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# HENRY MILLER, JR. & DAVID ALEXANDER MILLER: TMRCA AND RELATIONSHIP ANALYSIS

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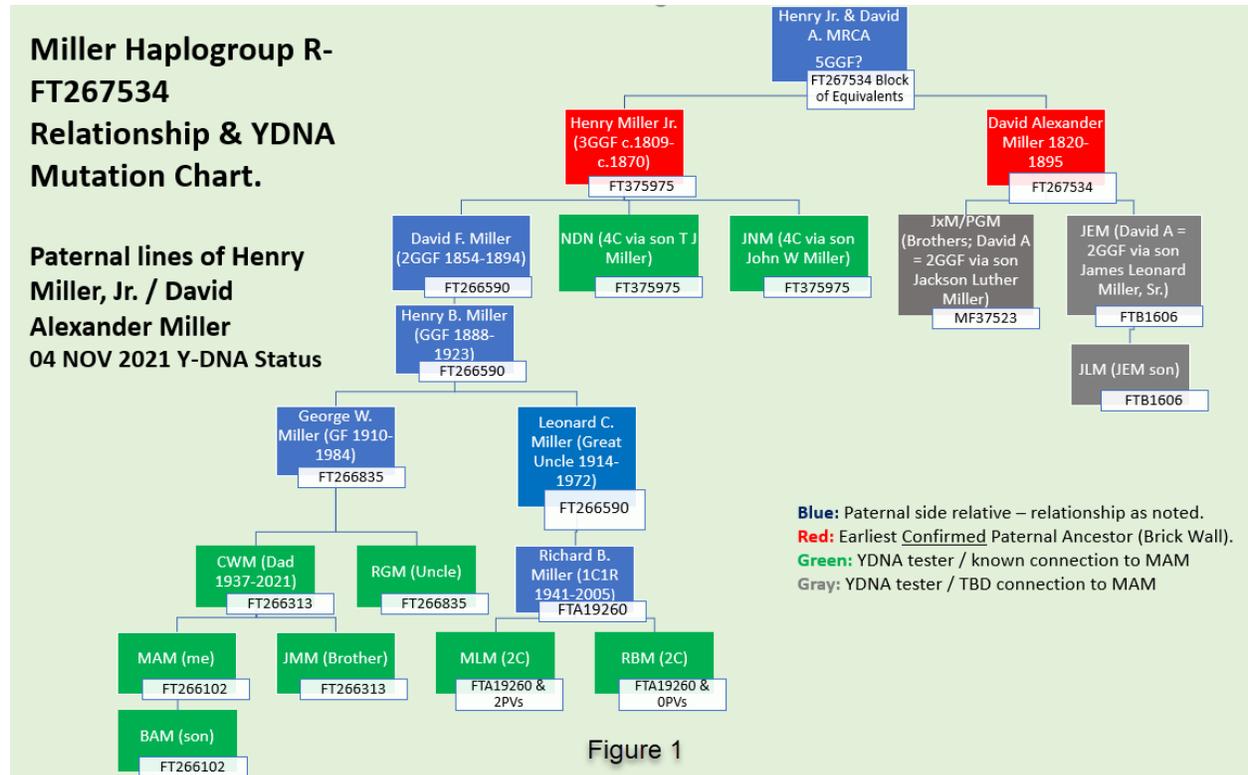
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## Henry Miller, Jr. & David Alexander Miller: TMRCA and Relationship Analysis

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18 DEC 2021

**Purpose.** Determine how the current group of YDNA test results and associated autosomal DNA data (atDNA data) support and guide further genealogical research to determine the relationship between Henry Miller, Jr. (“Henry”) and David Alexander Miller (“David”), both born in the first quarter of the 19<sup>th</sup> century.



**Background.** A team of amateur genealogists, led by Mark Miller (Colorado) and Brad Miller (Georgia), and supported by Joseph Miller (North Carolina), are utilizing traditional genealogy (atDNA testing at Ancestry, and YDNA testing at Family Tree DNA (FTDNA) to establish the patrilineal lines of descent that connect Henry and David Miller. The documented paper trail ends with each of these men, and we have been unable to establish their relationship. Henry was born in Ashe County, North Carolina in the first decade of the 19th century. David was born in neighboring Wilkes County in 1820. YDNA testing proves that Henry and David are related along their patrilineal Miller lines (Figures 1 and 4).

Because we have seemingly exhausted online genealogy resources, the team engaged local genealogist Jill Privott of Boone, NC. Ms. Privott is currently researching David’s line, with a goal of identifying his connection to Henry. Based on her report, we will recruit YDNA testers to validate, or invalidate Jill’s traditional genealogical research results. There are several unrelated Miller lines who migrated to this area of northwest North Carolina. The Miller surname is prevalent in the area. Identifying our Miller line

from the several local Miller lines has become a process of elimination. Our strategy is to identify the most probable connection between David and Henry through traditional research, followed by YDNA testing to validate or invalidate the research. YDNA testing is effective for verifying, and for excluding, connections between patrilineal lines. In the case of a common surname like Miller, including and excluding patrilineal lines are both important elements of the investigatory process.

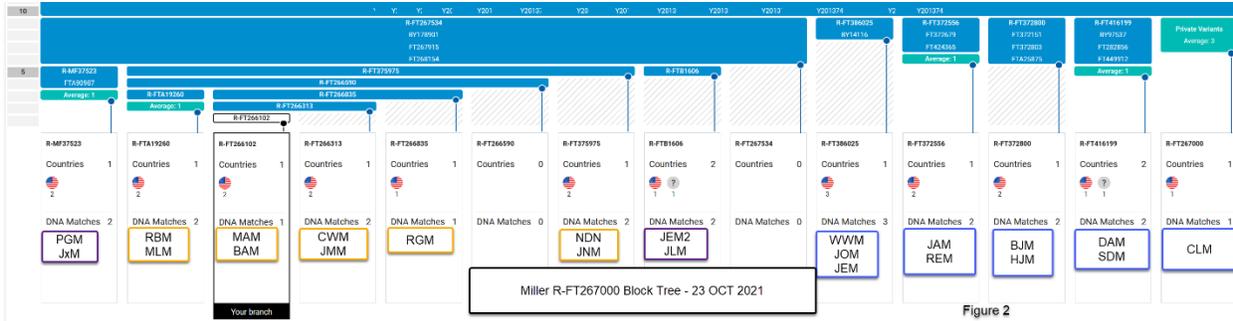
To date our YDNA testing has excluded the following local Miller lines as patrilineal connections to David and Henry. Each of these excluded lines is the source of many Miller descendants in the Ashe / Wilkes County area:

- 1) William Miller c. 1735 unknown – c. 1825, Lewis Fork, Wilkes, NC
- 2) Johannes Muller 1726 Ephrata, PA – 1780 Friedburg, Rowan, NC.

**Objectives.** Based on the 23 testers under the R-FT267000 Haplogroup (a genetically related group who share a common male ancestor), and the subgroup of 13 under R-FT267534, we estimated the following:

- 1) the patrilineal TMRCA (time to most recent common ancestor) of the FT267534 subclade,
- 2) the birth date of David’s and Henry’s common patrilineal ancestor, and
- 3) the most likely patrilineal relationship between David and Henry.

**Step 1: Estimate the TMRCA of the Miller R-FT267000 Haplogroup and the average SNP mutation rate of the R-FT267534 subclade.**



**Figure 2**

Figure 2 illustrates the status of the BigY-700 YDNA testing program of the Miller R-FT267000 group project through FTDNA. The average SNP mutation rate of 1 new SNP per 83 years (see <https://ydnawarehouse.org/benchmarks>) was utilized to calculate the project’s TMRCA because all the project tests are FTDNA BigY-700 tests. There are no BigY-500 tests whose average SNP mutation rate is 131 years due to its lesser test coverage (ibid.). The author’s Figure 3 spreadsheet was used to calculate the average number of SNPs per tester downstream of the project’s common patrilineal ancestor. The sum of 126 SNPs divided by 23 testers equals an average of 5.48 SNPs per tester from the project MRCA to the average birth year of the FT267000 test group, which is 1958. 5.48 SNPs x 83 years/SNP equals 455 years. 1958 – 455 = 1503 AD +/- . Because TMRCA estimates are only approximate we used 1500 AD +/- .

In his review of this paper, it is noteworthy that Dr. Iain McDonald believes the R-FT267534 block may be an anomaly of 4 SNPs that occurred over a very short period, possibly even one generation, skewing

the project TMRCA. To minimize the potential bias introduced by this possibility Dr. McDonald suggested:

*“[if you] treat R-FT257534 as its own line, you end up with 43 SNPs / 13 lines = 3.31 SNPs per line. If you then average R-FT257534 and the other [Miller project] lines together (4 [in the FT267534 block]+3.31 SNP + 2+2 + 4+4 + 4+4 + 4+4 + 3 = 38.31 SNPs / 10 lines = [3.81] SNPs per line), giving an average of about [315] years [1635 AD +/-]. In reality, that could be anywhere from about [250 to 400] years, or [1550 to 1700 AD]. I'd say this is a more realistic TMRCA estimate.”*

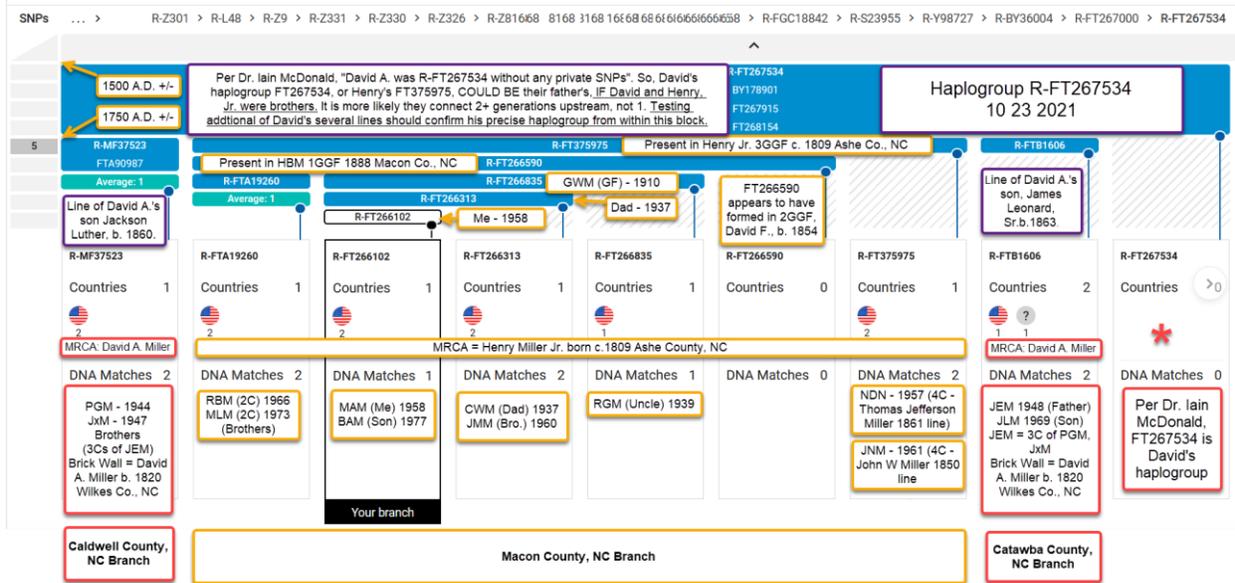
Dr. McDonald’s theory suggests we may be closer to discovering the MRCA of each R-FT267000 subclade (the subgroups of the R-FT267000 Haplogroup) and the corresponding project MRCA than we believe. Pending additional testing which should indicate which approach is more likely, the author is *staying the course* with an open mind to Dr. McDonald’s view, while seeking testers to break up and clarify the FT267534 block of equivalents

					Miller R-FT267534 Subclade	
Miller R-FT267000 Branch	SNPs (including Private Variants) below MRCA	Testers	SNPs x Testers	Average Branch SNP Mutation Rate (TMRCA years / SNPs per Branch)	Average Years per SNP (Subclade Rate)	Average Clade Generations per SNP @ 29 years / generation (Project Average)
MF37523	7	2	14	65	65	2.24
FTA19260	8	2	16	57		
FT266102	9	2	18	51		
FT266313	8	2	16	57		
FT266835	7	1	7	65		
FT375975	5	2	10	91		
FTB1606	5	2	10	91		
FT386025	2	3	6	228		
FT372556	4	2	8	114		
FT372800	4	2	8	114		
FT416199	5	2	10	91		
FT267000	3	1	3	152		
		23	126	83		
<b>TMRCA Calculations - Miller R-FT267000 Haplogroup</b>						
Average SNPs per tester from MRCA (SNP SUM/Testers)	5.48					
x average SNP mutation rate for BigY-700s	83					
= calculated TMRCA years	455					
Estimated TMRCA date	1503	Average birth year (1958) minus TMRCA years				
<b>TMRCA Calculations - Miller R-FT267534 Subclade</b>						
Average SNPs per tester from MRCA (SNP SUM/Testers)	7.00					
x average SNP mutation rate for BigY-700s	65					
= calculated TMRCA years	455					
Estimated TMRCA date	1503	Average birth year (1958) minus TMRCA years				

**Figure 3**

As shown in Figure 3, more SNP mutations have emerged down the lines of the FT267534 subclade than other associated lines. This suggests that the average SNP mutation rate of the FT267534 family clade is faster than the average 83 years/SNP factor. Over the 455-year period calculated above, the FT267534 subclade averages seven SNPs per tester or 65 years/SNP (455/7).

**Step 2: Estimate the birth date of the common patrilineal ancestor of David and Henry.**



**Figure 4**

Again, as shown in Figure 4, there are four SNPs in the FT267534 Block of Equivalents. The gap at the base of this block represents the MRCA of the Henry and David Miller lines. To estimate the TMRCA of David and Henry these four SNPs are subtracted from the FT267534 average of seven SNPs from the project TMRCA date to present. So, the average number of SNPs per tester for the David/Henry estimate is three (7-4), as also calculated in Figure 5. Three SNPs x 65 years/SNP = 195 years. The average birth year of the testers is 1957. 1957 – 195 years = 1762 A.D. +/- as the estimated birth date of David's and Henry's MRCA.

						R-FT267534 Miller Family Clade	
Miller R-FT267000 SNP Branch	SNPs (including Private Variants) below MRCA	Testers	SNPs x Testers	Average Branch SNP Mutation Rate (TMRCA years / SNPs per Branch)	Average Years per SNP (Clade Rate)	Average Clade Generations per SNP @ 27.4 years / generation (Sub-group Average)	
MF37523	3	2	6	65	65	2.37	
FTA19260	4	2	8	49			
FT266102	5	2	10	39			
FT266313	4	2	8	49			
FT266835	3	1	3	65			
FT375975	1	2	2	195			
FTB1606	1	2	2	195			
		<b>13</b>	<b>39</b>	<b>65</b>			
TMRCA Calculations for Miller R-FT267534 Sub-Group (24 OCT 2021)							
Average SNPs per tester from MRCA (SUM/Testers)	3.00						
x average SNP mutation rate for BigY-700s	65						
= calculated TMRCA years	195						
Estimated TMRCA date	<b>1762 Average birth year (1957) minus TMRCA years</b>						

**Figure 5**

David Vance's TMRCA calculator ([https://docs.google.com/file/d/1Wjye3-vYDZQyNFcyR6lwKONBmAkbc04a/edit?usp=doclist\\_api&filetype=msexcel](https://docs.google.com/file/d/1Wjye3-vYDZQyNFcyR6lwKONBmAkbc04a/edit?usp=doclist_api&filetype=msexcel)) was also applied (Figure 6).



common ancestor must be within one SNP timescale of 1820. That could be 83 years, or much shorter or longer. It's unlikely to be that much longer, otherwise the more distant Miller tests (WWM, JOM, JEM, ...) would show more SNPs”.

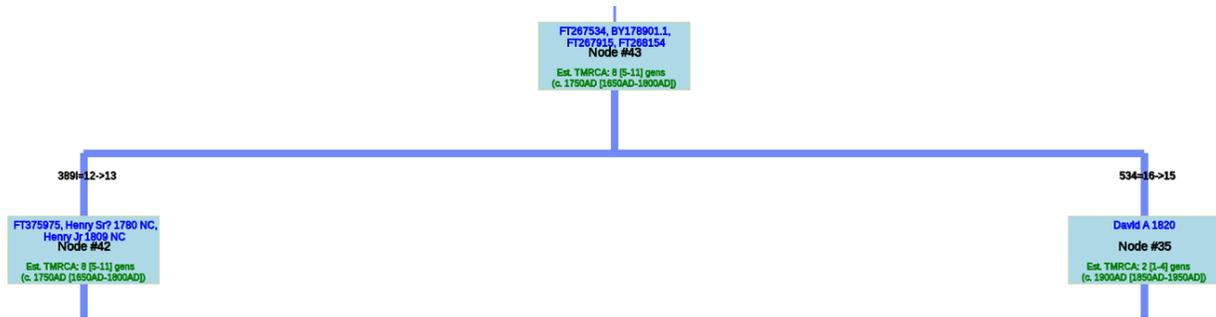


Figure 7

**Step 4: Estimate the generations from David A and Henry Jr. to their MRCA.**

Figure 8 calculates the average years per generation for the Miller R-FT267000 haplogroup (28 years) and the FT267534 subclade (27.4 years).

Initials	Father's Age	Branch Ave.	Branch
DAM	35	35.0	FT267000
2GGF DFM	45	27.4	FT267534
JxM	40		FT267534
PGM	37		FT267534
GGF HBM	34		FT267534
MLM	32		FT267534
RGM	29		FT267534
CWM	27		FT267534
GF GDM Sr.	26		FT267534
JEM2	26		FT267534
RBM	25		FT267534
JMM	23		FT267534
GF GWM	22		FT267534
MAM	21		FT267534
JLM	21		FT267534
NDN	19		FT267534
JNM	19		FT267534
BAM	19		FT267534
REM	36	33.5	FT372556
JAM	31		FT372556
BJM	37	33.0	FT372800
HJM	29		FT372800
JEM	36	26.3	FT386025
JOM	22		FT386025
WWM	21		FT386025
<b>Average</b>	<b>28</b>		

**Figure 8**

Applying 27.4 years per generation to estimate the number of generations from David Miller and Henry Miller to their MRCA yields:

- 1) David was born in 1820.  $1820 - 1755 = 65$  years.  $65 / 27.4$  yrs. per generation = 2.4 generations, .
- 2) Henry's birth year is between 1802 and 1810, say 1806.  $1806 - 1755 = 51$  years.  $51 / 27.4 = 1.9$  generations,

One of our working hypotheses has been that Henry and David may have been brothers. Steps 1 through 4 imply it is more likely they were 1<sup>st</sup> cousins, 1C1Rs, or 2<sup>nd</sup> cousins. If the TMRCA dates of 1500 and 1755 are valid, it seems unlikely that they would be much more distantly related than 2<sup>nd</sup> cousins, although possible.

**Step 5: What can we intimate from Henry's SNP FT375975 and David's SNP FT267534?**

Could David Miller and Henry Miller be brothers? Possibly. The FT267534 subclade demonstrates the ability to form SNPs at a faster than average rate. However, the 1755 MRCA implies it is more likely that

David and Henry connect two or three generations upstream, allowing for the possibility that they may have been brothers.

**Step 6: What clues do atDNA relationships between the FT267534 testers (plus the brother of JEM) provide?**

Figure 9 was built to identify potential atDNA patterns among the FT267534 YDNA test group. The relationship probabilities are taken from [The Shared cM Project tool v4](#) located at [dnainter.com](http://dnainter.com). As noted in the Figure, two observations emerged:

- 1) This is small sample set, but the data implies the FT267534 Miller family clade may tend to be more closely related than the highest probability block of the Shared cM Project, based on actual 3C1R, Half 3C1R and 3C relationships versus closest high probability block expected relationship of 4C1R.
- 2) David is the 2ggf of his descendant testers, JxM, JEM & GDM. Henry is the 2ggf of CWM & RGM, and the 3ggf of JNM & NDN. So, we know that JxM, JEM & GDM are at least 4th cousins from CWM & RGM. While the shared cM data and Observation 1 cannot inform us of the exact relationship of these testers to their patrilineal MRCA, if Observation 1 is valid, it seems likely that the MRCA is not further upstream than about the 5C1R or 6C range, or a maximum of about 3 generations upstream of JxM, JEM, GDM, CWM & RGM. This data also implies that the relationship between David and Henry is likely somewhere between brothers and 2nd cousins.

Does endogamy make the Miller patrilineal line relationships appear closer than actual? Henry Miller married his first wife, Mary Ann Nichols, in 1835 in Wilkes County, NC. Their first recorded child, Martha Jane, was born in 1837 in Haywood County, NC, about 135 miles to the west. So, Henry left the Ashe/Wilkes County area before the first child was born. This Miller branch never returned to the Ashe/Wilkes County area. This implies that endogamy is not a key factor between Henry's descendants and David's. Many of David's have remained in Caldwell and Catawba Counties, which are near Ashe and Wilkes Counties. While Caldwell and Catawba Counties are neighbors, examination of the family trees connecting the "Caldwell Millers" and the "Catawba Millers" does not indicate that endogamy is significant between these Miller lines. It does not appear that endogamy is significantly prejudicing Figure 9.

Subject	Subjects = David Alexander Miller Descendants												Subjects = Henry Miller, Jr. Descendants					
	JxM (BigY tester)						JEM (BigY tester)				GDM (JEM's brother)				CWM (BigY tester)		RGM (BigY/CWM bro.)	
Match	JNM	NDN	CWM	RGM	JEM	GDM	JNM	NDN	CWM	RGM	JNM	NDN	CWM	RGM	JNM	NDN	JNM	NDN
Shared cM	<8	<8	22	<8	24	13	21	<8	<8	<8	14	<8	<8	<8	26	19	<8	10
Known					3C	3C									3C1R	Half 3C1R	3C1R	Half 3C1R
Relationship Probabilities from The Shared cM Project 4.0 tool v4																		
8C or +	64%	64%	58%	64%	57%	61%	58%	64%	64%	64%	61%	64%	64%	64%	56%	59%	64%	62%
7C1R	64%	64%	58%	64%	57%	61%	58%	64%	64%	64%	61%	64%	64%	64%	56%	59%	64%	62%
7C	64%	64%	58%	64%	57%	61%	58%	64%	64%	64%	61%	64%	64%	64%	56%	59%	64%	62%
6C1R	64%	64%	58%	64%	57%	61%	58%	64%	64%	64%	61%	64%	64%	64%	56%	59%	64%	62%
6C	64%	64%	58%	64%	57%	61%	58%	64%	64%	64%	61%	64%	64%	64%	56%	59%	64%	62%
5C1R	64%	64%	58%	64%	57%	61%	58%	64%	64%	64%	61%	64%	64%	64%	56%	59%	64%	62%
5C	64%	64%	58%	64%	57%	61%	58%	64%	64%	64%	61%	64%	64%	64%	56%	59%	64%	62%
4C1R	64%	64%	58%	64%	57%	61%	58%	64%	64%	64%	61%	64%	64%	64%	56%	59%	64%	62%
4C	14%	14%	16%	14%	16%	15%	16%	14%	14%	14%	15%	14%	14%	14%	17%	16%	14%	15%
Half 3C	14%	14%	16%	14%	16%	15%	16%	14%	14%	14%	15%	14%	14%	14%	17%	16%	14%	15%
3C1R	14%	14%	16%	14%	16%	15%	16%	14%	14%	14%	15%	14%	14%	14%	17%	16%	14%	15%
Half 3C1R	14%	14%	16%	14%	16%	15%	16%	14%	14%	14%	15%	14%	14%	14%	17%	16%	14%	15%
3C	6%	6%	8%	6%	8%	7%	8%	6%	6%	6%	7%	6%	6%	6%	9%	8%	6%	7%
Notes and Observations																		
<8	Known relationship from YDNA testing, but not listed as a match on Ancestry. Assumed 4 cM match in Shared cM Project																	
%	Relationship probability based on assumed 4cM match in Shared cM Project																	
%	Relationship probability based on shared cMs per Ancestry																	
%	Actual relationship compared to relationship probability.																	
Observation 1: This is a small sample set, but the data implies that this Miller family clade tends to be more closely related than the highest probability block of the Shared cM Project. I.e.: Actual 3C1R, Half 3C1R and 3C relationships versus closest high probability block expected relationship of 4C1R.																		
Observation 2: David Alexander Miller is the 2ggf of each of his descendant testers JxM, JEM & GDM. Henry Miller, Jr. is the 2ggf of CWM & RGM. He is the 3ggf of JNM & NDN. So, we know that JxM, JEM & GDM are more distant than 3rd cousins from CWM & RGM. While the shared cM data and Observation 1 cannot inform us of the exact relationship of these testers to their paternal MRCA, if Observation 1 is valid, it seems likely that the MRCA is not further upstream than about the 5C1R or 6C range, or a maximum of about 3 generations upstream of JxM, JEM, GDM, CWM & RGM. This implies that the relationship between David A. and Henry is likely somewhere between brothers and about 2nd cousins.																		

Figure 9

### Summary of observations.

1. The TMRCA of the Miller R-FT267000 project is approximately 1500 AD, with acknowledgment of Dr. McDonald's hypothesis that the TMRCA may be in the 1550 to 1700 AD range. For determining the relationship between Henry and David the difference between these hypotheses is less important than the TMRCA for the R-FT267534 subclade and should resolve with further testing and genealogical research.
2. The TMRCA of the Miller R-FT267534 sub-clade is approximately 1755.
3. The current haplogroup status and block tree structure of the David and Henry lines implies it is not likely they were brothers, but the possibility cannot be excluded.
4. Using 27.4 years per generation for the FT267534 family group:
  - a. From David's 1820 birth date to the 1755 TMRCA is about 2-3 generations.
  - b. From Henry's 1806 +/- birth date to the 1755 TMRCA is about 2 generations.
  - c. These approximations imply that the TMRCA is Henry's grandfather, who would also be David's grandfather or great-grandfather, implying they are cousins or 1C1rs.
    - i. Assuming Henry's birth year is about 1806 and the MRCA's is 1755:
      1. If the MRCA is his grandfather, the birth year of Henry's father is roughly 1780.
      2. If the MRCA is his great grandfather, the birth years of his grandfather and father are roughly 1872 and 1889, or an average of 17 years old each when the grandfather and father were born.
      3. The first scenario is more likely than the second.
    - ii. Applying David's birth year of 1820 and the 1755 TMRCA:
      1. If the MRCA is his grandfather, the estimated birth year of his father is roughly 1788

2. If the MRCA is his great-grandfather the birth years of his grandfather and father are roughly 1777 and 1798, or an average of 22 and 21 years old when the grandfather and father were born.
3. Both possibilities are reasonable.
5. atDNA analysis implies that the likely relationship between David and Henry is in the range of brothers to 2<sup>nd</sup> cousins.

**Conclusion.** Recognizing that there is a margin of error, the most likely relationship between Henry and David is 1C1Rs or 1<sup>st</sup> cousins, with a 2<sup>nd</sup> cousin relationship possible. Pending further testing and research that supports a different theory, the hypothesis that 1C1R plus or minus is the most probable relationship between David and Henry because it most effectively reconciles the body of data:

- 1) The proximity of their birth locations and dates.
- 2) The migration history of northwest North Carolina, as briefly discussed below.
- 3) The estimated 1755 TMRCA compared to the generational analysis.
- 4) The block tree and atDNA data suggest they are closely related, but not brothers.

Migration south along the Great Wagon Road began prior to 1750. It appears the Miller family migrated to northwest North Carolina sometime after the conclusion of the French and Indian War in 1763, and prior to Henry's birth in the first decade of the 1800's. It is likely they migrated in the late 1700's as Henry's Miller line did not become well established in the area, and David's only became well established through his 10 children (seven sons and three daughters) who largely remained in the area. Whether the original patrilineal ancestor(s) migrated to northwest North Carolina with his family, or his descendants migrated on their own, the conclusions of this paper reconcile well with the birth dates and locations of Henry and David. The data support the hypotheses that the family migrated to Wilkes County prior to the 1799 creation of Ashe County. There is evidence that one of the branches of the family either moved, creating the Ashe and Wilkes birth locations, or the creation of Ashe County placed one branch in Wilkes and the other in newly formed Ashe County. Either option is possible.

#### **Next steps.**

1. After receipt of the Privott genealogy report, update this analysis, if needed.
  - a. Define the next YDNA testing plan.
  - b. Add one or more YDNA testers with a potential upstream connection to David and Henry, to test the report.
2. Add at least one YDNA tester down one or more of the untested lines of David's descendants to empirically define David's haplogroup.
3. Find one or more testers to validate or exclude the Eli Jackson Miller line as a third connection to the David and Henry lines.
4. Apply Dr. McDonald's advice from his review of this paper:
  - a. "The other important thing is to consider the more distant Millers in the tree. The overall haplogroup can't be that old, otherwise people would have different surnames. This acts as a safe upper limit for the age of the overall R-FT267000 block", and
  - b. "I would also pay attention to these more distant lines and see whether you can tie together a more distant line to any of these. Get any one of them back to the early 1700s or 1600s, and you may find your own ancestors among them."

I would like to express my sincere gratitude to Dr. Iain McDonald, Dr. Lee Martinez, and David Vance for reviewing this paper and providing insightful feedback that forced deeper thought. Not all review comments were incorporated, but all are greatly appreciated and may prove to be more correct than my conclusions as genealogical research and further testing bring the Miller team closer to the truth. The author is solely responsible for the accuracy and completeness of this paper.