generations at least when compared to the rest of the population.[26]

High extinction rates can occur due to a population bottleneck or genetic bottleneck. This is a sharp reduction in the size of a population due to environmental events such as famines, earthquakes, floods, fires, disease, and droughts; or certain human interventions.

There is a high probability that the line from any male ancestor will eventually hit a generation with no sons. The probability depends on the chance of each descendant having zero, one, two, three (and so on) sons who themselves become fathers, and, linked with that, the average population growth. The calculations of the likelihood of extinction first became known through the work of the Galton-Watson process. This process predicts that for a single ancestor there is

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a 91% chance of a surname being extinct by 20 generations if there is no average growth in population.[27]

For haplogroup R-Y129823, it experienced a split into two lineages from a node around 1550CE and an earlier split into two lineages around 1400CE. Prior to this it shows no split until one goes back to FGC13326, in about 1750BCE. At that time FGC13326 spit into nine lineages.

Fig. 15 shows an indicative route map of descendant clades of FGC13326, 1750BCE to 1000BCE. The purpose of the map is to represent, based on the evidence from FT timeline data and YFull data (accepting biases) where descendants of FGC13336 migrated to in the first few hundred years after its formation. After 1000 BCE, because descendants would have dispersed to such an extent, meaningful information would not be gleaned. This data suggests in the early (first few hundred years) stage, descendants of FGC13326, as represented by present day testers, migrated mainly in a West/North West direction; to Germany, The Netherlands, England, and France (modern country boundaries). Some migration to Austria and Belgium also took place.

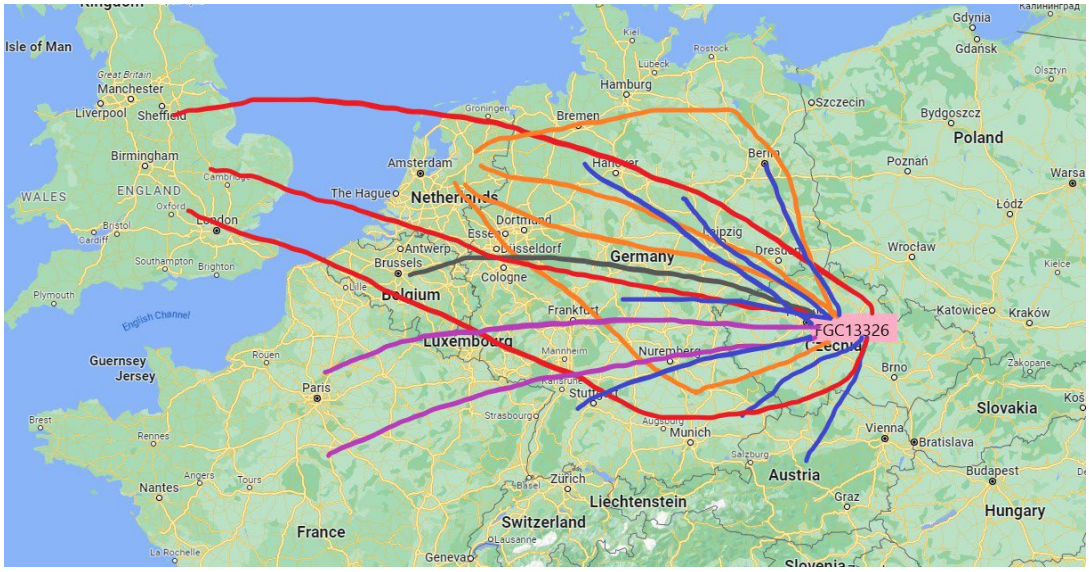

Fig. 15 Indicative migratory paths of descendants of FGC13326, 1750 BCE to 1000BCE
(Source: Kevin Terry)

Most descendants of FGC13326 came to England at various points after 400 CE, with the majority of them after the Norman Invasion.[28]

R-FGC13326 originated probably towards the end of the Únětice Culture. This culture ended around 1700 BCE. Did R-FGC13326 expand and spread as part of the power struggles in this collapsing cultural grouping, or did they ascend to glory through the rise of the nascent Tumulus Culture to the west? We would need more precise timing and geographical information to know.[29]

Conclusions

Paper records for Cork Terrys from the 12th century onwards show that there were several separate settlement locations in Cork for families bearing this surname with possibly distinctive genetic ancestry. The relationship between Terrys from different locations in Cork was not

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always clear. In Waterford, also, there were many Terry families. Paper records did not indicate how these Waterford families were related to the Cork Terrys.

From the 17th century paper records are extant on Cork and Waterford Terrys who emigrated to Continental Europe, Britain, the American continents, and Australia. In many cases there are records of their Irish roots. Sometimes, due to non-paternity events, the adoption of the surname Terry by families with different surnames and naming patterns of surnames in some countries, it is difficult to establish which families with the surname Terry are descended from Terrys of Cork.

The results of Y chromosome DNA have clarified a number of these questions. Genetic testing to-date is not able to answer all the questions due to limited testing. The largest number of Cork and Waterford Terry branches share a common ancestor from the 15th century. Within Cork these Terrys from Cloyne and Rathcormack share a common ancestor from the 16th century. There is a second Cork Terry branch, the Castlemartyr branch, with a distinctive genetic signature. Likewise, in Waterford, a second Terry branch, the Newcastle branch has a distinctive genetic signature. This branch is genetically linked to the McNeill's of Northern Ireland and Scotland.

Several DNA testers from the United States are connected to these various branches.

Paper records of Spanish and Peruvian Terrys show links back to Cork and Limerick. However, the two Peruvian Terrys, who have tested, are not genetically connected to Terrys in Cork and Waterford. One tester has Italian ancestry with the surname Terrile. The other tester has Spanish ancestry.

Author Biography

Kevin Terry, MA (Local History), is a retired public servant. Formerly City Engineer with Cork and Limerick, Kevin lives with his family near Cloyne.

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[1] A haplogroup is a genetic grouping defined by at least one single nucleotide polymorphism (SNP) occurring at a known location on the Y-chromosome DNA or in mtDNA. A genetic lineage, also known as genetic pedigree, is a series of mutations or changes in the genetic code which connect an ancestor's genetic code to their descendant's genetic code.

[2] García-Álvarez de la Villa, B., & Terry, K., (2016). Terrys in Spain and Latin-America: Exile and Rise of an Irish Merchant Family. *Estudios Irlandeses: Journal of Irish Studies*, (11), 69-81.

[3] Kevin Terry, The Terrys of Cork – Merchant gentry 1180-1644, Phillimore & Co. Ltd., 2013, pp 4-14.

[4] SNP (single nucleotide polymorphism)

[5] https://discover.familytreedna.com/y-dna/R-Y129823/globetrekker?loggedIn=true

[6] https://groups.io/g/R1b-U106/topic/86196098#:~:text= We%20think%20that% 20R%2DZ156,BC%20in% 20modern%20southern%20Germany; https://groups.io/g/R1b-U106/message/5759.

[7] https://discover.familytreedna.com/

[8] This data is of March13th, 2023.

[9] Private correspondence with Ewenn Gicquel, France. The demographic data used in the preparation of the map is from the 21st century.

[10] Kevin Terry, The Terrys of Cork – Merchant gentry 1180-1644, Phillimore & Co. Ltd., 2013

[11] Terry, Kevin, *Ancestral Journeys*, Kevin Terry, 2021, p18.

[12] https://www.familytreedna.com, July, 2023.

[13] https://www.familytreedna.com/public/terry?iframe=yresults

[14] YSEQ is a company established in 2013 to make traditional Sanger sequencing products for the Y-chromosome available direct to consumer (DTC).

[15] https://discover.familytreedna.com/y-dna/R-S18811/story

[16] Terry, Kevin, *Ancestral Journeys*, Kevin Terry, 2021, p18.

[17] Terry, Kevin, *Ancestral Journeys*, Kevin Terry, 2021, p128

[18] http://www.irishorigenes.com/content/gallowglass-do-you-belong-warrior-clan

[19] https://discover.familytreedna.com/y-dna/I-CTS6364/ancient

[20] Terry, Kevin, *Ancestral Journeys*, Kevin Terry, 2021, pp 137, 138

[21] https://discover.familytreedna.com/y-dna/G-Z31423/story

[22] https://discover.familytreedna.com/y-dna/G-Z31423/globetrekker

[23] https://www.familytreedna.com/my/snp-map, March, 2023.

[24] Branching here means that from known DNA results the lineage spit at this time.

[25] https://discover.familytreedna.com/y-dna/R-FGC13326/story, 12th March 2023.

[26] Wikipedia contributors. "Galton–Watson process." *Wikipedia, The Free Encyclopaedia*. Wikipedia, The Free Encyclopaedia, 26 Nov. 2021. Web. 16 Oct. 2022.

[27] https://www.academia.edu/44948637/The_dispersal_by_extinction_and_migration_of_surnames_linked_to_Old_Norse_personal_names_in_Norfolk, p3

[28] Iain McDonald's view as expressed in FamilyTreeDNA R-U106 discussion group.

[29] Iain McDonald's view as expressed in FamilyTreeDNA R-U106 discussion group.

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Journal of Genetic Genealogy

Identification of the Mitochondrial DNA Haplogroup of Elizabeth Martiau

Including her maternal line descendants:
Mildred Reade, Mildred Warner, Mildred Washington, &
Mildred Lewis

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Abstract

This is the first documentation of the mitochondrial DNA line of Elizabeth Martiau. This project verifies several lines of her descendants including some where documentation has been lacking. Her maternal line descendants included many noteworthy women in colonial Virginia. These findings can assist others researching their heritage.

Key words: mitochondrial DNA, Elizabeth Martiau, Mildred Reade, Mildred Washington, Mildred Warner, Mildred Lewis, Nicholas Martiau, George Reade, Lawrence Washington, Augustine Warner, John Lewis, Henry Willis

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Introduction / Overview

This work traces some of Elizabeth Martiau's matrilineal descendants and confirms the shared mitochondrial DNA (mtDNA) haplogroup of those lines.

This project was started as part of my effort to document my ancestral family tree. Like most people who work on their genealogy, there are branches that lead into "brick walls" when information seems to end without resolution. Among other brick walls, I have persistently tried to resolve two key links in one branch that I found puzzling. This branch included noteworthy people in American history, and I felt that surely the truth should be within reach.

Despite years of searching, I was unable to resolve these problematic links. This was due to a lack of documentation that is needed to verify the connection to their ancestors. I have seen numerous family pedigrees posted online and in books that contradict one another. Some state the relationship was uncertain or unproven while others state the relationship as fact, but without sources provided. Both become widely distributed as people copy other trees without pursuing primary sources. This can amplify errors that are very difficult to correct once perpetuated. The number of errors in published pedigrees is amazing. Very recently I looked at an individual using Ancestry.com and found over 11,000 family trees posted with incorrect parents attached.

In my pedigree, I specifically wanted to know if Elizabeth Wills who married John Clayton was the daughter of Henry Willis and his second wife, Mildred. And further, who was Mildred? Mildred has been an enigma being listed as either Mildred Howell or Mildred Lewis. My second goal was to verify her correct identity.

The research questions are:

1. Can Elizabeth Willis be verified as the daughter of Henry Willis and Mildred (Lewis) (Howell) (Brown) Willis?

2. Can Mildred (Lewis) (Howell) (Brown) Willis be verified as the daughter of John Lewis and Elizabeth Warner?

I have found good documentation showing that Elizabeth Willis was my 5th great grandmother and that she married John Clayton in 1753. But, in Virginia there were several people named Elizabeth Willis living at that time. She is usually stated to be the daughter of Henry Willis, but no source for that was found. Was she born to Mildred; the second wife of Henry Willis as often claimed? And, to find my ancestors further back I needed to identify the maiden name of Elizabeth's mother. Was Mildred who was variably reported to have married John Howell as her first husband, or was she the daughter of John Howell and married Dr. John Brown as her first husband?

Records show that Mildred Brown married Henry Willis as his second wife. If she was born a Lewis and then married Howell and then Brown, then Willis, she would be formally Mildred (Lewis) (Howell) (Brown) Willis. Because Henry's second and third wives were both named Mildred, some get confused and attach Elizabeth as

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a daughter of the third wife. Her birth date is not consistent with that attachment. Henry's third wife was Mildred (Washington) (Lewis) (Gregory) Willis.

The problematic links in my line were Elizabeth Wills and Mildred Lewis. Since documentation was unsatisfactory, inconsistent, confusing, or missing their identification rested on circumstantial evidence. To confirm their parentage (Elizabeth Willis as a daughter of Henry Willis and Mildred Lewis and Mildred Lewis as a daughter of Elizabeth Warner and John Lewis) would be possible with genetic testing of their ancestors and descendants.

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Material and Methods / Methods and Data

Traditional genealogical research was done to identify living women who potentially descend from matrilineal ancestors of the "top level" women in the pedigree of Elizabeth Martiau. The quality of documentation varied among lines and there were several where data conflicted among genealogists studying those lines. Over a 6-year period I was able to create a list of all female descendants and located several who are living. Several kindly agreed to participate with mtDNA testing to determine if they shared the same haplogroup.

Testing was done by identifying and recruiting living female or last generation male descendants to provide a buccal swab sample to FamiiyTreeDNA[1] (FTDNA), a company well-established in genetic testing. FTDNA compares the sampled DNA to two reference sequences, the Reconstructed Sapiens Reference Sequence (RSRS) and the Revised Cambridge Reference Sequence (rCRS).

For interested readers, a nice example of the use of mtDNA is illustrated by the identification of the remains of King Richard III. In September 2012, a set of bones was discovered beneath a parking lot in Leicester, England[2]. That location was thought to be at the former site of the Grey Friars Priory. A study was done at the University of Leicester to extract mtDNA from those bones and compare them to know matrilineal descendants of King match.

[1] *FamilyTreeDNA.com (Gene-by-Gene, Ltd.) Houston, TX*

[2] Wikipedia Link: Exhumation and reburial of Richard III of England
https://en.wikipedia.org/wiki/Exhumation_and_reburial_of_Richard_III_of_England

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Top Level Individuals

Nicholas Martiau and wife (wives)

Nicholas Martiau is said to have been born in 1591 in France. Documentation of his birth has not been found, and his parents are unknown[3]. The year of birth appears to be calculated from his age in the 22 Jan 1624/5 Jamestown, Virginia muster in which he is listed as 33.

He was trained as a Military Engineer, probably in France. He was a protestant and therefore at risk of persecution at that time in France, so he emigrated to England. There he was granted citizenship by royal decree. He then became associated with the Earl of Huntington who was a member of the Virginia Company that provided funding for the settlements in Virginia.

Nicholas is often identified as a French Huguenot. He was the godfather of Richard Toche and attended his baptism on 11 May 1615 at the French Huguenot congregation on Threadneedle Street, London. It seems unlikely that he was a Catholic; they were not allowed to emigrate to the colony of Virginia in early years. In England, he took the Oath of Supremacy, as all office holders were expected to do. In Virginia he was a member of the House of Burgesses and a justice. There was controversy in Virginia caused by those doubting his commitment to England, so he was asked to take another oath of loyalty, which he did. Nicholas and his family were members of the established Church of England while in Virginia.

According to research by John Frederick Dorman[4], Nicholas Martiau, was an agent of the Earl of Huntington and arrived in Virginia in the spring of 1620 on the ship Francis Bonaventure. He was 33 years of age in the 1624/5 muster so he would have been 29 years old when he arrived. John Frederick Dorman analyzed available dates and concluded that his daughter Elizabeth was born in or before 1625 to the first wife of Nicholas Martiau in England. A marriage location and name of his first wife have not been found. A baptismal record for Elizabeth in England has also not been found.

[3] Wikipedia Link: Nicholas Martiau https://en.wikipedia.org/wiki/Nicolas_Martiau

[4] John Frederick Dorman, *Adventurers of Purse and Person, Virginia, 1607-1624/5: Families G-P*, Genealogical Publishing Co., Inc., Fourth Edition, 2005, p. 503-5.

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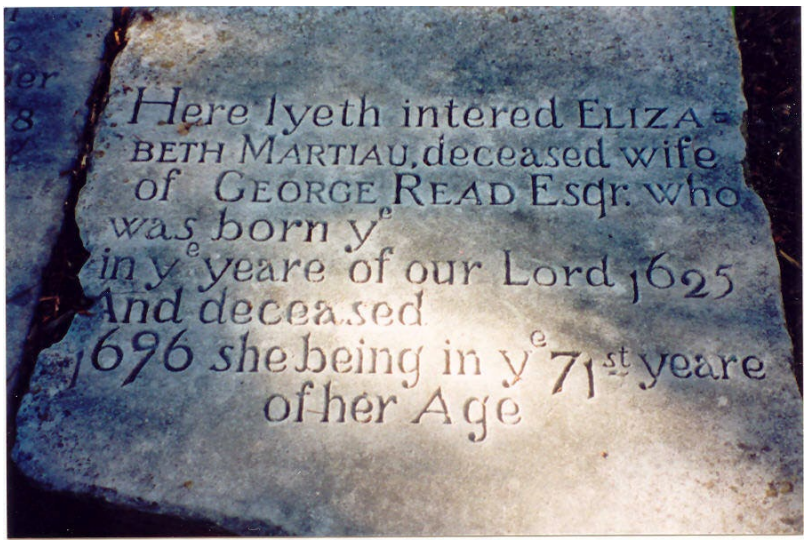

Most researchers list Elizabeth as a daughter of Jane and born in Virginia. Elizabeth's birthdate is somewhat uncertain due to the date on her tombstone.[5] The tombstones of George Reade and Elizabeth Martiau Reade were unearthed when Buckner Street in Yorktown was being graded in 1923. A descendant, Letitia Page Evans, apparently was responsible for the restoration of these stones. She had the surfaces "re-polished and re-cut" according to a 1941 newspaper article describing the re-interment of skeletons found and identified as the Reades (see abstract in appendix). Several lines of the tombstone epitaph were unreadable including Elizabeth's year of birth, year of death, and age at death.

The re-cut dates appear to be inconsistent with several known facts. Chiefly, her will was dated 1686 which means she died at 61 years of age, or her birthdate was wrong. If she was 71 then she was born about 1615.

The original date may have been 1605 or 1615, but it was re-cut as 1625, which implied Elizabeth was born in America and that Jane was her mother. However, if she was born in 1605 her father would have been 14 years old then, which is highly unlikely. Louise Pecquet du Bellet[6] says the will of Nicholas Martiau describes Elizabeth as his eldest daughter "who had crossed the ocean with him". There are 2 images of his will in Virginia court records that were transcribed by different clerks. Neither of those copies shows that phrase—perhaps it appears in the original. If there, it supports that Elizabeth was born in England and came to America with her father. But it could also be a phrase added by the author as no other published reference to his will was found that includes it.

Jane was the second wife of Nicholas Martiau. She was the widow of Edward Berkeley. She and her daughter arrived in Virginia on the Seaflower in Feb 1621/2. Her maiden name remains unknown. She might have been either Jane Scarsbrooke, Jane Eggleston, Jane Boykin, or Elizabeth Jane Page.[7] Jane is listed in the census of 1624/5 enumeration living on Hog Island along with her husband Edward Berkeley and her daughter, also named Jane. At that time, Nichols Martiau was listed in the Elizabeth City muster. Edward died and Jane then married Nicholas Martiau. Jane Martiau presented an inventory of Edward's estate on 5 July 1627. This gives an estimated marriage date between 22 Jan 1624/5 to 1627 for Nicholas and Jane.

Nicholas and Jane had two daughters, Mary, and Sarah. They also had 2 sons: Nicholas who died at age 9 and Richard who died at age 3. Dorman lists Nicholas as born to his father's first wife, but that isn't consistent with

[5] Photo Added by: *Kenneth Williams on 9 Jan 2004* https://www.findagrave.com/memorial/11591903/elizabeth-reade

[6] Louise Pecquet du Bellet, *Some Prominent Virginia Families*, Clearfield Company, Baltimore Maryland, 1994, Vol 4 page 4

[7] John Frederick Dorman, *Adventurers of Purse and Person, Virginia, 1607-1624/5: Families G-P*,Genealogical Publishing Co., Inc., Fourth Edition, 2005, p. 503.

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the headrights claim. Since both boys died young, there are no patrilineal descendants which would enable Y-DNA {patrilineal DNA} testing to define a male line haplogroup of the Martiau line.

If all 4 girls (Elizabeth, Jane, Mary, and Sarah) were daughters of Jane, then they would share the same mtDNA haplogroup. Attempts to trace the lines of Mary Reade, Sarah Reade, and Jane Berkeley to living descendants have not been successful to date. No known mtDNA tests on those lines have been performed, so currently no comparison to Elizabeth can be done. All of Elizabeth's maternal line ancestors would share the same haplogroup back to its time of formation which was sometime between 600 and 3800 years ago (see discussion in a following chapter).

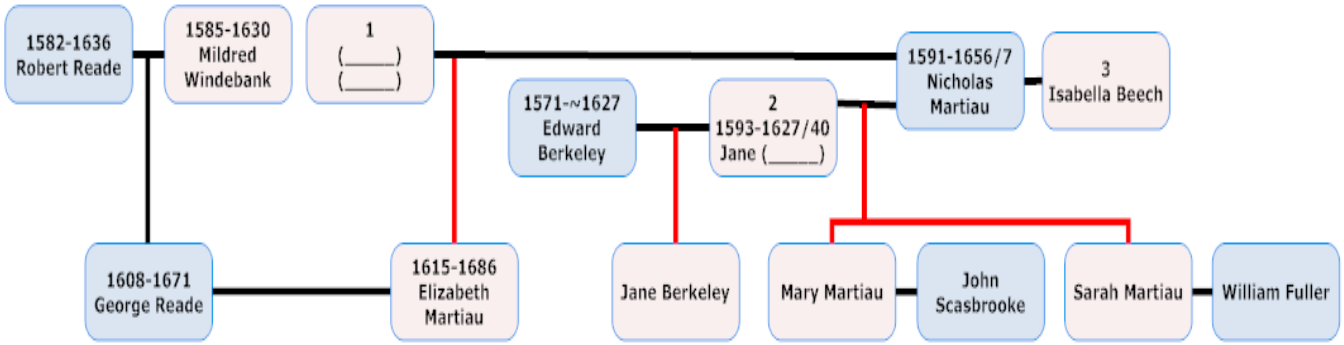
In a letter from Nicholas Martiau to the Earl of Huntington dated 12 Dec 1625 he wrote, "It was more my desire to have visited yr Ldp longe ere this, but I am now both a husband & a father, & so constrayned to staye a while longer by it, untill my little ones can rise & followe mee". The child referred to is probably Mary, but also "my little ones" implies that there was more than one child in 1625. Jane's daughter Jane Barkeley was also in the home then. Probably Elizabeth Martiau was there too. Since Nicholas and Jane married about 1625 and a daughter Mary was born about 1625 that conflicts with the assumption of Elizabeth also being born about 1625. Therefore, it seems most likely that Elizabeth was born about 1615 and in England.

However, the Will of Elizabeth (Martiau) Reade bears the date 10 Feb 1685 and probate date of 24 Jan 1686/7 and states her two young sons, Francis, and Thomas, were not yet 21 years of age, which means they were born after 1664. If Elizabeth was born in 1615 then she was at least 49 years old at the birth of one of those sons, and that is very unlikely in those times.

Nicholas married Isabella Beech after the death of his second wife, Jane. There are no known children born to that third marriage, and she was not mentioned in his will, so she probably predeceased him.

Since it is unclear whether Elizabeth was born to Nicholas' first or second wife, Elizabeth Martiau is emplaced as the most distant ancestor for this project—the trunk of the tree. All her daughters, grand-daughters, and their daughters, etc., share the same mtDNA haplogroup.

Here is a diagram showing the most likely relationship of Nicholas Martiau with his daughters. The red line in this and subsequent diagrams indicate the matrilineal descent and shared mtDNA.



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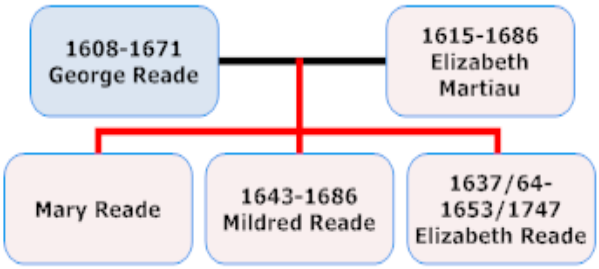
Elizabeth Martiau

As mentioned above, no baptismal record for Elizabeth or marriage record for Nicholas are identified in records in England. She was most likely born in 1615, but there is uncertainty about that.

George Reade married Elizabeth Martiau in 1641. He applied for control of land that had been awarded to Nicholas as “head-rights” for settling on the York River but was not seated. Court documents listed those transported including: Capt. Nich. Marteaw, Mrs. Jane Marteaw, Elizabeth Marteaw, Jane Bartlett…” and are cited in various court records from 1631 to 1651. The awarding of headrights to Nicholas is somewhat confusing. His initial passage to Virginia was paid by the Earl of Huntington. Nicholas was provided additional land grants for building fortifications after the 1622 Powhatan-Anglo War, or perhaps as an award for his settling the land that became York County.

George Reade was born in 1608 at the Linkenholt Manor, Hampshire, England to Robert Reade and his second wife, Mildred Windebanke. George and Elizabeth had 3 daughters and the second was named Mildred. The name Mildred is recurrent in the descendants and John Stoudt’s book on Nicholas Martiau states Mildred Reade was named after her grandmother, Mildred Windebanke who may have been the origin of that family naming tradition.

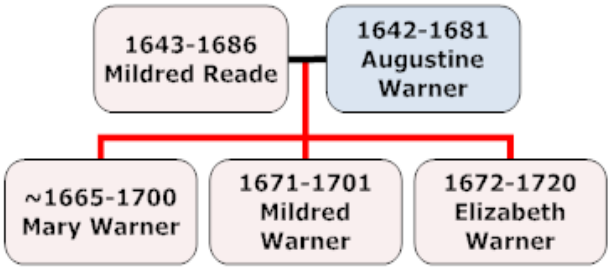
Here is a diagram showing the trunk of this family tree:



Elizabeth Martiau married George Reade and had three daughters:

Mary Reade — No records have yet been located. It is likely that she died young.

Mildred Reade married Augustine Warner and had three daughters. These are discussed further below.



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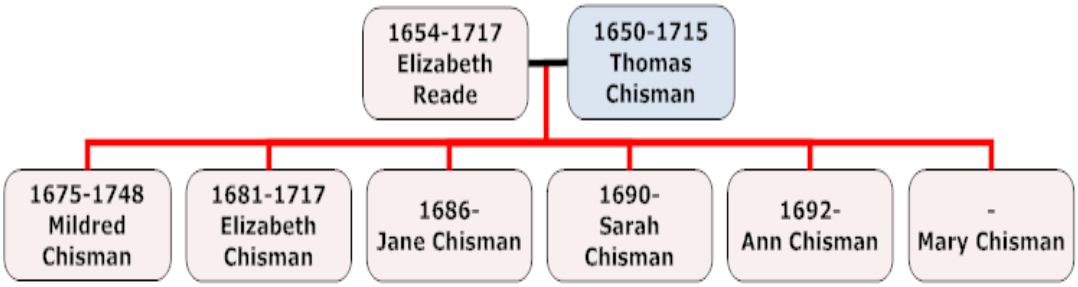
Elizabeth Reade and Thomas Chisman had six daughters:



1. Mildred Chisman married Lawrence Smith and had 4 daughters.
2. Elizabeth Chisman married a (____) Lucas and no children were found.
3. Jane Chisman married John Lily and had no daughters.
4. Sarah Chisman married:
   Thomas Barber and had 1 daughter, Elizabeth—no further information was found
   Robert Shields and had 3 daughters.
5. Ann Chisman—no further information was found.
6. Mary Chisman—no further information was found.

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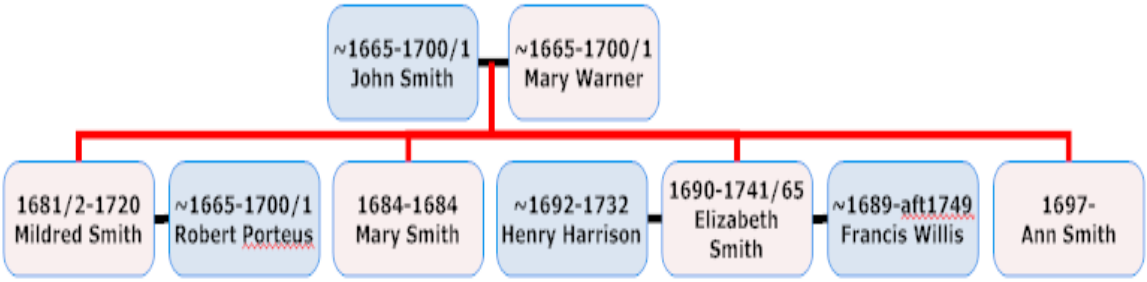
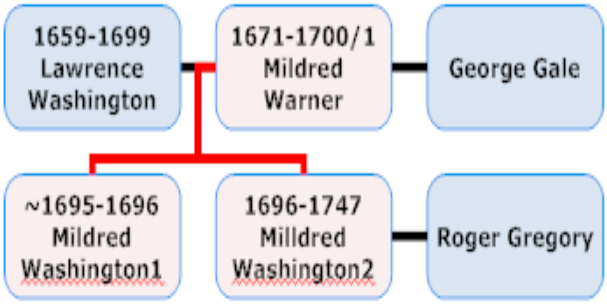
Mary Warner married John Smith and had 4 daughters:



1. Mildred Smith married Robert Porteus and had 3 daughters—no further information on descendants of those 3 daughters was found. Of note, Robert and Mildred Porteus are ancestors of King Charles III of England (and his mother Queen Elizabeth II, and her mother Queen Elizabeth I) through their son Robert Porteus who married Judith Cockayne. As both Robert Porteus Sr. and Mildred Smith were born in Virginia, they are known as the "American ancestors" of the current royal family in England.
2. Mary Smith—died in infancy.
3. Elizabeth Smith married:
   a) Henry Harrison and had 4 daughters—no further information on descendants of those 4 daughters was found.
   b) Francis Willis and had no daughters.
4. Anne Smith—no further information was found; probably died young.

Note: Some family trees include Martha Jacqueline Smith as another daughter, but she was a not mentioned in her father's will. Other trees list her as a daughter of Augustine Warner Smith and Sarah Carver. No records list her husband or any children for her.

Mildred Warner married twice:



1. Lawrence Washington and had 2 daughters
   a) Mildred Washington1—died in infancy
   b) Mildred Washington2 married:
      1) John Lewis and had no children
      2) Roger Gregory and had 3 daughters
         i) Mildred Gregory m John Thornton and had 4 daughters
         ii) Frances Gregory m Francis Thornton and had 2 daughters
         iii) Elizabeth Gregory m x 4 and had 1 daughter with Reuben Thornton

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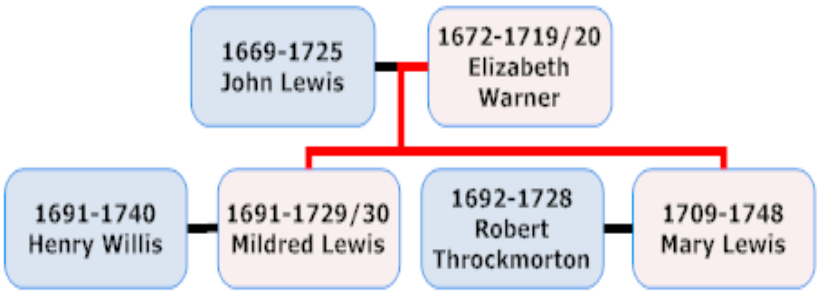
3) Henry Willis and possibly had 2 daughters—if so, both died in childhood

2. George Gale and had no children.

Elizabeth Warner married John Lewis. Her tombstone epitaph states she was the mother of 14 children. She may have had at least 6 daughters.



These are the ones most listed:

1. Mildred Lewis - no documentation lists her as a daughter—see below.
2. Catherine Lewis - twin died young.
3. Elizabeth Lewis - twin died young.
4. Elizabeth Lewis - m John Bolling but died shortly after leaving no children.
5. Isabella Lewis - m Thomas Clayton, had only 1 daughter Juliana who died at 4 years.
6. Mary Lewis - no documentation found; listed as a daughter by researchers—see below.
7. Anne Lewis - no documentation found—see below.
8. Others: names unknown - no documentation found—see below.

Mildred Lewis was not documented as a daughter in records of Elizabeth (Warner) Lewis or John Lewis and no baptismal record has been found in St Peter's Parish or Abingdon Parish. The year of her birth, 1691, was the year John Lewis was relocating from New Kent County to Gloucester County and from St. Peter's Parish to Abingdon Parish. He may also have attending various other churches during that time. They lived in Warner Hall by 1704.

Mary Lewis no records have been found to document her as a daughter, but many think she was. According to Merrow Edgerton Sorley[8] "…none of their daughters left any surviving issue (with the exception of Mary Lewis, who may not have been their daughter, as documentary proof of her parentage does not exist)."

Anne Lewis is also not named in records. Some attach her to this family, while others do not.

It is thought that some additional daughters may have died young.

The known sons are John, Charles, and Robert Lewis. Since Elizabeth had 14 children odds suggest there were other unnamed sons and daughters.

[8] *Merrow Edgerton Sorley, Lewis of Warner Hall: The History of A Family, Genealogical Publishing Co., Inc., 1935, page 59*

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The Problematic Links

Mildred Howell or Mildred Lewis?

A small book was published by Richard Henry Willis, MA PhD that was not dated but reported as either 1898 or 1901 called A Sketch of the Willis Family of Virginia and of their Kindred in other States. It is a book that combines a manuscript previously written (1834) by Byrd Charles Willis with material added by Richard Henry Willis[9]. This book has been used as a source of information by many genealogists, so it deserves some scrutiny.

Byrd was the son of Lewis Willis who was the son of Henry Willis and Mildred (Washington) (Lewis) (Gregory) Willis. Byrd Charles Willis was born in 1781 and died in 1846. His grandfather, Henry Willis died in 1740, so Byrd did not know his grandfather personally. The manuscript he wrote was based on family stories and records from a Willis family bible. That bible was reportedly owned by another descendant at the time the manuscript was published. The genealogist Lyon G. Tyler[10] reports in the history of the "Willis Family" that a copy of the bible was provided to the author by Prof. R. H. Willis and contained the following entries:

Marriages: Henry Willis and Ann Smith were married 2nd of November 1714. Henry Willis and Mildred Brown were married the 30th of October 1726. Henry Willis and Mildred Gregory were married the 5th of January 1733.

Births: John Smith, son of John Smith,' was born 17th of December, 1712. Ann Smith miscarried of a girl and boy in May 1715. Mary Willis was born 5th of August 1716. Francis Willis was born 12th of October 1718. David Willis was born the 17th of December 1720. Henry Willis was born the 22nd of September 1722. John Willis was born the 17th of August 1724. Robert Willis was born the 12th of March 1725. John Willis was born the 16th of July 1728. Elizabeth Willis was born the 12th of January 1729. Ann Willis was born the 14th of September 1731. Isabel Willis was born the 10th of June 1733. Lewis Willis was born the 11th of November 1734.

Deaths: Henry Willis departed this life the 14th of September 1740. Mildred Willis, the wife of Henry Willis, departed this life the 5th of September 1747. John Willis Elder departed this life the 5th of March 1750.

It was reported that the contents were copied in part from older bibles, and it is possible that some dates may have been changed. It would be helpful to carefully examine this bible to verify its contents.

Byrd states that Lewis Willis was named for the first husband of Mildred Washington, John Lewis. John died not long after marriage leaving no children. Byrd Willis reports several stories about Henry Willis which may be apocryphal: "It is said he courted his three wives as maids and married them as widows; he had children by them all" and "That upon hearing about the death of (Mildred Howell), Col. Henry Willis' second wife, Mildred Gregory wept immoderately; upon someone's remarking that it was so strange she should grieve so much for

[9] Byrd Charles Willis and Richard Henry Willis, MA PhD, *A sketch of the Willis family of Virginia : and of their kindred in other states : with brief biographies of the Reades, Warners, Lewises, Byrds, Carters, Champes, Bassetts, Madisons, Daingerfields, Thorntons, Burrells, Taliaferros, Tayloes, Smiths, and Amblers. Richmond, Va.: Whittet & Shepperson, 1898.*

[10] Lyon G. Tyler, *Willis Family",* William and Mary Quarterly, Vol 6 no 4, pages 212-3

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her cousin, she replied that the death of her relation was not the sole cause of her grief, though she loved her dearly as they were cousins and bore the same name, but that she knew that old Henry Willis would be down there to see her and she did not know what to do with him. The sequel proved that she knew the man for in a little month the old cock sat himself down before her door and commenced as regular siege; she held out for some time, but finally capitulated, so in less than two months after the death of his second wife (Mildred Brown) he marred (Mildred Gregory), formerly Washington, and sister to John and Augustine Washington. In due time my father, Lewis Willis, was the first of this union."

It is not clear where these stories originated, but they were clearly not directly told by Henry or Mildred to their grandson. Perhaps Lewis Willis or another relative or acquaintance had shared them with Byrd. The tenor and wording of these stories is consistent with other parts of Byrd's manuscript, so it's possible he created them. They do provide some potential clues. If the Mildreds were 1st cousins that would limit the possibilities. However, the term "cousin" was variably applied at that time and may not be specific to a first cousin as is most used today. It was often used to describe any relative who was not a sibling. There are also clues about the timeline of events. But there is also introduced additional confusion because this book reports the following children born to the 3 marriages of Henry Willis:

Ann (Alexander) Smith married Henry Willis Nov 1714; died Mar 1725/26

Children:	John	(Smith) Dec 1712
	Henry	no date in book; other sources cite b Sep 1722 and Robert b Mar 1725/26
	Francis	Oct 1718
	Mary	Aug 1716
	David	Dec 1720
	Robert	Sep 1722
	John	Jul 1728; other sources cite b Aug 1724

Mildred (Howell) Brown married Henry Willis 1726; died Jun 1733

Children:	John	Jul 1728
	Elizabeth	Jan 1729
	Ann	Sep 1731

Mildred (Washington) Gregory married Henry Willis Jan 1733

Children:	Isabell	Jun 1733
	Ann	Jan 1734
	Lewis	Nov 1734

There are several things to point out. It is recorded that Henry's second wife Mildred died about June 1733. During these years, a double-date system was used for months between January and March 25th. There are several events within those double-date rules: Mildred Washington's marriage to Henry was in January, so if that was 1732/3 then the second wife was still living, so it must be January 1733/34. This was 6 months after the death of the second wife (assuming June 1733 is correct), not 2 months as reported by the family story. Some report her death as Nov 1733, but that was probably a date calculated from the Byrd story that Henry and this third wife married 2 months after the death of his second wife. Isabell was born in Jun 1733 which would have been prior to the marriage of Henry and his third wife, so she was probably born to the second

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wife, and the timing suggests that Mildred died nearly the same time; this likely represents complications from childbirth, unfortunately a common event at that time. Ann Willis was recorded as born January 1734 which would more likely be 1734/5 as Byrd reports that his father Lewis was the first born to that couple. John Frederick Dorman[11] states that Lewis was the only child born to that couple. Lyon G. Tyler[12] wrote some corrections to his history of the Lewis Family and states that the copy of the Byrd Charles Lewis manuscript sent to him had the original wording "his father Lewis was the fruit born to that couple". Apparently, the word changed during the process of transcribing it for printing.

Byrd Willis lived in Fredericksburg in the house built by his grandmother. His father developed a horse-racing track there too. Byrd describes himself as more interested in horse racing than in business. Here is an excerpt describing himself: "I was an idle fellow, fond of fox hunting, racing, and convivial parties; paid no attention to plantation business, and but for the profits of my race-course and the sale of fire wood, would have run through the girths long before I did. In 1825, finding that things were getting worse and worse, I sold off, paid off, and came off to this Territory) 'Florida)."

From the tone of his descriptions, it seems that Byrd did not hold much respect for his father or grandfather. He also was self-critical. "As the only child of my mother, who had long despaired of such a blessing, I was much petted indeed. The poor lady did not know where to stop, for she persisted in treating me as a child, when I began to think myself nearly a man, and I fear in repelling these infantile caresses, I was not always mindful of the respect due to her. I had no cause to tax my father with being overfond of me; indeed, it was his disposition to conceal rather than display partiality, if he ever indulged in such a feeling, and I had never any reason to believe that I was ever its object, from having to launch out much money for the education of my eldest brother, to little purpose ; my father was slow to expend much upon his other sons, so that the cheapness, not the excellence of schools, was the best recommendation."

Besides the internal inconsistency in the book, there are other factual errors in later portions, so its value as a resource must be considered carefully.

Returning to Henry Willis, for those interested, a good description of the business and nature of Henry Willis can be found in the book Forgotten Companions, by Paula S. Felder[13]. She provides a description of his efforts to develop the town of Fredericksburg.

One interesting fact is that during his second marriage Henry Willis' household included 3 children named John; his wife's son John Smith, and 2 sons named John Willis. It is unknown why he named a son John with each of his first two marriages, but it was not unusual to repeat names within a family. It's said that to keep them straight he called them "Jack," "John," and "Johnny". John was referred to as "John Willis the Elder" in some later court documents and a family bible.

The second, and only other clue found about Mildred's maiden name involves a land transaction between Henry Willis and John & Charles Lewis. In summary it appears that the Lewis brothers purchased land that was then sold back to Henry designated as a sort of trust to benefit Henry during his lifetime, then to Mildred and

[11] John Frederick Dorman, *Adventurers of Purse and Person, Virginia, 1607-1624/5: Families G-P*,Genalogical Publishing Co., Inc., Fourth Edition, 2005, p. 552
[12] Lyon G. Tyler, *"The William and Mary Quarterly"*, Jul 1902, Vol. 11, No. 1, p. 40
[13] Paula S. Felder, *Forgotten Companions*, American History Company ,1982, pages 71-100

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her heirs. This transaction is shown in the Spotsylvania County, Virginia records[14]. This was during the time of Henry's marriage to his second wife. In Deed Book D, page 181 John Willis sold the same land 5 Sep 1749 (about 2 years after Henry died). He states that he inherited this land from Henry and Mildred Willis. At that time, he also sold several small lots in Fredericksburg that he also inherited. According to Robert N. Grant (personal communication), this sort of trust is usually set up between relatives and implies that John & Charles Lewis were related to Mildred. John & Charles were brothers and sons of John Lewis and his wife Elizabeth Warner. No other document has been found to show a link of Mildred to the Lewis family.

The lack of information on Mildred was summarized by this exchange on the Lewis Genforum message board in 2006:

> Mildred, d/o of John Lewis and Elizabeth Warner
> Posted by: Aleta Pope Hudson (ID *****1813) Date: January 31, 2006, at 12:47:46
> 17019 of 18823
>
> I am searching desperately for a valid source of information to document the "fact" that Mildred Lewis is a daughter of John Lewis and Elizabeth Warner. I have looked through the St. Peter's Parish, New Kent Co., VA records, and they do not show a child named Mildred being born to John Lewis. The minutes of a Vestry meeting for that Parish, dated 4 Mar 1702, show "Mr. John Lewis lately Departed of this County". Most birth dates given for Mildred place her birth date before 1702, so St. Peter's Parish seemed a likely place to look since that's where Chemokins (home of the Lewis's before they moved to Warner Hall) was located. We know that she's not shown in the Abingdon Parish Records. The website for The National Society of the Washington Family Descendants has a small article posted entitled "More about Mildred Washington and the three wives of Henry Willis." The article mentions Mildred Lewis, the daughter of John Lewis and Elizabeth Warner, who married first John Howell, secondly Dr. John Brown, and thirdly, Henry Willis. I'm assuming this "society" wouldn't publish an article like this without having factual resources to back up the information, and a query to that effect (which I sent to this organization) remains unanswered as of today. I have just purchased Sorley's book about the Lewis Family, and there is no mention of Mildred, a daughter of John Lewis and Elizabeth Warner, but he does mention Henry Willis's "second wife, who was born Mildred Howell and may have been related to the wife of Col. Charles Lewis of 'The Byrd'." Of course, I know that Henry Willis married the widow Howell, supposedly nee Lewis. Help, help, help, help, help!! I'd appreciate any and all comments, help, suggestions, etc.
> ---
> Re: Mildred, d/o of John Lewis and Elizabeth Warner
> Posted by: Lucy Grisham (ID *****2065) Date: February 24, 2006, at 04:46:11
> In Reply to: Mildred, d/o of John Lewis and Elizabeth Warner by Aleta Pope Hudson 17059 of 18823
>
> I don't know of any Mildred that was daughter of John Lewis- there was one who was daughter of Edward, brother to John Lewis, but according to her tombstone, she died as a little girl. I think that Zachary Lewis had a Mildred, but that would not be her either. There are many errors in the established history of these Lewis families, as there was two John Lewis's whose families were recorded in New

[14] *Spotsylvania County Deed Book B, pages 133-4 dated 3 Mar 1730 & page 181 dated 5 Sept 1749*

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> Kent records, John, son of David Lewis of York, Vestryman of St. Peters, and John Lewis III who married to Elizabeth Warner, he being son of John Lewis and Isabella Miller, d/o James Miller. They are related, probably thru their grandfathers. Their children are distinctly different, and I find no Mildred listed anywhere for them. I do find a Mildred Washington, daughter of Augustine Warner and wife Mildred, for whom she must have been named and Elizabeth Warner would have been her aunt. She was born 1697- and died 1747. She married first to John Lewis, (son of Edward Lewis and Susannah)- who died according to tombstone, in 1718. He apparently didn't live long because they had no children, then she re-married to Col. Roger Gregory and had three daughters who married Thornton brothers. Roger died 1731. Her third husband was Col. Henry Willis (1691-1740). their son was Col. Lewis Willis, who grew up with Geo. Washington. She was his third wife too.
> I know that Maj. John Lewis 1692-4, son of John and Elizabeth, who married Frances Fielding had a daughter named Mildred. She would have been born probably about 1727-8? tho. I do not know who she married?
> Col. Charles Lewis of "The Byrd" was married to Mary Howell, daughter of John Howell- but I can't tell you who his wife was.
> If you can find a copy of the "Wright-Lewis-Moore" book by Boyd Wright, there is documentation of tombstone records found after much of the established history was written, that refutes a good deal of it. It also brings to light things that help clarify some of the jumble of this Lewis History.
> Hope this helps some.
> Lucy Vickers Grisham, Lewisville, Texas.

John Frederick Dorman states as fact that Mildred was Mildred Lewis, daughter of John Lewis and Elizabeth Warner and that she married John Howell, then John Brown, then Henry Willis[15]. His references for this are: Pioneer Lewis Families, Vol 4 Cook Publications, 1978 [sic], p. 78-9, and the Byrd Charles Willis manuscript described above. The publication by Michael Cook did not contain references to sources[16].

I also wrote to John Augustine Washington asking about sources for his paper "More about Mildred"[17] and did not get a response. In that paper he states:

> "The National Society of the Washington Family Descendants"
>
> More about Mildred Washington and the three wives of Henry Willis.
> John A. Washington, January 1998
>
> "The second wife of Henry Willis was born Mildred Lewis, the daughter of John Lewis and Elizabeth Warner. She married first John Howell, by whom she had one child, a daughter Mildred Howell, who married a Lightfoot. John Howell died, and she married, second, Dr. John Brown, as probably his second wife. It is thought that she did not have any children by Dr. Brown. Her third husband was Henry Willis, and she was his second wife. By Henry Willis she had four children. After her death Henry Willis married Mildred Washington, daughter of Lawrence Washington and Mildred Warner, and they

[15] John Frederick Dorman, *Adventurers of Purse and Person, Virginia, 1607-1624/5: Families G-P*,Genalogical Publishing Co., Inc., Fourth Edition, 2005, p. 556.
[16] *Michael L. Cook, Pioneer Lewis Families, Cook Publications, Evansville Indiana, 1984, Vol 4 pages 78-79*
[17] This note is no longer visible on the website of the National Society of Washington Family Descendants since the website was updated in 2023 but it can be accessed via WayBackMachine at *http://washingtonfamilydescendants.org/wp-content/uploads/2014/08/More-about-Mildred.pdf*

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had one child, Lewis Willis. Notice that the two Mildreds are first cousins, since their mothers were the two Warner sisters."

"It is true that forty or fifty years ago there was considerable misunderstanding and confusion about these three wives of Henry Willis and their children, but it was all cleared up more than forty years ago, and any confusion can be traced to early, incorrect data."

While the author sounds very certain of his conclusion, no sources for the information were ever provided so I was unable to verify. John Augustine Washington died in 2020.

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Elizabeth Willis

Elizabeth Willis is stated to be the wife of John Clayton. John was the fourth with that name being son of John Clayton (referred to as one of America's first botanists), and his father John Clayton who was a landowner in Hanover and Gloucester Counties, Virginia. Both father and grandfather were active in their church and politically. Both served as clerks in Gloucester County, Virginia. A biography of the botanist and his family is detailed in John Clayton Pioneer of American Botany[18]. The book mentions that Elizabeth Willis was the wife of John Clayton but provides no details on her identity.

The book" Our Kin"[19] similarly states that John Clayton married Elizabeth Willis and names their children, but nothing about her parents.

According to Louise Pacquet de Bellet[20] she was provided with a copy of the manuscript written by Byrd Charles Willis which contained a marginal note written on the original that a daughter of Henry Willis married a Clayton. This reference was quoted by Peggy Frances Rush[21] in her book The Willis Family of the Northern Neck in Virginia 1669-1737, states that "Elizabeth Willis born 12 Jan 1729/30 (given only in bible records with an undocumented source claiming that she married John Clayton)" in reference to Elizabeth Willis as a daughter of Henry and Mildred Willis. And further that, "No appointment of a guardian was found for Elizabeth in Spotsylvania County after Henry's death." She would have been 10 years old when he died, and her stepmother Mildred was still living until she was 17. She married John Clayton in 1753 at 23 years of age, so where was she during those 6 years?

John Frederick Dorman[22] states Elizabeth Willis was a daughter of Henry and Mildred (Lewis) (Howell) (Brown) Willis and she married John Clayton. In a bit of circular sourcing, it refers to a chapter on Salter-Weld which includes John Clayton and his ancestors, does not mention Elizabeth Willis. There it refers to Mildred Lewis in the Martiau chapter. The Salter-Weld chapter lists source for John Clayton the Berkeley book on the botanist John Clayton.

There has also been confusion between Isabella Lewis, a daughter of John Lewis \ Elizabeth Warner with Isabell Willis (some cite her name as Mary Isabell Willis) who married Howell Lewis thereby becoming Isabell Lewis. Howell Lewis was a grandson of John Lewis \ Elizabeth Warner through their son Charles Lewis.

Isabella Lewis married Thomas Clayton. Some references mistake that marriage for Elizabeth Willis who married John Clayton. Isabella Lewis is documented via her baptism record in Abingdon Parish 18 Dec 1707. Isabella had 1 daughter who died young, and Isabella and Thomas also died a few years later leaving no other children[23]. These 2 Isabell(a) Lewis was a generation apart so their dates should help keep them straight.

---

[18] Edmund Berkeley and Dorothy Smith Berkeley, *John Clayton Pioneer of American Botany,* University of North Carolina press, 1963, page 151

[19] Mary Denham Ackerly & Lula Eastman Jeter Parker, *Our Kin, the Genealogies of Some of the Early Families who Made History in the Founding and Development of Bedford County Virginia* C. J. Carrier Co., 1999, pages 347, 348, 350 & 353.

[20] Louise Pacquet du Bellet, *Some Prominent Virginia Families,* J. P. Bell Publishers, 1907, Vol 2 page 282.

[21] Peggy Frances Rush, *The Willis Family of the Northern Neck in Virginia 1669-1737*, Heritage Books, 2007, page 83

[22] John Frederick Dorman, *Adventurers of Purse and Person, Virginia, 1607-1624/5: Families G-P*,Genalogical Publishing Co., Inc., Fourth Edition, 2005, pages 556-557

[23] Merrow Egerton Sorley, *Lewis of Warner Hall the History of a Family,* Genealogical Publishing Co., 1935, page 59.

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Viewing pedigrees posted on the Internet there are many variations noted. Some list Elizabeth Willis as married to John Sale, some list her as married to James Hayes, some list her parents as William & Ann Willis. Some list her as a daughter of Mildred (Washington) (Lewis) (Gregory) Willis. The circumstantial evidence of time and location support a link to Henry and Mildred (Lewis) (Howell) (Brown) Willis as parents, but the lack of documentation and conflicting alternatives is unsettling. The strongest primary source is the Willis family bible, but that has not been available for examination; that bible had a publication date of 1832 suggesting entries were copied into it later.

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Matrilineal Lines of Descent

Identification of the descendants was done using traditional genealogic methods of looking for all extant documentation: census records, wills, land transactions, bible records, obituaries, tombstones, etc. When those are not found secondary sources, such as works published by genealogists were reviewed. Some pedigrees posted on the Internet have source information provided.

Sorting these families can be confusing because of frequent intermarriages and repeated use of names within family lines. Using broad Internet searches helps to locate living individuals using sites such as LinkedIn, Facebook, or public records documents found by name searches. Some people post their pedigrees in Ancestry and messages can be sent through that system. Contact was also attempted by email or letter. It is easier to interest those who are already working on family genealogy. Letters or emails from a stranger are often sent directly to trash. About 10% of attempts to contact resulted in a response.

Testing was done on those who volunteered to assist with the project. A buccal swab was obtained and processed by FamilyTreeDNA (Genes by Genes, Ltd.) a commercial genetic DNA testing company in Houston, Texas. Full-sequence mtDNA tests were performed and compared to the two human reference standards and to other contributors who have been tested by FamilyTreeDNA. They hold a very large database from participants worldwide and report that over 400,000 full sequence mtDNA tests have been performed (May 2023)[24].

[24] Personal Communication

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Results

The trunk described above led to a total of 6 branches (great granddaughters of Elizabeth Martiau) whose descendants were studied further. The goal was to identify living matrilineal descendants eligible to have mtDNA testing. Of the 6 branches, 7 led to finding living female descendants eligible for mtDNA testing. Those 6 Branches and 7 Lines are:

Mildred Warner m Lawrence Washington
- Branch 1 Mildred Washington — 1 participant recruited: Line 1

Elizabeth Warner m John Lewis
- Branch 2 Mildred Lewis — 4 participants recruited: Lines 3, 4, 8, & 9
- Branch 3 Mary Lewis — 1 participant recruited: Line 2
- Branch 4 Anne Lewis

Elizabeth Reade m Thomas Chisman
- Branch 5 Mildred Chisman — 1 participant recruited: Line 7
- Branch 6 Sarah Chisman

In addition, there were 2 additional lines with participants recruited:

Another descendant thought to be of Elizabeth Willis and John Clayton was recruited, but her haplogroup did not match others. A further view of her genealogy disclosed an attachment was found to be an error, so results were excluded. 1 participant recruited: Line 5 (not shown)

A descendant of Jane Lane, the sister of Mary Lane who married John Howell, was recruited as she would share the same mtDNA as Mary Lane. See the discussion following explaining the logic for this test. A diagram of her line appears on the following page.

1 participant recruited. Line 6

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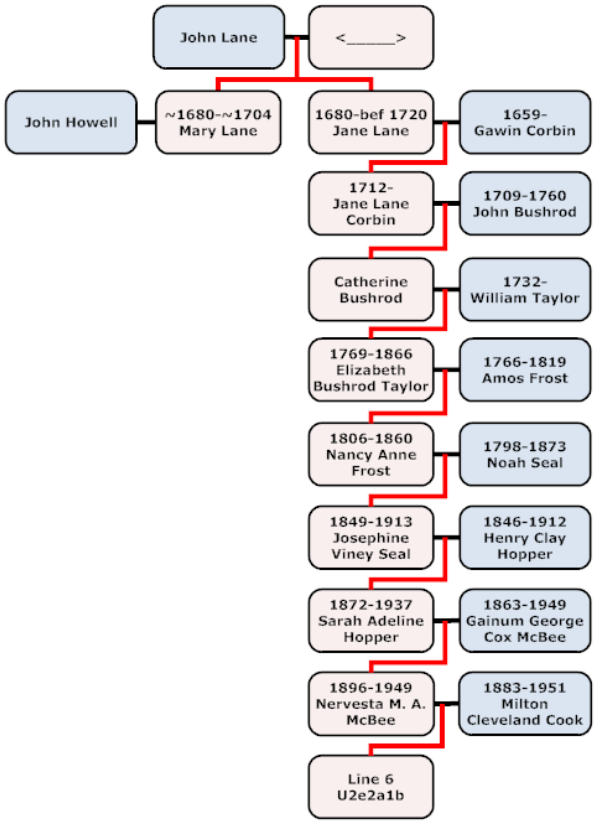

Below is a diagram of the maternal lines of the participants—this puts all the pieces together. The green boxes share a matching haplogroup. The pink boxes are female who would share the same haplogroup if descendants could be found for testing. The blue boxes show some of the husbands to help with orientation. The colorless boxes are those who do not share matching haplogroups. The red lines show the mtDNA line of descent along each line.

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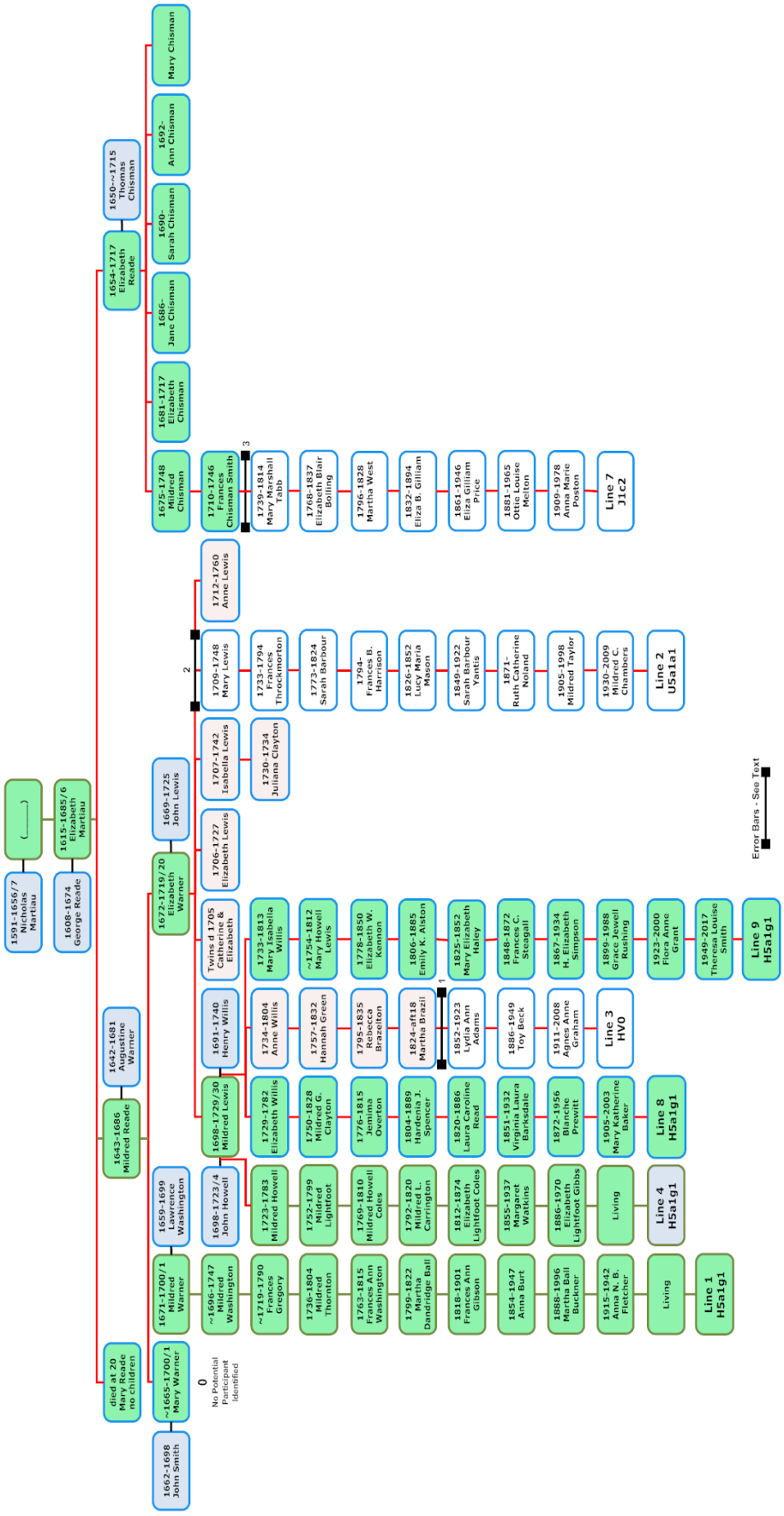

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There are also “error bars” that shows those lines who do not match and the point the match is lost. A description of each of those follows.

Error Bar 1 on Line 3:

Many family pedigrees posted on Ancestry list Martha Brazil as the daughter of Rebecca Brazelton and the wife of Cuthbert Adams. The 1850 census in Seminole, Chattooga Co GA lists Martha Brazeale at age 26, daughter of Morris and Rebecca Brazeale. The 1850 census in Laurens Co GA lists the wife of Cuthbert Adams as Elizabeth B. born about 1825. Therefore, Martha Brazil daughter could not be the same person as Elizabeth B. Adams.

The 1860 census lists Elizabeth’s birth as ~1820; the 1870 census lists her as Brazil Adams with birth ~1819; the 1880 census lists her as Brazila with birth ~1815. Laurens Co GA marriage records show Elizabeth Brazil Culpep(p)er marrying Cuthbert Adams 4 Jan 1838. Her tombstone in China Grove Cemetery, Mitchell Co GA has the name Martha Brazil Adams b 1824 d 1881. A pedigree posted on FamilySearch lists her as Elizabeth Brazil Culpepper daughter of Henry F. Culpepper and Edith Smith.

Martha Brazil (Brazeale) appears with her father at age 44 in the 1870 census. It appears she did not marry. No death record has been located. She probably did not have children.

Therefore, it appears that Martha, the daughter of Rebecca Brazelton and Morris Brazil is not the same person as Elizabeth Brazil Culpepper, the wife of Cuthbert Adams. But it is confusing why the name Martha Brazil appears on the tombstone of Elizabeth Brazil (Culpepper) Adams. A few Ancestry pedigrees list Martha Elizabeth Brazil (Culpeper) Adams as a full name, but no source is provided. The mismatch in mtDNA supports that Lydia Ann Adams does not share the same haplogroup as this matrilineal group.

Error Bar 2 on Line 2:

The line from the participant to Mary Lewis is well documented, but as mentioned previously, there is no documentation of her parentage.

Isabella Lewis who married John Clayton had one daughter who died young. The mtDNA results suggest that Mary Lewis was not of this matrilineal group and therefore not the daughter of John Lewis & Elizabeth Warner. Possibly she was the daughter of Nicholas Lewis per this birth record in St. Peter s Parish, New Kent Co., VA: Mary daughter of Nicho Lewis baptis. Jan. the 16th, 1708/9.

Error Bar 3 on Line 7:

Some pedigrees posted online list Mary Marshall Tabb as a daughter of Frances Chisman Smith. Others list her as the daughter of Thomas Tabb and Rebecca Booker. The former appears incorrect as Frances married Matthew Wills as his second wife and they had 7 children from 1730 to 1741. She died in 1746 and her husband, Matthew, married a third wife Mary Johnson. He died in 1761.

Mary Marshall Tabb was born in 1739, so she could not be the daughter of Frances Smith. The mtDNA haplogroup does not match the other matrilineal descendants confirming this.

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Key Findings

This project defines the haplogroup for Elizabeth Martiau and her matrilineal descendants. Downstream, all daughters, granddaughters, and so on also share the same haplogroup. Sons of the last generation also have their mother's mtDNA. The matching results confirm that the shared haplogroup has been identified as mtDNA H5a1g1. This confirms the haplogroup of Elizabeth Martiau's downstream descendants: Mildred Reade, Mildred Warner, Mildred Lewis, and Elizabeth Willis, etc. Mildred Washington was also in this line and therefore shares the same haplogroup.

The answer to the research questions posed in the introduction are:

1. Yes, Elizabeth Willis was the daughter of Henry Willis and Mildred (Lewis) (Howell) (Brown) Willis.

2. Yes, Mildred (Lewis) (Howell) (Brown) Willis was the daughter of John Lewis and Elizabeth Warner.

In addition to answering the research questions there are additional findings that became evident:

1. Mildred (Lewis) (Howell) (Brown) Willis was a first cousin to Henry's third wife, Mildred (Washington) (Lewis) (Gregory) Willis. They share the same mtDNA haplogroup H5a1g1. The apocryphal story by Charles Byrd Lewis cited previously was likely true.

2. To confirm Mildred Lewis was not a Howell, a Howell line matrilineal descendant from the sister of Mary Lane who married John Howell was tested. If Mildred was a Howell, then her descendants would also match that line. The haplogroup did not match, therefore Mildred was not a Howell.

3. Mary Lewis either was not a daughter of John Lewis and Elizabeth Warner or an adoption occurred in a female descendant. The one descendant tested has a different haplogroup.

4. Mary Marshall Tabb probably either was not the daughter of Frances Chisman Smith or an adoption occurred in a female descendant. The one descendant tested has a different haplogroup.

5. Martha Brazil (Brazeale) was a daughter of Rebecca Brazelton, but she did not marry Cuthbert Adams. More likely he married Elizabeth Brazilla Culpeper. The haplogroup of one descendant of Brazilla (Elizabeth B.) Adams does not match the other lines, but it remains unclear why her name appears as Martha on Elizabeth's tombstone as shown on her FindAGrave web page.[25]

[25] *https://www.findagrave.com/memorial/43885156/martha-brazil-adams*

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Looking at the matches available to all participants at FamilyTreeDNA there are 51 fully identical within the H5a1g1 haplogroup and there are 39 participants with a genetic distance = 1.

There are no fully identical matches to Line 4 and 49 that have a genetic distance = 1, including Lines 1, 8, and 9. These 1-step matches are the same participants that exactly match each other which indicates that the single mutation occurred in Line 4 sometime between Mildred Howell and the participant. Testing descendants who were born since Mildred Howell would pinpoint at which generation the new sub-branch in that line was created.

Lines 1, 8, and 9 match each other exactly when comparing their full genomic sequence mtDNA. Their results share Haplogroup H5a1g1. Line 4 matches the other 3 lines with a genetic distance of 1. That single mutation difference must have occurred in Mildred Howell or one of her descendants, otherwise the 4 lines would be identical.

Lines 2 and 3 did not have matching results. Their records were further examined to determine why these did not match. The diagram below shows those who match colored in green while those who do not match without color. Pink lines should match if testing could be done on any descendants. A few husbands were included to help with identification of the lines.

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Test results compared to reference standards.

The mtDNA sequence is compared to 2 human reference sequences: the Reconstructed Sapiens Reference Sequence (RSRS) and the Revised Cambridge Reference Sequence (rCRS). The tables below were copied from the results table at FamilyTreeDNA for each participant. They list the specific site along the mtDNA change that has a marker different from the reference. Lines 1, 8 & 9 match each other exactly and share the same differences when compared to the RSRS and rCRS sequences. Line 4 has a single mutation difference from those (highlighted in yellow).

RSRS Comparison to Lines 1, 8 & 9

RSRS Values | rCRS Values

Extra Mutations	315.1C C16519T
Missing Mutations	

HVR1 DIFFERENCES FROM RSRS				
A16129G	T16172C	T16187C	C16189T	T16223C
G16230A	T16278C	T16304C	C16519T	

HVR2 DIFFERENCES FROM RSRS				
G73A	C146T	C152T	C195T	A247G
315.1C	A444G	C456T		

CODING REGION DIFFERENCES FROM RSRS				
A769G	A825t	A1018G	G2706A	A2758G
C2885T	T3594C	G4104A	T4312C	T4336C
T7028C	G7146A	T7256C	A7521G	T8468C
T8655C	G8701A	C9540T	G9804A	G10398A
T10664C	A10688G	C10810T	C10873T	C10915T
A11719G	A11914G	T12705C	G13105A	G13276A
T13506C	T13650C	T14766C	C15833T	

RSRS Comparison to Line 4

RSRS Values | rCRS Values

Extra Mutations	315.1C G6465R C16519T
Missing Mutations	

HVR1 DIFFERENCES FROM RSRS				
A16129G	T16172C	T16187C	C16189T	T16223C
G16230A	T16278C	T16304C	C16519T	

HVR2 DIFFERENCES FROM RSRS				
G73A	C146T	C152T	C195T	A247G
315.1C	A444G	C456T		

CODING REGION DIFFERENCES FROM RSRS				
A769G	A825t	A1018G	G2706A	A2758G
C2885T	T3594C	G4104A	T4312C	T4336C
G6465R	T7028C	G7146A	T7256C	A7521G
T8468C	T8655C	G8701A	C9540T	G9804A
G10398A	T10664C	A10688G	C10810T	C10873T
C10915T	A11719G	A11914G	T12705C	G13105A
G13276A	T13506C	T13650C	T14766C	C15833T

CODING REGION DIFFERENCES FROM rCRS

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The Matrilineal Pedigree Tables

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Line 1: Descendant of Elizabeth Martiau > Mildred Reade/Warner/Washington

The first participant is a well-documented descendant of Elizabeth Martiau. Her mtDNA haplogroup was the standard to compare with other lines. The person ID number is the ID used by Dr. Justin Glenn and is shown as the "Glenn #"). References are shown at the end of this section.

Gen	Maternal Line	Lived	Glenn #	Husband	Yrs/Gen	Reference
1	(_____) (_____)			Nicholas Martiau		
2	Elizabeth Martiau	1615-1685/6	41	George Reade		1-3
3	Mildred Reade	1643-1695	42	Augustine Warner	28	1
4	Mildred Warner	1671-1700/1	43	Lawrence Washington	28	1,2
5	Mildred Washington	1696-1747	11	Roger Gregory	25	1
6	Frances Gregory	~1720-1790	35	Francis Thornton	24	1
7	Mildred Thornton	1736-~1804	107	Charles Washington	16	1
8	Frances Ann Washington	1763-1815	103	Burgess Ball	27	1
9	Martha Dandridge Ball	1799-1822	351	Jonathan Catlett Gibson	36	1
10	Frances Ann Gibson	1818-1901	1041	James Creth Burt	19	1
11	Anna Burt	1854-1947	2983	Aylette Hawes Buckner	36	1
12	Martha Ball Buckner	1888-1996	16654	William Meade Fletcher	34	5-10
13	Anna Nancy Buckner Fletcher	1915-1942		Francis Percival Smith	27	7-10
14	Living				21	9-10
15	Participant #1				24	11-15
	Total Years =	345		Average =	27	

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Line 4: Descendant of Elizabeth Warner

This is the only male participant. He inherited his mother's mtDNA. His line is also well documented but shares the problematic link to Mildred Lewis. His test provided verification of the haplogroup shown in Line 1 as well as providing verification that Mildred Lewis shared the same haplogroup. His test shows a one-step difference from Lines 1, 8 & 9. As a full-sequence mtDNA test the single step difference remains "closely related". This line descends from Mildred Lewis' first marriage to John Howell.

Gen	Maternal Line	Lived	Glenn #	Husband	Yrs/Gen	Refer-ence
1	(_____) (_____)			Nicholas Martiau		1-3
2	Elizabeth Martiau	1615-1685/6	41	George Reade		1
3	Mildred Reade	1643-1695	42	Augustine Warner	28	1
4	Elizabeth Warner	1672-1719/21	†	John Lewis	29	1
5	Mildred Lewis	1691-1733		John Howell	19	16
6	Mildred Howell	1723-1783		William Lightfoot	32	17
7	Mildred Lightfoot	1752-1799		Walter Winston Coles	29	18
8	Mildred Howell Lightfoot Coles	1769-1810		Paul Carrington	17	19
9	Mildred Lightfoot Carrington	1792-1820		Issac Howell Coles	23	12, 20
10	Elizabeth Lightfoot Coles	1812-1874		William Joel Watkins	20	21
11	Margaret Watkins	1856-1937		George William Gibbs	44	22
12	Elizabeth Lightfoot Gibbs	1886-1970		Joseph Dunning Weed	30	23
13	Living				35	13, 14
14	Participant #2				36	13-15
	Total Years =	342		Average =	29	

† Cited as the youngest daughter of Mildred Reade and Augustine Warner but no ID number was assigned.

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Line 8: Descendant of Mildred Lewis

She is a key participant to verify the lineage of Elizabeth Willis to Mildred Lewis as she descends from those ancestors. She descends from Mildred Lewis and her third husband, Henry Willis. She descends from George Reade and Elizabeth Martiau through the matrilineal line shown below:

Gen	Maternal Line	Lived	Glenn #	Husband	Yrs/ Gen	References
1	(_____) (_____)			Nicholas Martiau		1-3
2	Elizabeth Martiau	1615-1685/6	41	George Reade		1
3	Mildred Reade		42	Augustine Warner	28	1
4	Elizabeth Warner	1672-1719/20	†	John Lewis	29	1
5	Mildred Lewis	1691-1733		Henry Willis	19	2, 24-28
6	Elizabeth Willis	1729-1782		John Clayton	38	24-28
7	Mildred Gregory Clayton	1750-1828		James Overton	21	26, 29
8	Jemima Overton	1778-~1815		Thomas Harris Spencer	28	30
9	Hardina Jefferson Spencer	1804-1889		Sion Spencer Read	26	31, 32
10	Laura Caroline Read	1820-1886		Harrison Barksdale	16	33-35
11	Virginia Laura Barksdale	1851-1932		John Claude Prewitt	31	36, 37
12	Blanche Prewitt	1871-1956		Richard Downing Baker	20	38, 39
13	Mary Katherine Baker	1905-2003		Ethelbert Carter Stanley	34	40, 41
14	Participant #8				36	13-15
	Total Years =	326		Average =	27	

† Cited as the youngest daughter of Mildred Reade and Augustine Warner but no ID number was assigned.

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Line 9: Descendant of Isabella Willis

Isabella Willis was one of the daughters of Mildred and Henry Willis. There was uncertainty about who was her mother, Mildred Lewis, or Mildred Washington. Isabella (aka Mary Isabella) was most likely born to Mildred Lewis as discussed previously. Ironically, it doesn't matter for this project as Mildred Washington and Mildred Lewis were first cousins and share identical mtDNA from their common grandmother, Mildred Reade. This result provides additional verification of the shared haplogroup.

Gen	Maternal Line	Lived	Glen #	Husband	Yrs /Gen	Refer-ences
1	(_____) (_____)			Nicholas		1-3
2	Elizabeth Martiau	1615-	41	George		1
3	Mildred Reade	1643-1695	42	Augustine	28	1
4	Elizabeth Warner	1672-	†	John Lewis	29	1
5	Mildred Lewis	1691-1733		Henry Willis	19	2, 16
6	Mary Isabella Willis	1733-1812		Howell	42	
7	Mary Howell Lewis	~1754-		Charles	21	42
8	Elizabeth Warner	1778-		John T.	24	42
9	Emily Kennon	1806-1885		Coleman	28	43,
10	Mary Elizabeth	1825-1852		John Jacob	19	43,
11	Frances C.	1848-1872		John Peter	23	43,
12	Harietta Elizabeth	1867-1934		Millard	19	46-50
13	Grace Jewell	1899-1988		Charles A.	32	50
14	Flora Anne Grant	1923-2000		Robert	24	51-54
15	Theresa Louise	1945-2017		Gary Foster	22	55
16	Participant #9				31	13-15
	Total Years =	330		Average =	26	

† Cited as the youngest daughter of Mildred Reade and Augustine Warner but no ID number was assigned.

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Discussion / Conclusion

Limitations and future research

It is possible that some of the lines of non-matching participants contained an adoption event that was not recorded. Additional testing to stepwise triangulate on the ancestors of that line might identify if such an event occurred.

Additional testing that would add to these findings.

Additional verification of descendants of Elizabeth Martiau showing they share the same haplogroup will depend on living maternal line women (or last generation sons) performing a full-sequence mtDNA test. This represents a finite number of individuals. Having traced many lines to develop this project it is interesting to notice how many lines end without living female descendants. This occurs when a child or young woman dies before having children, or she only has sons so her mtDNA is no longer passed forward beyond one more generation.

To further confirm Elizabeth Martiau's haplogroup, it would be useful to find a matrilineal descendant from Elizabeth Reade along the Chisman line who could be tested.

To further confirm Mildred Reade, finding a matrilineal descendant of Mary Warner would show results from all 3 Warner daughters. This would involve locating female descendants of Ann or Nancy Porteus most likely in Yorkshire, England.

Another participant who descends from Mary Lewis might verify that she was not the daughter of Elizabeth (Warner) Lewis.

Could these matches have occurred by chance?

H5a1g1 haplogroup frequency

The frequency of mtDNA has been counted in various regions and countries. For the H haplogroup counts show the following as reported by Eupedia:[26]

Haplogroup H is found in about 40% of Europeans.
It makes up about 28% of American mtDNA.
Subclade H5 is found in 2.4-4.1% of those in England (highest in Wales (8.5%) and lower in other regions).
Subclade H5a1 is found in 1.8-2% of those in Europe.

[26] *https://eupedia.com/europe/Haplogroup_H_mtDNA.shtml (last accessed 18 Aug 203)*

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Frequency of subclade Haplogroup H5a1g1 has not yet been published, but it is likely well below 1.8% in Europeans. That means that finding a match at random would only occur less than once or twice in a hundred; so, any two who match are at least 98-99% likely to share a common ancestor.

The company, FamilyTreeDNA.com (Gene by Gene, Ltd.) occasionally reports on the number of tests run. Currently they report that over 400,000 full-sequence mtDNA tests have been done (personal communication). They report identification of over 5,000 distinct lines from nearly 200 countries. If participants were equally random between groups, then there would be 400,000/5,000 people per haplogroup = 43. Diversity is huge.

Among the 400,000+ tested, only 246 were identified within haplogroup H5a1g1 including all downstream subgroups. That is 0.0615% of total tests. There are 51 test takers (49 excluding Lines 8 & 9) who are exact matches compared to Line 1 participant (49/400,000 = 0.012% = 99.99% chance that it is not a random match).

There are 39 with a 1-step genetic distance (about 0.018% of total tests). Three of the exact matches and 1 of the 1-step matches are included in this project which leaves 48 other exact matches and 38 other 1-step matches. Given that the diversity is high and the number of matches per haplogroup is low, there is less chance that the project participants matched due to random chance.

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HVR1, HVR2, AND CODING REGION MATCHES

EXACT MATCH

Country	Match Total	Country Total	Percentage
Austria	1	780	0.1%
England	7	11214	0.1%
Finland	1	6373	< 0.1 %
Germany	1	9739	< 0.1 %
Ireland	3	8789	< 0.1 %
Scotland	1	4106	< 0.1 %
Switzerland	1	1144	0.1%
United States	4	14813	< 0.1 %

GENETIC DISTANCE -1

Country	Match Total	Country Total	Percentage
Belgium	1	363	0.3%
England	3	11214	< 0.1 %
Germany	5	9739	0.1%
Ireland	2	8789	< 0.1 %
Netherlands	1	1187	0.1%
Scotland	1	4106	< 0.1 %
United Kingdom	2	3647	0.1%
United States	1	14813	< 0.1 %

Country of origin of the most distant ancestor was reported by 11 of exact match testers in H5a1g1 who identify United Kingdom, England, Scotland, or Ireland (total 58%), and an additional 4 identify United States as the origin country. FamilyTreeDNA reports 11,214 mtDNA results who list England as the origin of their ancestor; of those there were only 7 in the H5a1g1 exact match group = 0.062% (table from FTDNA).

Being among H5a1g1 exact matches is obviously rare among test takers and among those with ancestors from England. From a biologic viewpoint there is no doubt that the participants who match share a common ancestor most likely from England.

At the time Mildred Lewis lived (1690-1733) the population of Virginia (in 1730) was 84,000 white people. Using the maximum of 1.8% chance of random selection of H5a1g1, there would be about 1,500 people with that haplogroup in Virginia. The odds of picking 1 of those 1500 is 1/1500 = 0.00067 = 0.067%, a very small chance. The other way to state that is there was 99.93% chance the person was not randomly selected from the population.

The question then is who was that common ancestor? Because the H5a1g1 haplogroup is a more recent branch, FamilyTreeDNA states that an exact match on full-sequence mtDNA testing implies that the common ancestor lived 125-500 years ago. The timeframe of the ancestor documented by Line 1 is consistent within that range. We also know from the documentation that does exist on the other lines that these also match to location and that time range. And since 3 of the 7 exact matches listing England as the country of origin, this is consistent with this haplogroup defining the lineage of Elizabeth Martiau.

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Examination of the pedigrees of others in haplogroup H5a1g1 did not reveal any other family who could link as the common ancestor of Elizabeth Martiau. Some of the exact matches had origins in England, but there were no common families found in reviewing their pedigrees. This most likely means that they shared an ancestor in distant past generations—perhaps over a thousand years ago as the haplogroup formation period was as far back as 518 CE.

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By measuring time that occurred between specific changes one can arrive of an estimated rate of change and allow calculation of when a branch formed. Generally, it is predicted that 1 random change in the DNA strand will occur in each 70 generations. A new meiosis has occurred with each pregnancy. A new generation is assumed to be started each 25 years. This calculates to 1 change every 1,750 years. Published studies have measured the change in various populations and they find a range of 1 mutation in every 2,454 to 3,624 years.[27] However, since a random change can occur at any time, it may also happen within a recent generation. These time estimate studies make some assumptions used in their methods that can lead to somewhat different results: Did they evaluate part or all the mtDNA for example? Did they make assumptions about number of offspring and reproductive variation?

It is interesting to calculate the mutation rate for various intervals along the timeline from L0 to present. There was a period of no change in about 250 generations, but in general, the more recent intervals show a decrease in generations for a change to occur. For example, the interval from H5 to H5a1g1 had 7 mutations in about 7700 years or 1 per 44 generations while there were 9 mutations from R to H5 or 1 per 233 generations. Mutation rate may be increasing.

In this project tree there were about 9-14 generations between the MRCA (Elizabeth Martiau) and each participant. In the 4 matching lines, there was 1 DNA nucleotide change; this was in the 44 total generations and 1,095 total years represented. The intergenerational time used for most studies is 25 years per generation giving an average calculation of 1 change in 41 generations. In this project the average intergenerational time was 26.9 years. Having 1 change is not unexpected.
H5a1g1 formed 1250 ybp (CI=95% 1900-750 ybp) with average TMRCA 425 ybp (CI=95% 600-275 ybp) yfull.org (accessed: 20230501). FamilyTreeDNA gives an estimate of the Most Recent Common Ancestor being a 50% chance between 125-400 years ago. In this project the average years from participant to Elizabeth Martiau is 336 years which fits neatly within that range.

H5a1g1 is defined by having these 3 new mutations from parent branch H5a1g: A444G, G9804A, T16311C! which means that at base pair site 444 Guanine was substituted for Arginine, at site 980 Arginine was substituted for Guanine and at site 16311 Cytosine was substituted for Thymine.

[27] Doron M Behar, Mannis van Oven, Saharon Rosset, et al. *"A "Copernican" Reassessment of the Human Mitochondrial DNA Tree from its Root", Supplemental Data,* The American Journal of Human Genetics, Volume 90 (v) 2012, Apr 6.

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On finding the tomb of Elizabeth Martiau

Abstracted from the newspaper article[28]:

About 1923 Mr. Minson Cook had charge of the grading of Buckner Street in Yorktown VA, which apparently had never been graded. The plow or scraper turned up two large stone slabs between lots 5 & 11. Upon examination these stones were found to be the gravestones of Col. George Read and his wife Elizabeth Martiau Read. These stones were polished, recut, and mounted on brick foundations in the churchyard of Colonial Grace Church, Yorktown, VA by Mrs. Arthur Kelly Evans of Hot Springs, VA. She was a descendant of Colonel Read.

During the month of May 1936, the national park service ran into this burial ground while laying a water main along Buckner Street. They uncovered 18 skeletal remains at the exact spot between lots 5 and 11. Two skeletons, one of a man past middle life, the other of a woman past middle life were found at that point in the street where the two Read stones were found in 1923. A broken corner of Colonel Read's stone was also found there by the park service. All the 18 remains were scientifically examined by Dr. Hopkins the curator of the park museum who classified them as to age, sex, size, and approximate length. Mr. Bennett T. Gale, park engineer was assigned to supervise the disinterment and to make a full report to superintendent B. Floyd Flickinger. They reported that considering all the evidence that this was the burial ground of the Reads. A blueprint was made of the locations of each grave and concluded that Grave 6 was Nicholas Martiau and Grave 7 was Jane Berkeley. A youth skeleton in Grave 9 was likely Nicholas Martiau, Jr. and Grave 4 may be the burial of Jane Berkeley, the daughter of Jane who married Nicholas.

The remains were reinterred at the Grace Colonial Church on May 30, 1941, by the Thomas Nelson chapter, Sons of the American Revolution. The Rev. John Baer Stoudt of Allentown PA delivered the memorial oration A firing squad and bugler from Fort Monroe fired the military salute and sounded taps. At that time there were 5 generations of Martiau, and his descendants buried in this churchyard.

[28] Col. A. A. Pruden, *"Gives Records Of Bodies Re-Interred May 30"* Daily Press, Newport News, Virginia, 8 Jun 1941, p 38

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Acknowledgements

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I thank all the volunteers who have transcribed documents making them available enabling research over the Internet.

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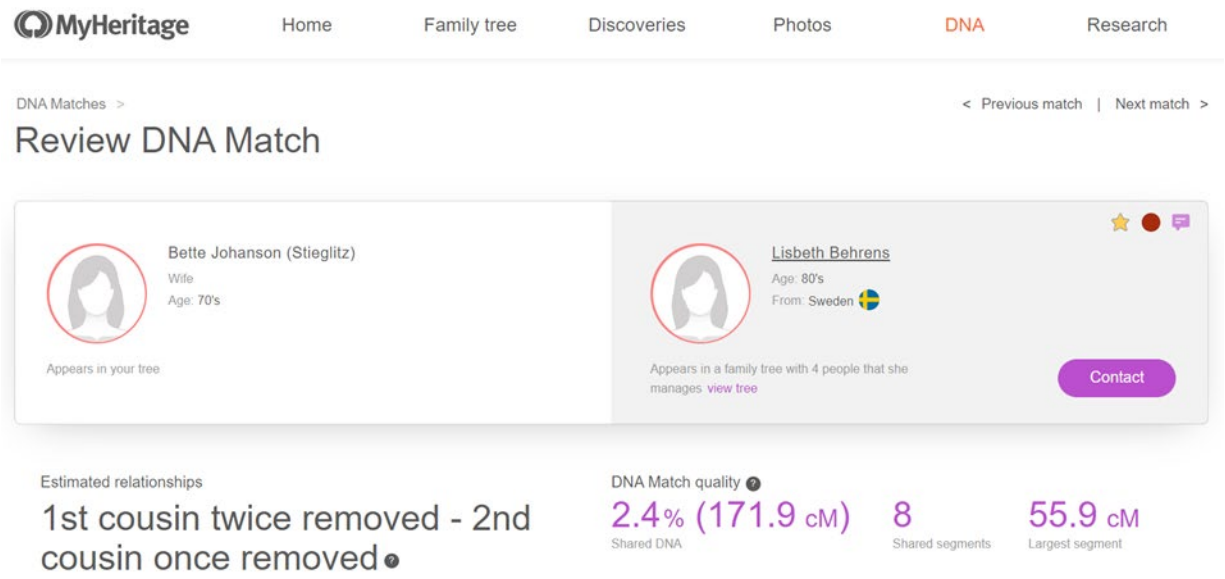
Journal of Genetic Genealogy

Who Was Lisbeth's Great Grandfather?

Rob[t.] Flanagan Stieglitz

There are several reasons for individuals to have their DNA evaluated by genealogy companies. The majority test for ethnicity results, others for genealogy matching and some for more personal reasons. Recently I was contacted by an individual regarding a genetic match on *MyHeritage DNA*. She wrote, "Hej. Mitt namn är Lisbeth, jag har en matchning med 4% med din DNA, som jag förstår på fäderna sida. Jag föddes 1940 i Arvika och undrar om din släkt har anknytning."[1] (English translation from *Google* – Hello, My name is Lisbeth, I have a 2.4% match with your DNA, which I understand is on my father's line. I was born in 1940 in Arvika, and I wonder if your family has a connection).[2] The match Lisbeth is referring to is with my wife Bette. The question then is, who was the common ancestor(s) of Lisbeth Behrens née Ahlén and Bette Stieglitz née Johanson?



According to genealogists Angie Bush and D. Joshua Taylor, "Genetic genealogy is the use of DNA testing in combination with traditional genealogical and historical records to infer relationships between individuals."[3] It is important to emphasize that DNA analysis cannot be used alone, your matches need to have accurately sourced family trees.[4] "By understanding basic patterns of genetic inheritance, genealogists can very effectively use DNA

[1]"MyHeritage Message Inbox," *MyHeritage*, Lisbeth Behrens, 27 Dec 2021 (https://www.myheritage.com/inbox/thread/186339392 : accessed 27 Dec 2021).
[2]"Google Translate," 2001, *Google.com*, Swedish to English, 2001. https://translate.google.com/ : 27 Dec 2021).

[3] Alona Tester, "Beginners Guide to DNA and Genealogy," *FamilyHistory.link*, 12 December 2017, website (https://www.familyhistory.link/dna-genealogy-guide/ : accessed 25 May 2020).
[4] Angie Bush and D. Joshua Taylor, "You Need Both! Uniting DNA and Traditional Research," *Devils Lake Library* (Devils Lake, ND, March 2019), online document (https://devilslakendlibrary.com/wp-content/uploads/2019/03/You-Need-Both-Uniting-DNA-and-Traditional-Research.pdf : accessed 17 April 2020).

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testing to answer questions of kinship and identity, and in some cases, reconstruct kinships for which no records exist." [5]

Family Trees

Bette's ancestry consists of four ethnicities, Norwegian, Swedish, German and Dutch. Only one of Bette's great grandparents, Adolf Olsson Nord, has Swedish ancestry and in fact emigrated from there to America in 1883.[6]

The ancestral line below was provided by Lisbeth indicating that she was never told who the father of her grandmother Signe was. As per Lisbeth's original correspondence, she believes her genetic connection with Bette is within her father's line but nothing definitive has been determined yet.[7] Fortunately, Bette has multiple cousins that tested their DNA that descend from all four of her grandparents and Lizbeth matches only those from her Nord line. Therefore, this is the line we will research.

Emma Lovisa Fryklund
b: 22 Jul 1875 in Värmland, Sweden
d: 17 Oct 1933 in Karlstad, Värmland, Sweden

= **Unknown**
b:
d:

Signe Klara Maria Johansson
b: 21 Jan 1895 in Värmland, Sweden
d: 05 Mar 1966 in Kungsholmen, Stockholm

Gösta Eugen Lundell (Örtendahl)
b: 23 Jun 1917 in Glava, Värmland, Sweden
d: 04 Aug 2003 in Enköping, Uppsala

Lisbeth
b: Arvika, Sweden
d:

[8]

Signe was born in Värmland County, Sweden located in west central Sweden.[9] Bette's Swedish ancestors came from Högerud, Värmland.[10]

[5] Angie Bush and D Joshua Taylor, "You Need Both! Uniting DNA and Traditional Research," *Lake Region Public Library-Great Stories Start Here…,* Mar. 2019 (https://devilslakendlibrary.com/wp-content/uploads/2019/03/You-Need-Both-Uniting-DNA-and-Traditional-Research.pdf : accessed 25 Dec 2020).
[6] Adolf O. Nord, Declaration of Intention for United States Citizenship, 3 May 1888, No cert #, arrived 1883 in the port of Portland, County of Ramsey, Territory of Dakota, USA, Naturalization Records; *North Dakota State Archives*, 612 East Boulevard Ave. Bismarck, North Dakota.
[7] Lisbeth Ahlen Behrens per Rikard Behrens, "Permission to Use DNA and Family Tree Information," received by Rob Flanagan Stieglitz, communication through email, 25 Apr 2022.
[8] Robert Flanagan Stieglitz, "Lisbeth and Bette Tree," *Family Tree Maker*, personal computer database, Fargo, North Dakota, 1 May 2022.
[9] "Värmland County," *Wikimedia Foundation,* 22 Sep 2021 (https://en.wikipedia.org/wiki/V%C3%A4rmland_County : 1 May 2022).
[10] "Riksarkivet - Sök I Arkiven," *Riksarkivet*, 2022, Olof Olsson and Inga Maria Andersdotter family (https://sok.riksarkivet.se/folkrakningar?Fornamn=olof+&Efternamn=olsson&Fodelseforsamling=H%c3%b6gerud&Folk1860=false&Folk1870=false&Folk1880=false&Folk1890=true&Folk1900=true&Folk1910=false&Folk1930=false&Lan=17&AvanceradSok=False&page=7&postid=Folk_103530691&tab=post#tab : 1 May 2022).

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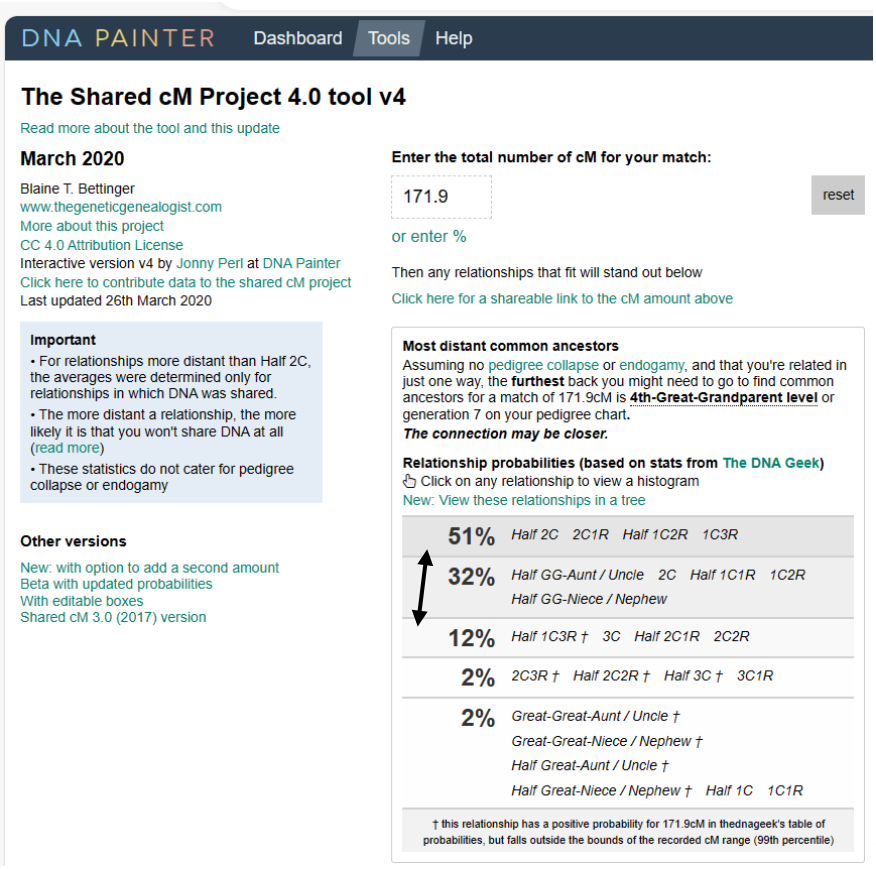
To begin, we will look at the shared DNA reported by *MyHeritage*. The amount of DNA is significant, meaning it is highly likely a common ancestor(s) can be determined.

The Shared cM Project 4.0 tool v4 found on *DNAPainter* is a collaborative data collection and analysis project created to understand the ranges of shared cM (centiMorgans) associated with various known relationships. The image below includes the entered total of shared DNA between Lisbeth and Bette. The total reported by *MyHeritage* is 171.9 cM and there is a 95% (51+32+12%=95%) probability it is a third cousin or closer relationship between Bette and Lisbeth. This means their most recent common ancestor(s) are more than likely great-great-grandparents or closer.



[11]

[11] Blaine Bettinger, "Version 4.0! March 2020 Update to the Shared CM Project!" *The Genetic Genealogist*, 27 Mar. 2020 (https://thegeneticgenealogist.com/2020/03/27/version-4-0-march-2020-update-to-the-shared-cm-project/ : accessed 11 Aug. 2021).

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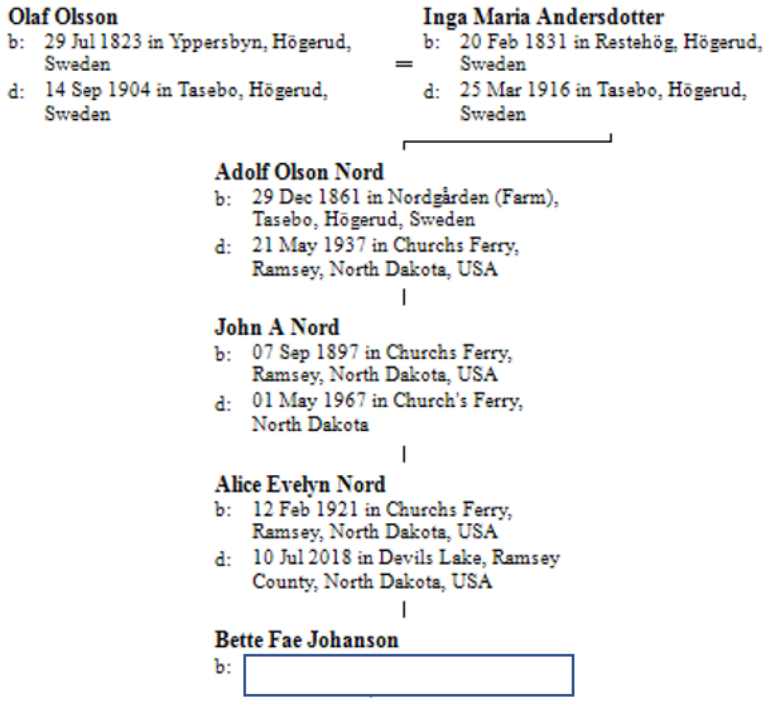
Bette's ancestral tree is seen below.[12]



Based on known family trees and the fact Bette's great grandfather immigrated to the United States in 1883, the relationhip is most likely third cousins. If this is the case then Lisbeth's unknown great-grandfather would have to be a brother to Bette's great-grandfather Adolf Olsson (Nord).

As previously mentioned traditional genealogical reseach has to coexist with genetic genealogy. Vital record search uncovered the 21 January 1895 birth record in Värmland for Lisbeth's grandmother Signe Klara Maria Johansson. Her mother, Emma Lovisa Fryklund was documented but although listed as an illegitamate birth, a father by the name of Emanual Johansson was reported.[13] So if this is accurate, the hypothesis that Lisbeth's biological great-grandfather is Adolf Olsson Nord's brother is incorrect.

According to Blaine Bettinger Ph.D., *The Genetic Genealogist*; "even the best documentary research can be wrong. Our ancestor's times were no simpler than our own and they were no less complex. Sometimes the relationships they reported on paper were not the same relationships they lived. We are the benefactors of the complex lives that our ancestors lived, and DNA testing can help unravel some of the complexity."[14]

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[12] Robert Flanagan Stieglitz, "Lisbeth and Bette Tree," *Family Tree Maker*, personal computer database, Fargo, North Dakota, 1 May 2022

[13] " Sweden, Indexed Birth Records, 1859-1947," *Ancestry.com*, Signe Klara Maria, 21 Jan 1895, Gunnarskog, Värmland, Sverige, Emanual Johansson, Emma Lovisa Fryklund, born 22 Jul 1875, Volume 1140, page 0/0 (https://www.ancestry.com/discoveryui-content/view/4209963:2262?_phsrc=dzw3118&_phstart=successSource&gsfn=signe&ml_rpos=14&queryId=d3fff513e9b3ea2159074c38fea6aabb : accessed 31 May 2022).

[14] "3 Reasons Every Family Historian Should Take a DNA Test | Blog," *Findmypast - Genealogy, Ancestry, History Blog from Findmypast*, 2 Jan. 2020 (www.findmypast.com/blog/dna/why-every-family-historian-should-take-findmypast-dna-test : accessed 17 Dec 2022).

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Further research into the life of Lisbeth's great-grandmother found three years after the birth of Signe, Emma gave birth to a son named Karl Martin in Gunnarskog, Värmland. His birth was also listed as illegitimate and this time no father was named.[15]

Research of birth records for the children born to Olaf Olsson and Inga Andersdotter of Högerud, Värmland between 1858 and 1880 found seven children that included five sons, including Adolf (below).[16]

- Christina Olsdotter - born 08 Sep 1857 in Värmland, Sweden, died unknown
- Olaf Olsson - born 26 Jun 1859 in Värmland, Sweden, died 14 Jun 1910 in Värmland, Sweden
- Adolf Olsson (Nord) - born 29 Dec 1861 in Värmland, Sweden, died 21 May 1937 in North Dakota, USA
- Mathilda Olsdotter - born 03 Oct 1865 in Värmland, Sweden, died 01 Dec 1948 in Värmland, Sweden
- Johan Olsson - born 25 Jan1869 in Värmland, Sweden, died 13 Jan 1895 in Värmland, Sweden
- Lars Albin Olsson - born 12 Feb 1872 in Värmland, Sweden, died 24 Jan 1890 in Värmland, Sweden
- Karl Emil Olsson – born 14 Feb 1878 in Värmland, Sweden, died 1957 in North Dakota, USA

DNA

Was Emanual Johansson the biological father of Signe? DNA does not lie, but sometimes people do. So, to determine the genetic connection to Bette's great-grandfather, Adolf Olsson (Nord), more descendants of his parents, Olaf Olsson and Inga Andersdatter are needed to be found and genetically compared to both Bette and Lisbeth. Once located, the following tools will be used to analyze the data (shared DNA in cM).

- *DNA Painter* for a chromosome matching and for atDNA triangulation.[17]
- *The Shared cM Project 4.0 tool v4* for relationship probabilities.[18]
- *WATO* (**W**hat **A**re **T**he **O**dds) for relationship probabilities.[19]
- *Family Tree Maker* to construct hypothesized family trees (models)[20]
- *Ethnicities* for comparison of *Genetic Groups*.[21]

"The GPS (*Genealogical Proof Standard*) is an adaptation of the scientific method applied to genealogical research questions."[22] The scientific method involves collecting data, developing a hypothesis, building models, assessing these models, and drawing conclusions.[23] Combining the provided family trees and the relationship

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[15] "Sweden, Indexed Birth Records, 1859-1947," *Ancestry*, Karl Martin, birth 6 Jul 1898, Gunnarskog, Värmland, Sverige, mother Emma Fryklund, birth 23 Jul 1875, no father listed (www.ancestry.com/discoveryui-content/view/221642:2262?_phsrc=QHb587& : accessed 27 Feb 2023).

[16] "All Sweden, Indexed Birth Records - 1859-1947," *Ancestry DNA,* children of Olof Olsson and Inga Andersdotter (https://www.ancestry.com/search/collections/2262/?birth=1870_hogerud-varmland-sweden_1493148&birth_x=10-0-0_1-0&count=50&father=Olof&father_x=1&mother=Inga&mother_x=1 : accessed 25 Apr 2022).

[17] "Chromosome Maps," *DNA Painter* (https://dnapainter.com/tools/sharedcmv4 : accessed April 17, 2020).

[18] "Shared CM Project 4.0 Tool v4 with Relationship Probabilities," *DNA Painter* (https://dnapainter.com/#profiles : accessed April 17, 2020).

[19] Andrew Millard and Mike Mulligan, "What Are the Odds?" *DNA Painter* (dnapainter.com/tools/probability : accessed 10 Nov. 2020).

[20] "Family Tree Maker," n.d., *Software MacKiev* (https://www.mackiev.com/ftm/ : accessed 17 Feb 2022).

[21] "What Are Genetic Groups?" *MyHeritage* (https://faq.myheritage.com/en/article/what-are-genetic-groups accessed May 1, 2022).

[22] Angie Bush and D Joshua Taylor, "You Need Both! Uniting DNA and Traditional Research," *Lake Region Public Library-Great Stories Start Here…,* Mar. 2019 (https://devilslakendlibrary.com/wp-content/uploads/2019/03/You-Need-Both-Uniting-DNA-and-Traditional-Research.pdf : accessed 25 Dec 2020).

[23] Wikipedia Contributors, "Scientific Method," *Wikipedia*, Wikimedia Foundation, 4 Mar. 2019, (en.wikipedia.org/wiki/Scientific_method : accessed 25 Dec. 2020).

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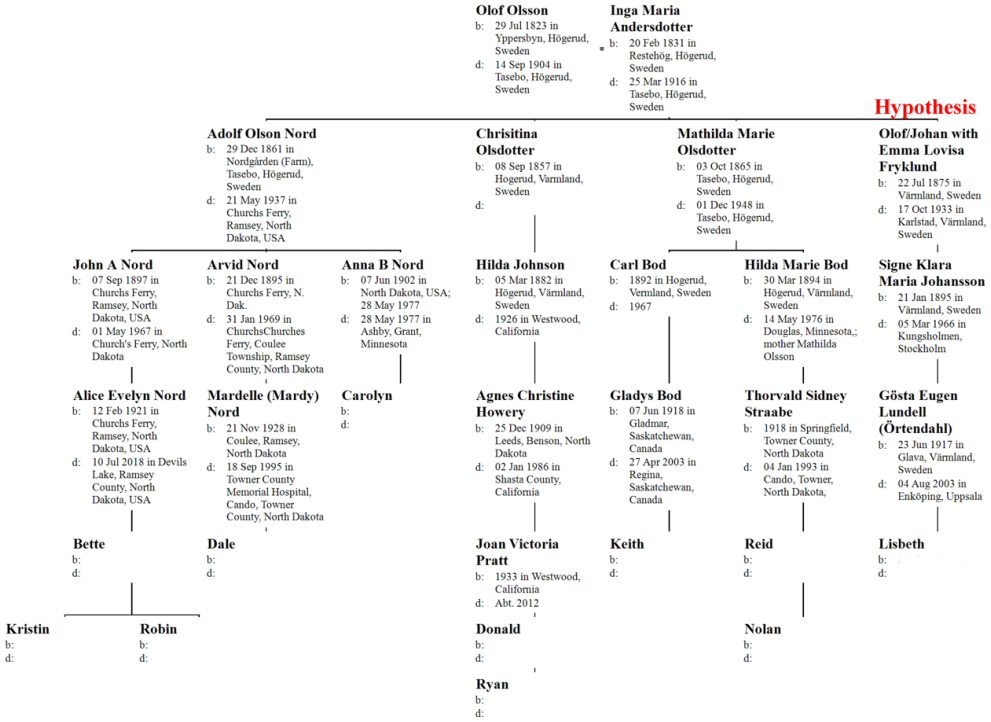
probabilities, a visual model depicting a hypothesized relationship between Lisbeth and Bette was constructed.[24] The process of how to apply the Scientific Method to solve genetic genealogical questions can be found in my article published in the 2023 July/August issue of *Family Tree Magazine*.[25]

Hypothesis: Looking at the family trees the most reasonable ancestral connection would be a great grandfather to Lisbeth and therefore a sibling to Bette's great-grandfather, Adolf Olsson Nord, and a son of Olaf Olsson and Inga Maria Andersdotter.

Model: A Family Tree with hypothesis that Lisbeth's biological great grandfather was the son of Olaf and Inga was created. To develop a workable and testable model, the more data one can secure, the more accurate the predicable result will be. The data used to determine the most likely relationship will be additional shared DNA from matches to both Bette and Lisbeth that were found. The model includes, Bette, her daughters, Kristin, and Robin as well as five additional matches (descendants of Olaf and Inga) found on *MyHeritage*: Dale, Keith, Carolyn, Nolan and Ryan, all with established family trees.[26] Dale and Carolyn are also descendants of Adolf, Keith and Nolan descendants of his sister Mathilda and Ryan his sister Christina. To ensure accuracy of the hypothesized Swedish genetic connection, all the individuals are verified biological descendants of Olaf Olsson (1823-1904) and Inga Maria Andersdotter (1831-1916) of Tasebo, Högerud, Sweden.[27]



[24] David Wood, "Scientific Models: Definition & Examples - Video & Lesson Transcript," *Study.com*, 21 Aug 2021 (study.com/academy/lesson/scientific-models-definition-examples.html : Accessed 30 Jan 2022).
[25] Robert Stieglitz, "6 Steps for Applying the Scientific Method to Genetic Genealogy," *Family Tree Magazine*, 21 Jun 2023 (familytreemagazine.com/dna/scientific-method-genetic-genealogy/ : accessed 24 Sep 2023).
[26] Dale Knutson, "Permission to Use DNA and Family Tree Information," received by Rob Flanagan Stieglitz, communication through email, 31 May 2022.
[27] Robert Flanagan Stieglitz, "Lisbeth and Bette Tree," *Family Tree Maker*, personal computer database, Fargo, North Dakota, 3 Feb 2023.

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The model family tree is pictured above.[28] The relationship prediction of each individual to Lisbeth within the model are shown below.

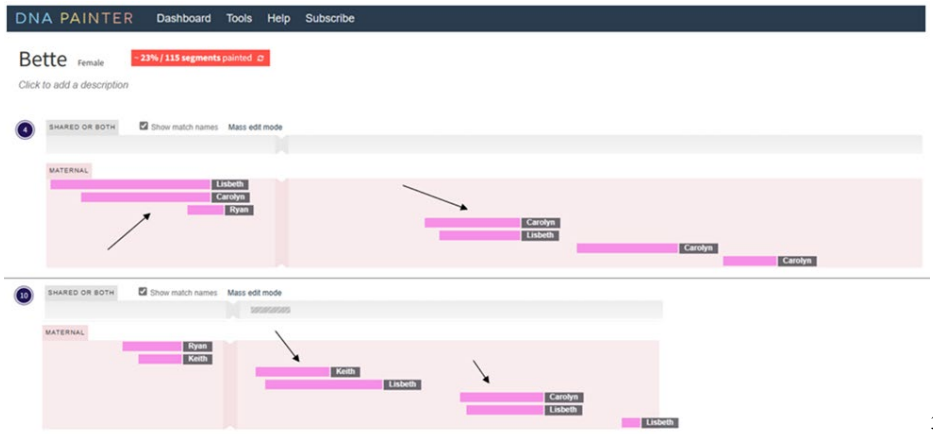
- Carolyn - 2nd Cousin Once Removed
- Bette, Dale and Keith - 3rd Cousin
- Kristin, Robin and Nolan - 3rd Cousin Once Removed
- Ryan - 3rd Cousin Twice Removed

***DNAPainter* and Triangulation**

- 4 30,652,525 – 38,509,827 8.6cM 3,840 SNPs Lisbeth with Bette & Ryan
- 4 7,639,550 – 35,558,460 36.9cM 14,976 SNPs Lisbeth with Bette and Carolyn
- 4 82,122,122 - 102,936,592 18.9cM 9,472 SNPs Lisbeth with Bette and Carolyn
- 10 48,331,883 – 62,320,330 17.3cM 7,296 SNPs Lisbeth with Bette and Keith
- 10 92,008,807 –108,686,065 14.5cM 8,576 SNPs Lisbeth with Bette and Carolyn

The bullet points above contain the location on the chromosome, the size and SNPs (Single nucleotide polymorphisms) within the shared segments of DNA for those listed on chromosomes #4 and #10.[29] "Triangulated segments are segments that all the selected DNA Matches (three in this case) share with each other. This capability is important for understanding DNA Matches' relationships because triangulated segments are more likely to be inherited from a common ancestor."[30]

DNAPainter chromosome painter will map the locations of the shared DNA on Bette's 23 chromosomes with each individual match. The shared DNA is separated by paternal or maternal inheritance. The images of the triangulated segments on Bette's chromosomes #4 and #10 are seen below. On chromosome #10 for example, Bette, Keith and Lisbeth share a 17.3 cM segment whereas Bette, Carolyn and Lisbeth share a 14.5 cM segment, confirming descent from a common ancestor(s).



[31]

[28] Ibid.
[29] "23andMe - Genetics 101: What Are SNPs?" *23&Me*, (www.23andme.com/gen101/snps/ : accessed 5 Apr 2023).
[30] "What Are Triangulated Segments in the Chromosome Browser — One To M23&Meany?" *MyHeritage* (https://faq.myheritage.com/en/article/what-are-triangulated-segments-in-the-chromosome-browser-%E2%80%94-one-to-many : accessed 21 May 2022).
[31] "DNA Painter | Chromosome Mapping," *DNAPainter,* maternal chromosome #4 (dnapainter.com/profile/210933 : accessed 7 Feb 2023).

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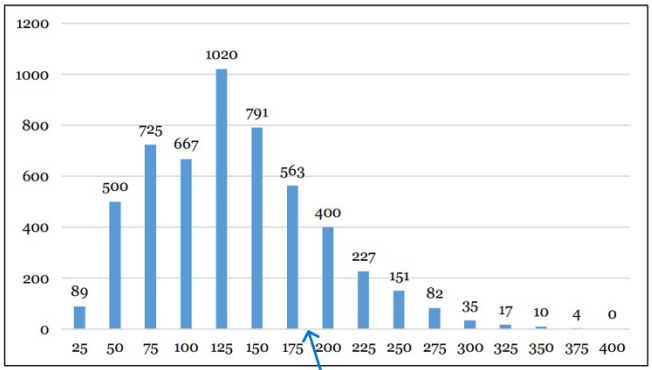
DNA Analysis – Shared DNA between each individual measured in centiMorgans (cM).

Match[32]	Bette	Kristin	Robin	Dale	Carolyn	Ryan	Keith	Nolan	Lisbeth
Bette		3,517. 1	3,528.3	290.4	294.5	48.9	91.4	35.1	171.9
Kristin	3,517. 1		2,792.7	241.3	173.1	23.8	55	0	38.2
Robin	3,528.3	2,792.7		85.3	221.9	17	14.9	0	53.2
Dale	290.4	241.3	85.3		495.1	45.7	192.4	67.5	72.2
Carolyn[33]	294.5	173.1	221.9	495.1		17.5	106.8	0	190.6
Ryan[34]	48.9	23.8	17	45.7	17.5		41.9	0	50.1
Keith[35]	91.4	55	14.9	192.4	106.8	41.9		155.9	145.7
Nolan[36]	35.1	0	0	67.5	0	0	155.9		110.0
Lisbeth	171.9	38.2	53.2	72.2	190.6	50.1	145.7	110.0	

Evaluating the Model – **Relationship histograms from *The Shared cM Project 4.0 tool v4***

The histograms for 2C1R, 3C, 3C1R and 3C2R from *The Shared cM Project 4.0 tool v4* are pictured below. The model's relationship predictions of 2C1R for Carolyn, 3C for Bette, Dale and Keith, 3C1R for Kristin/Robin/Nolan and 3C2R for Ryan are placed within the appropriate histograms and indicated with an arrow. For all eight matches to Lisbeth, their actual shared cMs were placed in the appropriate predicted relationship histograms. Your data points on the histogram should follow the *Empirical Rule* to support your hypothesis. The *Empirical Rule* states that a normal distribution of data follows a specific pattern.[37] The pattern is 68% of your data will fall within one standard deviation (SD) of the mean, while 95% and 99.7% within two and three standard deviations, respectively. For our hypothesis, six of the eight fall with one SD of the mean and two fall in the upper second SD. This means 75% fall in the first SD.

Relationship	#	Min	Average	Max	SD	Histogram
2C1R (Grouping #6)	5281	14	122	353	59	

[38]

Carolyn with Lisbeth

[32] "Chromosome Browser – Shared DNA Segments?" 2022, *Myheritage.com*, Bette Johanson (Stieglitz) and Dale Knutson share 13 DNA segments (https://www.myheritage.com/dna/match/D-7FCDE737-B56B-453B-B9A5-5BAD7A17FD07-D-2821EF4F-609D-452C-9C58-28912B2BF3C1/324729771?p : accessed 21 May 2022).
[33] Carolyn Johnson Vacek, email confirmation to Rob Stieglitz, authorizes use of her name and DNA data, 29 Dec 2022.
[34] Ryan Rath, email confirmation to Rob Stieglitz authorizes, use of his name and DNA data, 6 Nov 2022.
[35] Keith, email confirmation to Rob Stieglitz authorizes, use of his name and DNA data, 7 Dec 2022.
[36] Nolan, email confirmation to Rob Stieglitz authorizes, use of his name and DNA data, 9 Feb 2023.
[37] "Empirical Rule" *Basic-Mathematics.com* (www.basic-mathematics.com/empirical-rule.html : accessed 15 Mar 2023).
[38] Blaine Bettinger, "The Shared cM Project Version 4.0 (March 2020)," *The Genetic Genealogist*, Second Cousin-once removed, page 32 of 56 (https://thegeneticgenealogist.com/wp-content/uploads/2020/03/Shared-cM-Project-Version-4.pdf).

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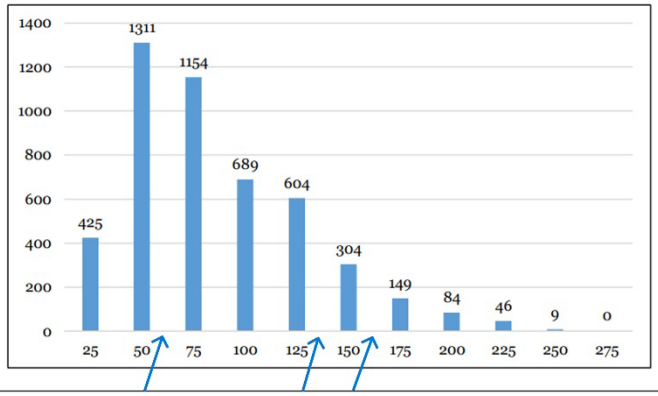
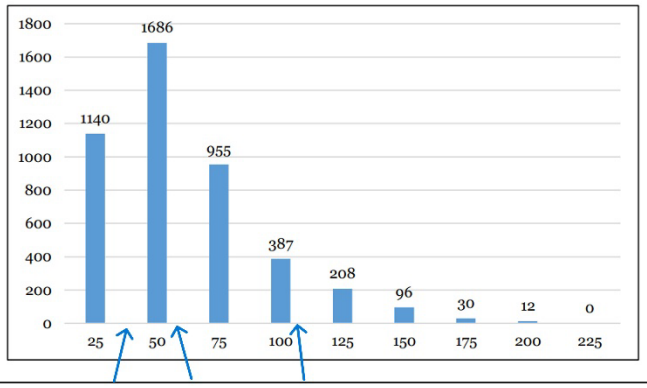
3C (Grouping #7)	4775	0	73	234	43	

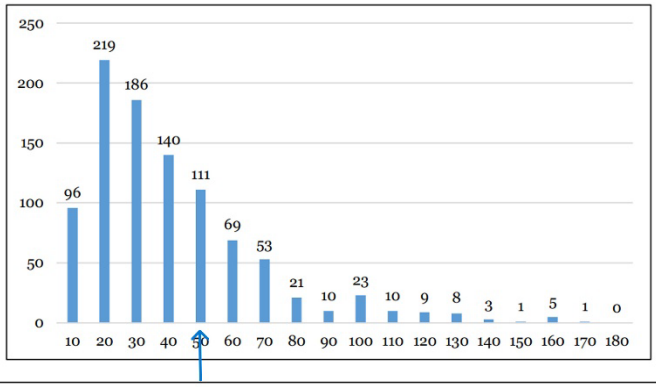
[39]

Bette, Dale, Keith with Lisbeth

3C1R (Grouping #8)	4514	0	48	192	32	

[40]

Kristin, Robin and Nolan with Lisbeth

3C2R (Grouping #9)	965	0	36	166	27	

[41]

Ryan with Lisbeth

[39] Bettinger, "The Shared cM Project Version 4.0 (March 2020)," *The Genetic Genealogist*, Third Cousin, grouping #7, page 34 of 56 (https://thegeneticgenealogist.com/wp-content/uploads/2020/03/Shared-cM-Project-Version-4.pdf : access 13 May 2022).

[40] Blaine Bettinger, "The Shared cM Project Version 4.0 (March 2020)," *The Genetic Genealogis*t, Third Cousin Once Removed, grouping #8, page 36 of 56 (https://thegeneticgenealogist.com/wp-content/uploads/2020/03/Shared-cM-Project-Version-4.pdf : access 13 May 2022).

[41] Bettinger, "The Shared cM Project Version 4.0 (March 2020)," *The Genetic Genealogist*, Third Cousin Twice Removed, grouping #10, p 38 of 56 (https://thegeneticgenealogist.com/wp-content/uploads/2020/03/Shared-cM-Project-Version-4.pdf).

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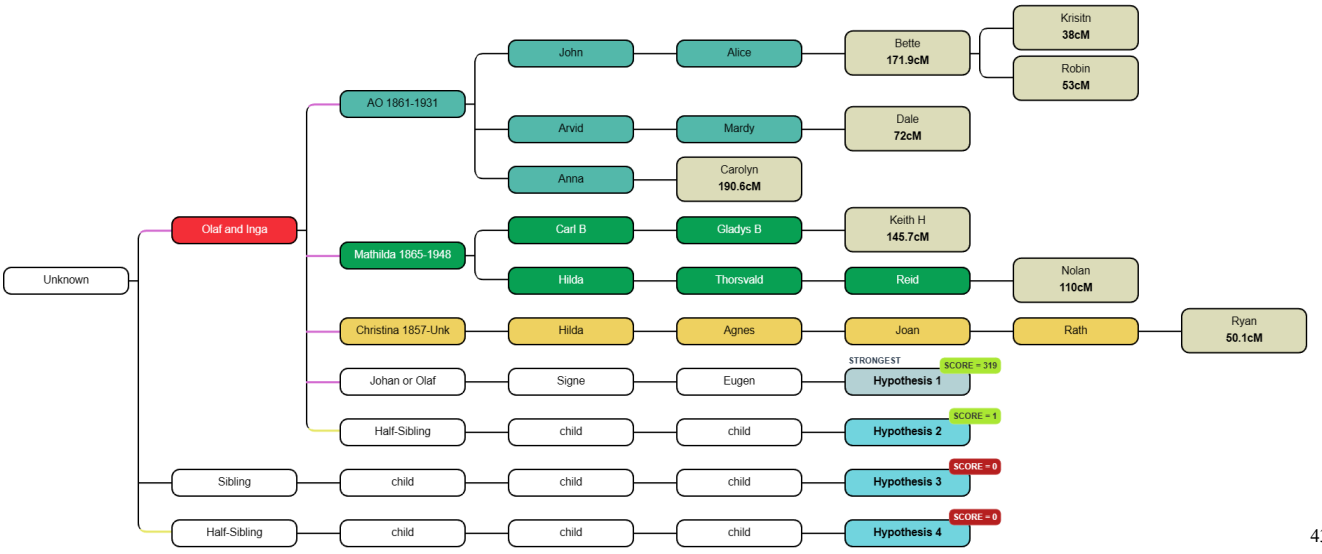
WATO (What Are The Odds)

"This tool **(WATO)** is designed to help you work out how one person, the "target", is related to a family group of people who have taken atDNA tests." The target is Lisbeth (hypothesis) where the WATO tool will calculate the most likely relationship with the family group consisting of Bette, Kristin, Robin, Dale, Keith, Carolyn, Nolan and Ryan by entering their shared DNA in cM (centiMorgans). Each relationship tree will contain three hypotheses, beginning with Adolf being the sibling of the target's ancestor. A score is then calculated for each relationship level. "The scores indicate how your hypotheses compare to one another. First, any hypothesis that is not possible given the data gets a score of zero. Then the possible hypotheses are ranked, starting with a score of 1. When more than one hypothesis is possible, they are ranked with higher scores being direct comparisons to the score = 1 hypothesis. For example, if you have three hypotheses with scores 100, 5, and 1, the highest is one hundred times more likely than the lowest and twenty times more likely than the second-place hypothesis."[42]



[43]

Match name & Shared cM		Hyp. 1	Hyp. 2	Hyp. 3	Hyp. 4
Carolyn	190.6	2C1R 48.76%	Half 2C1R 7.07%	3C1R 0.00%	Half 3C1R 0.00%
Bette	171.9	3C 11.84%	Half 3C 2.49%	4C 0.00%	Half 4C 0.00%
Keith H	145.7	3C 17.88%	Half 3C 5.70%	4C 1.10%	Half 4C 0.00%
Nolan	110	3C1R 16.68%	Half 3C1R 4.30%	4C1R 0.00%	Half 4C1R 0.00%
Dale	72	3C 28.41%	Half 3C 31.65%	4C 14.64%	Half 4C 4.09%
Ryan	50.1	3C2R 21.85%	Half 3C2R 24.46%	4C2R 24.46%	Half 4C2R 24.46%
Combined odds ratio		**319.07**	**1.00**	**0.00**	**0.00**

Match name & Shared cM		Hyp. 1	Hyp. 2	Hyp. 3	Hyp. 4
Carolyn	190.6	2C1R 48.76%	Half 2C1R 7.07%	3C1R 0.00%	Half 3C1R 0.00%
Keith H	145.7	3C 17.88%	Half 3C 5.70%	4C 1.10%	Half 4C 0.00%
Nolan	110	3C1R 16.68%	Half 3C1R 4.30%	4C1R 0.00%	Half 4C1R 0.00%
Dale	72	3C 28.41%	Half 3C 31.65%	4C 14.64%	Half 4C 4.09%
Robin	53	3C1R 29.75%	Half 3C1R 20.65%	4C1R 23.28%	Half 4C1R 23.28%
Ryan	50.1	3C2R 21.85%	Half 3C2R 24.46%	4C2R 24.46%	Half 4C2R 24.46%
Krisitn	38	3C1R 18.71%	Half 3C1R 18.41%	4C1R 49.58%	Half 4C1R 49.58%
Combined odds ratio		**98.45**	**1.00**	**0.00**	**0.00**

[42] "WATO - Frequently Asked Questions," *DnaPainter.com* (dnapainter.com/help/wato-faq : accessed 26 Dec. 2020).
[43] "What Are the Odds? – Original," *DNA Painter,* Lisbeth and Bette relationship hypothesis (https://dnapainter.com/tools/probability/146822 : accessed 3 Feb 2023).

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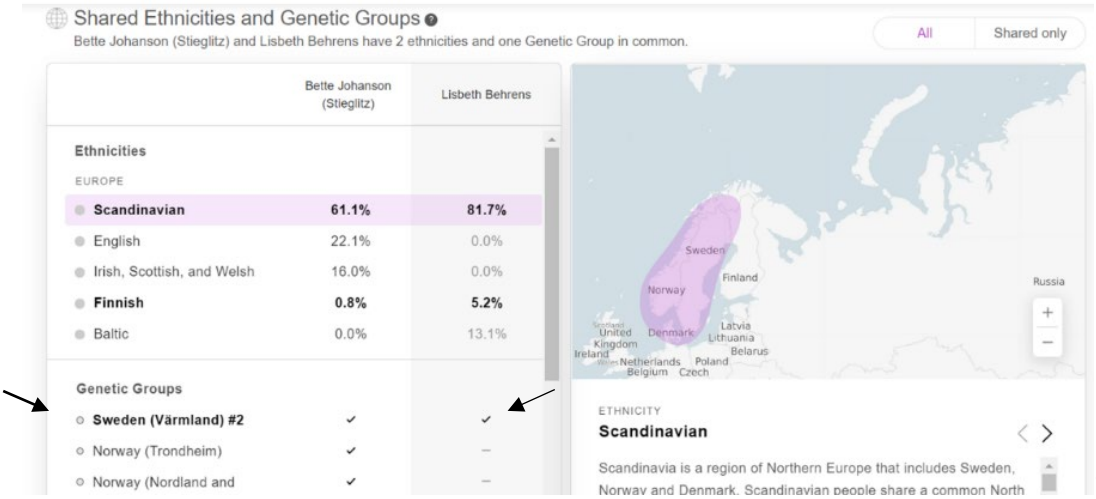
WATO predicts a ~319 to 1 probability that the relationship between Adolf and Lisbeth's great grandfather is a full sibling and therefore Lisbeth a third cousin to both Bette, Dale and Keith second cousin once removed to Carolyn, Kristin/Robin/Nolan third cousins once removed, and Ryan third cousin twice removed. This *WATO* tree does not consider the shared values of Bette's daughters, therefore a second *WATO* was prepared that removes Bette, so that daughters Kristin and Robin shared cM values are calculated. The prediction is the same with a probability ratio of ~99 to 1.

Ethnicities

"DNA cannot detect ethnicity, but there is sometimes an overlap with a person's genetic ancestry. For example, people who share the same heritage will often live in the same places and marry people from similar backgrounds."[44] With this understanding *MyHeritage* has created genetic groups. "Descendants of a group originated from the same location, at a specific point in time, have shared DNA segments that they inherited from the group's founding fathers and mothers."[45] The image below indicates both Bette and Lisbeth belong to the same Genetic Group – Sweden (Värmland) #2. Dale, Keith, Nolan and Carolyn also have ethnicity results that indicate their DNA is part of the Värmland Genetic Group.[46]



[47]

[44] Debbie Kennett, "How Can DNA Tests Determine Ethnicity?" *Who Do You Think You Are Magazine*, 2 Nov 2021 (https://www.whodoyouthinkyouaremagazine.com/tutorials/dna/what-do-dna-test-results-mean/ 1 May 2022).
[45] "What Are Genetic Groups?" *MyHeritage* (https://faq.myheritage.com/en/article/what-are-genetic-groups accessed May 1, 2022).
[46] Shared Ethnicities and Genetic Groups," *MyHeritage.com*, Bette Johanson, Dale Knutson, and Carolyn Johnson, Värmland genetic group in common (https://www.myheritage.com/dna/match/D-7FCDE737-B56B-453B-B9A5-5BAD7A17FD07-D-2821EF4F-609D-452C-9C58-28912B2BF3C1/324729771?p : accessed 21 May 2022).
[47] "Shared Ethnicities and Genetic Groups," *MyHeritage.com*, Bette Johanson and Lisbeth Behrens, two ethnicities and one genetic group in common (https://www.myheritage.com/dna/match/D-7FCDE737-B56B-453B-B9A5-5BAD7A17FD07-D-AFD0704D-92A4-445E-8325-8B9898BC5451/324729771?p=1&ps=10&sort=total_shared_segments_length_in_cm&siteId=324729771&individualId=7500008 : accessed 13 May 2022).

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Conclusion

One cannot conclusively state with 100% certainty the identity of Lisbeth's great grandfather although the combination of historical records, family trees and DNA provide solid indirect evidence that the connection was in Värmland. According to *AncestryDNA* the accuracy of genetic relationships is extremely high for seeing if two people are related at the 3rd or 4th cousin and closer level.[48] The sizes of the shared DNA establish the most likely relationship level, the shared matching of the descendants of the three siblings (Adolph, Christina and Mathilda) confirm the genetic connection to Olaf Olsson and Inga Marie Andersdotter**.** There were two sons that could be the biological great-grandfather of Lisbeth, Olaf (1859-1910) or Johan (1869-1895). Both were unmarried and living in the same location as Emma in 1894 at the time of conception. Emanuel Johansson was also in the same area at the time. It is then plausible Emma had multiple partners which included one of the Olsson brothers and may have believed Emanuel was the father. The genetic data is very convincing and the family connection too close not to conclude Johan or Olaf were most likely the father of Signe Klara Maria Johansson and not Emanuel Johansson.

One more issue must be addressed and that is endogamy. According to DNA Educator, Diahan Southard, "Endogamy is the practice of marrying within the same group of people for several generations. Genetically, what this means is that instead of only sharing DNA with the relatively few people in the world with whom you share a recent common ancestor, you share DNA with hundreds of people who are a wider part of your population. This means that those from endogamous communities will often share more DNA with each other than we would expect given their relationship."[49] The shared DNA found within the research group is on the higher side for each relationship level, indicating that endogamy is likely.

Genealogy, including genetic genealogy, is an unfinished project that is still being added to or developed. Just as all scientific research, it is "a work in progress."[50] Further research would than be directed in finding information on Emanuel Johansson, specifically confirmed descendants, if any, for DNA comparison.

Dedication

This narrative is dedicated to the memory to Ryan Rath, a young man I never met. Ryan, 45 years old, passed away unexpectedly in December of 2022. The use of genetic genealogy in solving ancestral mysteries requires a significant amount of luck. The most important would-be having individuals related to you on the specific ancestral lines you are researching test with any of the "big four" DNA testing sites. If fortunate enough to find a significant match (large enough shared atDNA that finding a common ancestor is possible) contacting them and securing their permission to use their raw data is a major challenge. This was not the case with Ryan. From the moment we connected regarding a common ancestral history, his excitement and epistemic curiosity to establish Lisbeth's relationship inspired me never give up reaching out.

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[48] "AncestryDNA® Test Accuracy | AncestryDNA® Learning Hub," *Ancestry.com* (https://www.ancestry.com/c/dna-learning-hub/ancestrydna-test-accuracy : accessed 26 May 2022).
[49] https://www.yourdnaguide.com/ydgblog/endogamy-dna-test-jewish
[50] "Science: A Work in Progress," *Smithsonian Science Education Center* (https://ssec.si.edu/science-work-progress : , accessed 8 Jan 2024).

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Journal of Genetic Genealogy

GENETIC GENEALOGY STUDY: THE GRIGSBY FAMILY- UNCOVERING PATRILINEAL DESCENDANTS THROUGH Y-DNA ANALYSIS

By Donald L. Grigsby, PhD; Michael Whitehead Grigsby, MBA; Corresponding author: Marcia Johnson, MBA, MPA, RHIA

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Short title: Grigsby Patrilineal Y-SNP Analysis

Key words: Grigsby, Y-SNP, Y-DNA, Patrilineal

Abstract

The Grigsby Family, as verified in church records, wills and other genealogical documents, has been an established family in Virginia since the 1600s. While traditional genealogy methods are a cornerstone of proving lineage in Grigsby family pedigrees, establishing a genetic connection to the original immigrant through DNA testing has been undertaken to substantiate lineage as conclusively as possible with significant supporting evidence.

The Grigsby Y-DNA Project started in 2008 with subjects who underwent Y-67 DNA testing at FTDNA. providing 67 site STR information, followed in later years by additional tests, including Y-111 STR, the Big Y, Big Y-500 and Big Y-700 tests, culminating in both STR and SNP data for subjects, some of whom could give primary source documentation for families dating back to the 1600s.

Initial testing indicated a possible relation among participants, leading to the later STR and SNP testing. The study focused on SNP FGC48457. The advent of the Big Y, Big Y-500 and Big Y-700 tests, as they became available from Family Tree DNA after 2013, allowed for expanded analysis of the hypothesized relationships among subjects. We found that the SNP data provided from testing to be both valid and reliable, based upon additional testing and analysis.

Consequently, Grigsby lineages in America were extensively confirmed through Y-DNA testing and SNP analysis with the ability to identify whether or not a subject was descended from a single identifiable individual who was born in 1623 (known as "Immigrant John Grigsby, who by his will acknowledged his five sons by name) four of whom are responsible for having produced the patrilineal test pool subjects that have formed the basis of this study. In three of the four lines, downstream branches have been identified by downstream SNPs. Grigsby lineages not descending from "Immigrant" John born in 1623, resulting from immigration from England well after the year 1800 were also identified

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by SNP analysis. All Grigsby surname Y-DNA test subjects, to date, whose lineage is traced to the period 1660-1800 are patrilineal descendants of the "Immigrant" John Grigsby (1623-1730) and exhibit the SNP FGC48457along with other SNPs such as JFS0012, JFS0014, JFS0015, JFS0016, found only in the four patrilineal lines of descent from "Immigrant" John Grigsby. In some lines, additional branching was also determined by a downstream SNP. Grigsby lineages not descending from the "Immigrant" John Grigsby born in 1623 were also identifiable based upon the SNP test results.

Introduction

History of the Grigsby Surname: The Grigsby surname has English origins, possibly derived from the name Grig, a pet form of Gregory. The largest concentration of the surname is found in Marden, Kent. The name has spread from its origins in the British Isles to the United States, Canada, Australia, and Germany. (Grigsby, 2023) (geneanet.org, 2023). Grigsbys have also moved to various counties in the United Kingdom. The genetic connection to Kent is still unconfirmed.

The Grigsby family history spans 400 years based on DNA research and 40 years of traditional genealogical research in the United States and the United Kingdom since the founding of the National Grigsby Family Society in 1981. The National Grigsby Family Society has done extensive traditional genealogy research. The Appendix to this article charts the first three generations of American Grigsbys as documented by wills, church records and other verified paper documents and researched and recorded by C.T. Denys in her seminal work. (Denys, 1995). This article aims to explore the ancestral lineage of "Immigrant" John Grigsby (1623-1730) and his descendants, drawing on

DNA research and extensive genealogical records of more than 40,000 Grigsbys maintained in an Ancestral Quest database and connect tested descendants not only through traditional genealogical methods but even more reliably through testing to the "Immigrant" and to family branches of that Immigrant.

While not yet genetically confirmed, genealogical research supports that in its English origins, "Leeds Castle" John Grigsby (1455-1550), an attorney, served on the Privy Council to Queens Catherine of Aragon and Anne Boleyn in the court of King Henry VIII. "Leeds Castle" John Grigsby married Margaret Sharpe, a wealthy and progressive heiress with a fortune and thousands of acres. (Denys, 1995). Their great grandson, Thomas Grigsby, married Elizabeth Banks, the aunt of Sir John Banks, one of the wealthiest men in England. (Coleman, 1975). Based on documents of christening in Maidstone in 1624, his cousin, John Grigsby, Elizabeth's oldest son, is believed to be the same as the "Immigrant" John Grigsby noted in Colonial Virginia in the parish of Stafford County to have been born 1623 and died 1730, age 107 according to the church records. (St. Paul's Parish Register Stafford-King Charles Counties, 2009).

According to the Powhatan Patawomeck tribal tradition, he may have married a sister to Pocahontas. Grigsbys are listed and accepted in the Patawomeck Gedmatch Project. (A mitochondrial DNA project, separate from the Y-DNA research examined in this article, is underway with respect to determining if living descendants of "Immigrant" John Grigsby carry evidence of Native American genes).

The union of "Immigrant" John Grigsby and his wife produced five sons, including Revolutionary War heroes and others who contributed to westward

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migration. Several of these early Grigsbys were childhood friends of Abraham Lincoln and played a significant role in his boyhood and young adulthood, as detailed in biographies by Doris Kearns Goodwin, William Bartelt and Joshua Claybourn. (Goodwin, 2018) (Bartelt, 2019). Aaron Grigsby married Lincoln's beloved sister Sarah.

Grigsbys fought on both sides in the Civil War and served in conflict after conflict throughout the settlement of America from coast to coast and in the many wars the U.S. was involved in throughout its history. The Grigsby family has been the subject of a PBS *Finding Your Roots* segment. (Rudolph, 2016). Grigsby family history includes its own share of the good and bad in American history. The Grigsby story is truly the story of America.

Methods and Data

Understanding Ancestral Descent

Prior to the completion of the Human Genome Project in 2003, proving ancestral descent from generations past was challenging. Today, genetic analysis provides an indisputable record of ancestry, revealing how DNA is passed from generation to generation. In males, the Y chromosome carries valuable information as it remains nearly identical through generations of patrilineal descendants.

Y-DNA Analysis in the Grigsby Family

How Do We Really Know We Descend from an Ancestor Who Lived Many Years Ago?

The answer to that question is not as simple as one might initially believe. Before April 2003, the date of the completion of the worldwide Human Genome Project, there was in reality no way to establish that we were descendants of an ancestor many generations ago. All that we had to rely upon prior to 2003 were family oral traditions and paper records, some of which proved to be incorrect.

Today, however, we can learn the story of our ancestry from a record that is indisputable, and we now understand how to read its language code, and we understand the process by which it is passed from generation to generation. Every male has both sex chromosomes X and Y along with 22 pair of autosomal chromosomes making 23 pairs total. Females have two X sex chromosomes as one pair along with 22 pair of autosomal chromosomes making 23 pairs total. During the production process of ova for the female and sperm for the male, the paired chromosomes separate with one half of each pair being included in each ovum and each sperm cell. When sperm and ovum unite to form a zygote cell, the zygote cell has once again 23 pair of chromosomes. Each ovum has one or the other of the female's X chromosome pair, while the sperm with which it unites may contain either an X chromosome or a Y chromosome.

When two X chromosomes unite, the child will be a female. When an X and a Y chromosome unite to make a pair, the child will be a male. The DNA instructions on the Y chromosome will produce itself identically to be passed on to each new generation of males. Each Y chromosome is made up of millions of nucleotides.

There are four kinds of nucleotides (adenine, cytosine, guanine, and thymine) indicative of the acid base of the

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nucleotide. Think of them as a four-letter alphabet upon which the instructions are encoded to create an individual and maintain its function throughout its life. Just as on a product assembly line, occasionally a defective item is produced. Although the body has an extremely effective system which eliminates the rarely created defective products, on very, very rare occasion, a defect gets by.

If that mutated nucleotide is on the Y chromosome and results in the creation of a son, that son will have a Y chromosome like his father's and brother's Y chromosome's millions of nucleotides – with the EXCEPTION of ONE nucleotide on ONE gene which we label a Single Nucleotide Polymorphism (SNP). That SNP for that individual will be replicated by that individual (it is all he has to replicate) and passed on to each of his sons, and they to their sons, generation after generation until another SNP may occur again, changing one nucleotide of the millions of nucleotides passed to ONE son who then passes it to ALL of his sons.

In the case of the Grigsby family in America, the original "Immigrant" John Grigsby of Stafford County (later Prince George County, Virginia), passed his identical Y chromosome on to each of his five sons, and they to their sons, and on and on, generation after generation in an unbroken chain. "Immigrant" John had five sons and one daughter.

Results and Discussion

At some stage, either in 1623 or in some generation before, a SNP occurred and all subsequent males in the Grigsby family descended from that family carry the FGC48457 marker.

This study involved testing at the FTDNA genetics lab in Houston, Texas, and at the YSEQ genetics lab in Berlin, Germany. The participants primarily consisted of 77 individuals, 66 from the United States, and 11 from the United Kingdom. It was found that the UK participants belonged to different Y-DNA haplogroups, indicating no shared common paternal ancestor among haplogroups within historic time. No UK haplogroup was related to the USA FGC48457 haplogroup. Fifty subjects were tested at the YSEQ genetics lab in Berlin, Germany. Some subjects were tested at both labs to serve as a control in testing validity and reliability. None of the individuals from the UK descended from the same patrilineal family as did John Grigsby (1623-1730). In fact, the 11 Grigsby surname individuals from the UK proved to be from five different Y-DNA haplogroups, meaning that those five groups have not shared a common paternal ancestor for several thousands of years. No UK or American Grigsby has traced their ancestry to "Leeds Castle" John Grigsby or to a date prior to 1600. Although this result was unexpected, it does not preclude relatedness on an "autosomal DNA" basis.

Of the five sons of "Immigrant" John Grigsby, four are known to have produced offspring. Descendants of all four sons have been Y-DNA tested. Descendants of those four of the sons exhibit FGC48457. The only Grigsbys in America prior to 1800 were that haplogroup. There were no brothers, uncles or cousins documented. The one daughter has traceable mitochondrial DNA through multiple generations that include living descendants but that is a subject for another article. Discussion and analysis are limited herein to the male descendants of "Immigrant" John Grigsby (1623-1730), said in recorded documents at the St. Paul's Parish Church in Stafford County, Virginia, to have died at the age of 107. (Saint Paul's Parish Register, 2009)

Our study identified a group of individuals who were believed to belong to the haplogroup R-U198. Forty-eight (48) of those individuals were determined to carry

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the SNP FGC48457, a SNP not found in any individual who has been tested to date with the exception of the forty-eight (48) patrilineal descendants of one John Grigsby (1623-1730). A Y chromosome nucleotide mutation (SNP) in a birth of a son occurs roughly, on average, about once every 150 years in each of the four Grigsby lines from John Grigsby (1623-1730). In that span of time, variance exists between surname families and among surname family lines.

"Immigrant" John Grigsby (1623-1730) had five sons who received his Y chromosome and a daughter who received his X chromosome. We can look at the living male descendants of John Grigsby and the Y-DNA he has passed down that is shared by ALL of his patrilineal descendants (this excludes the SNPs which have occurred later and are exhibited by some but not all of his patrilineal descendants) and we discover what "Immigrant" John" Grigsby's Y-DNA exhibited that he inherited from his father.

The Y-DNA that "Immigrant" John passed to sons John, Charles, and William was identical to his own (exact copies with no mutations/changes). The Y chromosome that he passed to James, however, was different from that inherited by the brothers of James. On one of the genes, one nucleic acid base on one nucleotide had switched from thymine inherited by his brothers, to cytosine (T to C), which we discovered and named the SNP JFS0016. All of the sons and later patrilineal descendants of the "Immigrant" John Grigsby son James Grigsby will exhibit the SNP JFS0016 nucleotide, which has cytosine as an acid base, while all other "Immigrant" John patrilineal descendants will exhibit thymine as an acid base at that same location. This one SNP "marker," therefore, allows us to easily identify any patrilineal descendant of the James Grigsby (I) line.

In the line of "Immigrant" John, son Charles Grigsby passed a mutated Y chromosome to his son "Soldier" John Grigsby (1620-1694). While the other sons received an identical Y chromosome that Charles himself exhibited, "Soldier John" Grigsby received a chromosome with a mutation/change in one of the millions of nucleotides. On the chromosome inherited by "Soldier John," the SNP JFS0014, which had one nucleotide that had switched from thymine to cytosine. While his father, brothers, and all of his Grigsby male cousins exhibit thymine at the SNP JFS0014 position, "Soldier John" and all of his patrilineal descendants exhibit the acid base cytosine at that location on the Y chromosome, marking their SNP JFS0014 branch of the FGC48457 haplogroup.

In the John Grigsby (II) line, the third generation Benjamin Grigsby exhibited a mutation in one novel nucleotide at the SNP location occupied by JFS0012 when the acid base adenine had switched to guanine. So, while his father and brothers and all of his Grigsby male cousins exhibit the nucleotide adenine at the location of the SNP that we have named JFS0012, all of those who descend from the John Grigsby (II) son Benjamin Grigsby exhibit the nucleotide guanine at that SNP location, identified as SNP JFS0012. See the Table at the end of this article which shows the SNP markers exhibited by John Grigsby and subsequent mutations which permit identification from which son a tested male is descended.

Other SNP markers that we have discovered and analyzed designate branching at various generational points in the Grigsby family tree. For the American family who are patrilineal descendants of "Immigrant" John Grigsby (1623-1730), we have discovered that in addition to the Grigsby surname, some of his patrilineal descendants are currently named Chambless [from the SNP{4} JFS0012 {5} branch of the John Grigsby (II) line of patrilineal descent]. There are also three separate White surname families [one from the line of the "Immigrant" John Grigsby, son James Grigsby line of JFS0016{5}]; a second White surname group from the JFS0015 Grigsby branch; and a third White surname group from the SNP Y659 who are genetically patrilineal descendants of "Immigrant" John.

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Furthermore, there is a Lay surname family group, descended from the JFS0015 Grigsby branch.

We have recently tested four descendants of William Barksdale Grigsby, born ca.1798 in Pittsylvania County, Virginia, to Moses Grigsby and wife Abigail Fritter. All four have proven not to be patrilineal descendants of the "Immigrant" John Grigsby. This line has existed in controversy for 25 years or so. The NGFS prior to that time believed and published that Moses Grigsby [son of John Grigsby (II) and his wife Jane Redman Grigsby], who married Catherine Branson (with whom he had children Henry Grigsby and Elizabeth Grigsby), also married a second time to Mary Matheny (with whom he had a son Moses Grigsby (II), among others). Research proved this to be in error – that Catherine Branson and Mary Matheny were married to two different men named Moses Grigsby. The Moses Grigsby who married Catherine Branson died, and his will was probated ca. 1780. He was married only to Catherine Branson. The Moses Grigsby (who married Mary Matheny) and his son Moses Grigsby (II) (who married Abigail Fritter) were both still alive and on the Pittsylvania County, Virginia, tax list ca. 1800 and later – 20 years after the death of the Moses Grigsby who married Catherine Branson.

If John Grigsby (II) was the father of the Moses who married Catherine Branson (and genetic testing of his descendants prove that he was), who was the father of the Moses Grigsby who married Mary Matheny and produced the line of Moses Grigsby (II) and son William Barksdale Grigsby? Our testing proves that four Barksdale descendants from two different sons are not patrilineal descendants of John Grigsby (1623-1730), which does not prove, but casts serious doubt, on whether William Barksdale Grigsby is a patrilineal descendant of "Immigrant" John Grigsby. The Barksdale descendants have not been shown, after testing three descendants of two sons, to be descendants of FGC48457. Information is insufficient to conclude a genetic connection at this time.

Conclusion and Next Steps

Through Y-DNA analysis, the Grigsby Y-DNA Project has successfully identified patrilineal descendants of the "Immigrant" John Grigsby. To date, all non-Grigsby surname individuals who carry the novel SNP FGC48457 also carry one additional Grigsby novel SNP, either JFS0012, JFS0014, JFS0015, or Y659. Therefore, we conclude that the non-Grigsby surname individuals who carry the novel SNP FGC48457 inherit that from "Immigrant" John Grigsby because they also inherit a downstream SNP from "Immigrant" John Grigsby, either JFS0012, JFS0014, JFS0015, or Y659. The study's findings shed light on the genetic history of the Grigsby family and provide valuable insights into ancestral connections.

Further research and analysis may uncover additional details and expand the understanding of the Grigsby family's genetic genealogy. Research is ongoing to discover possible links between descendants of "Immigrant" John Grigsby FGC48457 to the United Kingdom family of "Maidstone" John Grigsby (Baptized 1624) and his ancestor, "Leeds Castle" John Grigsby (1495-1550). Other areas of important research include Native American heritage from early Colonial connections to the Patawomeck/Powhatan tribe. Chief Wahanganoche often married daughters, as a diplomatic gesture, to prominent Colonial figures which created a joint Native American/Anglo ancestry. Native American oral tradition has been that "Immigrant" John Grigsby, whose land bordered that of the Chief, married one of the Chief's daughters.

In addition, testing has included African-American male Grigsbys to determine if they are descendants of the FCC48457 haplogroup. In the Colonial Virginia Overwharton Parish Tobacco Tenders List of 1723-24, the Grigsby family is listed as owning five plantations. (Boogher, 1899). Descendants of that Grigsby group were frequent owners of slaves. Initial testing has indicated that individuals of African descent with the

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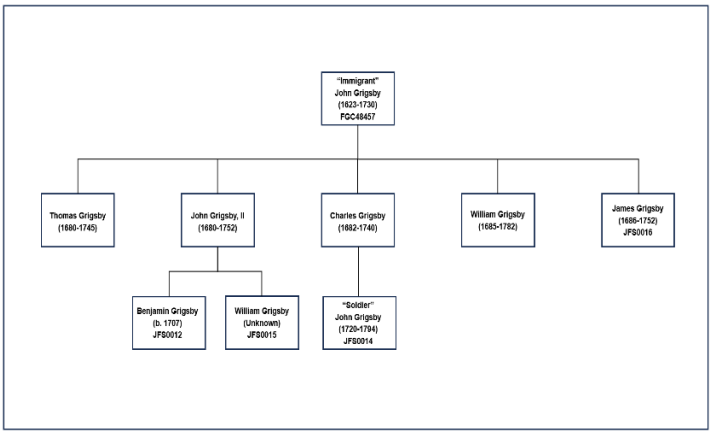
Grigsby surname have descended genetically from FGC48457 while other African-American individuals with the Grigsby surname have not. The National Grigsby Preservation Foundation would like to extend research interests to include historical information for these individuals regarding their known ancestral history and their possible ancestral enslavement, through wills and other records, regardless of whether or not a genetic relationship exists.

Table



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Conflicts of Interest

The authors declare no conflicts of interest and no commercial interests in the subjects covered by this study. No author has a financial or personal interest in Family Tree DNA or any other commercial DNA service used in testing.

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Appendix: Genealogy Chart of Three Generations Descendants of Immigrant John Grigsby

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1. John ' Immigrant John' GRIGSBY I-1 (b.1623 d.1730)
sp: UNKNOWN-2 (m.1678)
|-2. Mary Ann GRIGSBY-7 (b.1675 d.1747)
| sp: Benjamin NEWTON-45 (b.1669 m.1695 d.1710)
| |-3. Benjamin NEWTON-48 (b.1694 d.1722)
| | sp: Elizabeth GREGG-139 (b.1686 d.1732)
| |-3. Mary Elizabeth NEWTON-49 (b.1698 d.1747)
| | sp: John ROGERS-440 (b.1703 m.1720 d.1760)
| |-3. Margaret NEWTON-46 (b.1702)
| | sp: William HEABERD-4199 (m.1720 d.1721)
| | sp: John TRAVIS-134 (m.1722 d.1724)
| |-3. Letitia NEWTON-47 (b.1704 d.1725)
| | sp: Phillip CRAFFORD-138
| sp: John MEESE-518 (r.1681 m.1710 d.1733)
|-2. Thomas GRIGSBY-8 (b.1680 d.1745)
| sp: Rose NEWTON-50 (b.1695 m.1715 d.1785)
|-2. John GRIGSBY II-4 (b.1680 d.1752)
| sp: UNKNOWN-37332
| |-3. Benjamin GRIGSBY I-4130 (b.1707)
| | sp: Ann (widow Foley) LEITCH-4131 (m.1727)
| |-3. Mary GRIGSBY-30201
| | sp: John FEWELL-30202 (m.1726)
| |-3. William GRIGSBY-30200
| sp: Jane REDMAN-18 (b.1680 m.1705 d.1756)
| |-3. John GRIGSBY III-20 (b.1705 d.1771)
| | sp: Anne LAMPTON-131 (b.1708 m.1730 d.1771)
| |-3. Thomas GRIGSBY-19 (b.1707 d.1756)
| | sp: Anne DISHMAN-130 (m.1729)
| |-3. Aaron GRIGSBY-21 (b.1711 d.1764)
| | sp: Margaret PROCTOR-4384 (b.1690 m.1757 d.1764)
| | sp: Verlinda WHITE-133 (m.1762)
| +-3. Moses GRIGSBY I-22 (b.1715 d.1780)
| sp: Katherine BRANSON-132 (b.1724 m.1742 d.1751)
|-2. Charles W. GRIGSBY I-6 (b.1682 d.1740)
| sp: Sarah WILKERSON-33 (b.1695 m.1710 d.1756)
| |-3. Margaret GRIGSBY-34 (b.1712)
| | sp: John SMITH-164 (m.1728)
| |-3. Rose GRIGSBY-35 (b.1714)
| | sp: Benjamin SPICER-140 (m.1734)
| |-3. James GRIGSBY-36 (b.1717)
| | sp: Sarah SUDDUTH-22539 (m.1742)

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| |-3. CAPT John ' Soldier John' GRIGSBY-37 (b.1720 d.1794)
| | sp: Rosanna ETCHISON-142 (b.1730 m.1746 d.1761)
| | sp: Elizabeth Hawkins PORTER-148 (b.1734 m.1770 d.1807)
| |-3. Barbara GRIGSBY-38 (b.1722)
| | sp: RUNNELS-159 (m.1740)
| |-3. Charles GRIGSBY II-39 (b.1725 d.1827)
| | sp: Elizabeth LYTLE-158 (b.1720 m.1773 d.1777)
| | sp: Mary BRADFORD-972 (m.1778)
| | sp: Mary SEARS-4655 (b.1762 m.1816 d.1861)
| |-3. Rachel GRIGSBY-42 (b.1728)
| | sp: Isaac ROSE-161 (m.1751)
| |-3. Priscilla GRIGSBY-41 (b.1728)
| | sp: Abraham FLETCHER-160 (m.1746)
| |-3. Wilkerson GRIGSBY-40 (b.1730 d.1782)
| | sp: Sarah -5210 (b.1740 m.1759 d.1788)
| |-3. Mott Calville “Mott” GRIGSBY-4132 (b.1735 d.1795)
| | sp: Grace “Gracy” SANFORD-458 (b.1757 m.1778)
| |-3. Elisha GRIGSBY-43 (b.1738 d.1790)
| +-3. Reuben GRIGSBY-44 (b.1740 d.1769)
|-2. William GRIGSBY I-5 (b.1685 d.1782)
| sp: Ursley MANN-23 (b.1690 m.1705)
| |-3. Ann GRIGSBY-24 (b.1710 d.1794)
| | sp: William ROWLEY-169 (b.1711 m.1773 d.1774)
| |-3. William GRIGSBY II-28 (b.1713 d.1804)
| | sp: Sarah OWENS-656 (b.1710 m.1763)
| |-3. James GRIGSBY-25 (b.1714)
| |-3. Richard GRIGSBY-26 (b.1717 d.1787)
| | sp: Amy RUSH-165 (m.1742)
| |-3. John GRIGSBY II-27 (b.1719 d.1788)
| |-3. Margaret GRIGSBY-30 (b.1722 d.1793)
| | sp: George FOSTER-166 (b.1723 m.1746 d.1778)
| |-3. Alice GRIGSBY-29 (b.1726 d.1815)
| | sp: Benjamin RUSH-167 (b.1717 m.1744 d.1801)
| +-3. Lettice GRIGSBY-31 (b.1730)
| sp: Joshua OWENS-168 (b.1725 m.1747 d.1777)
+-2. James GRIGSBY I-3 (b.1686 d.1752)
sp: Susanna REDMAN-9 (b.1690 m.1710 d.1783)
|-3. James GRIGSBY II-10 (b.1712 d.1797)
| sp: Frances -51 (m.1755)
|-3. Lt. Enoch GRIGSBY-11 (b.1714 d.1794)
| sp: Susan Mary BUTLER-52 (b.1743 m.1763 d.1795)

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|-3. Nathaniel GRIGSBY Sr.-12 (b.1716 d.1801)
| sp: Elizabeth BUTLER-53 (b.1731 m.1747 d.1771)
| sp: Susannah Linton SMITH-5641 (b.1729 m.1765 d.1822)
|-3. Elizabeth GRIGSBY-13 (b.1718 d.1783)
| sp: Edward HUGHES-432 (b.1700 m.1734)
|-3. Redman GRIGSBY-14 (b.1721 d.1809)
| sp: Susannah JARVIS-65 (m.1746 d.1755)
| sp: Elizabeth THOMAS-103 (b.1737 m.1760 d.1778)
|-3. Samuel GRIGSBY I-15 (b.1724 d.1781)
| sp: Nancy Anne GRIGSBY-163 (b.1742 m.1762 d.1825)
+-3. Susannah GRIGSBY-16 (b.1727 d.1783)
sp: Charles STUART-417 (m.1752)

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