John Haacke and Hannah Adams: Pioneers of Markham Township, Ontario, Canada and Pivotal Ancestors for DNA Validation of Their Own Descendants

Abstract:

Purpose: To determine the dominance of a given haplotype for Johann Haacke (born circa 1775) and his descendants and estimate the probability of loci change.

Methods: A standard 26 or 43 loci test was performed in 9 descendants of Johann Haacke and 3 supposed descendants. Studies were also performed on three other Haacke families in England, Canada and the United States. To test the estimated probability of change, a second family by the name of Rittenhouse was investigated dating back to William Rittenhouse (born 1644).

Results: All subjects tested who descended from Johann Haacke had the same DNA signature at all 26 or 43 locations. One family agreed with 41 of 43 places while others varied by a dozen or more locations and were clearly not related. The probability for a given loci to change was found to be roughly 0.0004. The descendants of William Rittenhouse also followed the expected deviations for a probability of change of 0.0004.

Conclusions: If two men have a match over 43 loci, and have had the same surname for many generations, this implies that they are related at some point in the last few hundred years. A match of 41 or 42 would indicate a relationship further back, perhaps even hundreds of years earlier. Given the very small probabilities of change in a given loci, a combination of primary sources and DNA analysis can lead to verification of family connections, family lore and changes in surname.

Introduction

The focus in this paper is on the family and descendants of Johann Haacke, and his wife, Hannah Adams who settled in Markham, Ontario, Canada prior to 1800 (1,2). By 1794, they are in Toronto with the Berczy settlers (3,4). Johann was probably one of the young men who helped clear Yonge Street with the Berczy settlers (3). By 1800, as young adults, he is farming land in Markham (just north-east of modern day Toronto) on Lot 17, West ½ of Concession 4 (3). Here John and Hannah begin raising a large family that will, over time, migrate across North America. Some family members changed their name from Haacke to Hickey, some claimed a relationship to the famous presidential Adams family, some took the name of Haacke but were in fact genetically not Haackes, and no-one seemed to know the Haacke ancestry in Europe. How Johann and Hannah arrived in Ontario remains a mystery and where this branch of the Haacke family came from in Germany also remains unknown.

These are not unique problems in genealogical studies. There are always difficulties in family research as we probe further into the past. Some of these can be solved with enough detective work via conventional records and some through family lore. In the case of the early pioneers from Toronto, Ontario, Canada around the turn of the century in 1800, records were few and far between. Land records are available, but church records are sparse, wills almost non-existent, civil records 100 years from being available, and bible records exist for the lucky few. Still, it is possible to infer a great deal about the families as the children of the early pioneers of Toronto grew up and appeared in census records from 1841 onward. Over 30 years of research, the relevant Canadian records have been exhausted. In this paper, we show that a combination of conventional genealogical research and DNA analysis leads to answers to many of these questions (5) and, if not answers, then DNA opens the door for future directions of primary research.

The family of John Haacke and Hannah Adams

John and Hannah had at least 9 children. There were four boys. Descendants from all of these have participated in the DNA study that is at the core of this research. The results of this case study will give some answers to questions relating to proof of relationship to John and Hannah, validation of family lore, proof of name changes, and an example of a non-paternity event.

Elisabeth, born circa 1797, married Dietrich Steffens (3,6).

Mary Anne, born circa 1799, died young (3).

David, born 1801, moved to Illinois in 1822. He went to Fort Peoria and then settled south of this in Canton, Fulton County, Illinois (7). One descendant of this line agreed to take the DNA test.

Amalia, (probably born between 1802 and 1804) married John Gray. They had at least two children (4): Mariana (born 1818) and Margaretha (born 1821) (6). The latter, known as Margaret in later life, married a Peter Hutty from Yorkville (now part of Toronto). A brief history of Peter Hutty (8) reveals his wife's connection to John and Hannah and tells the same story as that given by David Haacke published in 1878 in a far away place in the United States (7).

Rachel, (probably born between 1802 and 1809) married Christian Tipp and had two children: Johann and Nancy. Christian's father was William Tipp (originally Tippe) formerly in the Braunschweig militia in Uhler's company of the von Rhetz Regiment (9).

Henry, was baptized in 1810 with his brother George (10). One branch of his family through a son David moved to Montana. Multiple descendants of this line agreed to take the DNA test. In this group, we find the creation of a new Haacke DNA as there was a non-paternity event in an earlier generation.

Mary Anne, married Joseph Fisher descended from a line of Fishers who came from Somerset County in Pennsylvannia. This family is so large and of such great interest historically that it would be ripe for a DNA evaluation.

George, like Henry was baptized in 1810 (10,11). He stayed in Markham and married Sophia Quantz a grand-daughter of Melchior Quantz (also a veteran of the Braunschweig/Hessian troops. They raised a family of 15 children. His children were: Hannah (b 1838) m John J. Lunau; Mathilda (b 1839) m William Fierheller; Mary Anne (b 1842) m Daniel S. Miller (a son of Ben Miller after whom the town near Goderich was named); William (b 1840, the author's great-great-grandfather) m Martha Ramsey; George (b 1843) m Hannah Ramsey a sister to Martha; Christina (b 1845) m John Barker; Caroline (b 1844) m John Lounsborough; Margaret (b 1848, d 1861); Sophia (b 1849) m William H. Heise; Amelia (b 1852) m George Heise a brother to William; Jane (b 1855, d 1861); John David (b 1856) m Zilpha E. Locke; Henry Edward (b 1858, d 1861); Arthur A. (b 1860) m Margaret C. Pearson and then Minnie M. Campbell; and Hannah Ellin (b 1863) m George Simpson. George and Henry were listed jointly on a mortgage in 1834 between them and Thomas Robson (Toronto land records). It was marked paid in 1836 and signed by Joseph Ridout. George Haacke signed in German (under Georg).

(names and dates from the George Haacke family bible) Multiple descendants of this line agreed to take the DNA test.

Christina, married Jacob Braendle.

Edward, born 1816 (6) moved to Canton, Illinois to join his brother David in 1836. He had 11 children all of whom changed their name to Hickey (the name Haacke is pronounced as Hickey in this farming community and in the mid-west United States). There is no primary documentation that this is the Edward Haacke from Toronto. There was in 1976 one person alive descended from this family, Mrs. Delma Carter, who remembered her father telling her the name was Haacke. She had an old obituary card that was "In loving remembrance of Edward Haake". Even by Edward's death in 1894, the family had forgotten how to spell the name. Here DNA will play a key role in determining if this is indeed the Edward baptized by Rev. Peterson in Markham Ontario (6). Multiple descendants of this line agreed to take the DNA test.

Methods: DNA as a tool to validate primary documentation and family lore

The rapid growth in our understanding of human DNA and the means to probe local structures within it are finding interesting applications in genealogy (5,12,13). On the male side, the Y chromosome is, for the most part, inherited intact from father to son (14). The good news for genealogists is that the structure of the Y-chromosome mutates slowly. The changes are fast enough that we can see them in a few hundred years, but slow enough that we can draw conclusions about how people are related. In a sense, from a genealogist's perspective, they serve as nature's church records and as primary sources of information.

There are places on the chromosome referred to as markers or loci where some patterns of the gene's building blocks repeat themselves (short tandem repeats or STR). The number of times this group repeats itself is called an allele and the entire group containing all these repeats is a segment. For example, when the number 12 appears after the loci DYS439 it means that the number of STR is 12, hence the allele for DYS439 is 12. In some of the results reported here, there are 43 loci, each with a unique allele. We are still developing statistical models describing the relationship between genealogical connections and empirically observed Y-chromosome mutation rates. However, the more direct genealogical information that is available with documented evidence of family relationships, the better DNA analysis will be understood as it relates to individual families. The results presented here on the descendants of John and Hannah already demonstrate how slow mutation rates can be.

Results

Four separate sons of Johann were followed 5 to 8 generations. Each person tested is marked with one or two asterisks. Those with a single asterisk all had the same haplotype. Those with the two asterisks had a different haplotype to the main branch of the family and to Henry marked with three asterisks. This change in haplotype was an indication of the creation of a new Haacke lineage. A total of 6 people in the sixth generation, 5 in the seventh generation and 1 in the eighth generation were tested (see Table 1). There were no deviations in the alleles for any of those tested and marked with a single asterisk. There are 41 separate generational nodes leading to all the end points of each line. (Had all 8 people come from 8 separate lines and been in the 5th generation that would have represented 40 separate generational pathways.)

Further, three other separate Haacke lines from Dayton, Ohio; Winnipeg, Manitoba; and Salt Lake City, Utah were also tested. Two of these had different haplotypes, while one was only different from the line of Johann Haacke in two locations.

Discussion

Clans 1 and 3: The fact that after 230 years all descendants of Johann Haacke have the same DNA in all places makes a strong statement as to the stability of a given family's DNA. Still, after three or four hundred years, it is not surprising to find 1, 2 or more rarely 3 changes. Therefore, sometime prior to 1775, Joe Haacke and myself are likely related. This discovery has significant implications for how to proceed with future research. This family is known to come from the State of Hanover (12). Military records from Wolfenbettel indicate that five soldiers with the name of Haacke came from Braunschweig to fight for the British in the Revolutionary War (15,16). Braunschweig is also in the state of Hanover. If a town or parish were known for Joe Haacke's ancestor, then his family could be researched in Germany with the hope of finding a connection to John Haacke. The collection of further DNA samples from other Haacke families may eventually lead to either a town which connects all related families or to the town where the family originated.

Clan 2: The Jim Haacke anomaly and the birth of a new Haacke line: The first 12 sites agree pretty well with each other. There is only one deviant result. The chance of this happening over 5 generations and 8 separate tests in the same generation is pretty high. These early studies of only 12 sites are today referred to as low resolution studies and only show broad relationships in the population at large (5). At first glance then, if we had only these markers to work with, it would seem that all family members are related. As the number of markers increases, more differences are seen. If the first 22 sites were chosen, only 2 sites would disagree. Over many generations this is not unreasonable either (17). Finally, testing with the current 43 markers reveals 13 differences. This indicates that this line is not related to the rest of the family members. Family lore suggested who the father might have been and recent DNA testing has in fact validated this with a very positive outcome. However, care must be taken in revealing such information and it should always be with the permission of both families.

The role of mitochondrial DNA studies: The DNA material presented so far has focused on the male descendants of John and Hannah. However, a study of mitochondrial DNA to test female relationships can also be used to prove connections to the male ancestry. There is no primary documentation showing that Amalia Gray, Rachel Tipp or Mary Anne Fisher were children of John and Hannah. Using mtDNA, one can try to show that separate families along a continuous female line of descent are related. If the mtDNA for all three female lines is the same, then we can be confident they are all descended from Hannah and assuming no infidelities from John Haacke as well.

Finally, we were lucky enough to have a well documented family history on the Rittenhouse side to a William Rittenhouse of Germantown, Pennsylvania who was born in 1644 in Muelheim, Germany. This family has multiple lines connected to today that represented roughly 10 generations (although some in this family extend to the 12th or higher generations). We show this data as validation of the theory developed based on the Haacke results quoting the probability of change as 0.0004 (17). Using this value, for the 7 cases studied, in the tenth generation we can predict the ratio of no change to one change to two changes to three changes as: 1:1.2:0.72:0.58. For 7 cases (which is not really enough for a proper statistical analysis) this would imply 2.00:2.40:1.44:1.16 when in fact we found 3:2:1:1 which is not a bad estimate. Clearly, after 10 generations, one can begin to see major deviations. A summary of the variations of the haplotype of this family is given in Appendix I.

Summary and Conclusions

The field of DNA analysis continues to mature. The ability to extract meaningful information from both a family's history and genetically will benefit from studies of families that have records over several hundred years. Care must be taken in drawing conclusions based on a small number of subjects until a given family has been carefully analyzed over many generations. The most reliable conclusions are best drawn from a study with as many markers as possible (a high resolution study). Despite these warnings, the preliminary evidence presented here is suggestive that some families change very slowly even over 43 markers. One direct application for those searching for their European roots would be to match a family with their DNA. If this were to be successful, then the location of the ancestors of that family can be assumed to be at some point the location of the root ancestor to both families. For those who thought the doors to tracing one's family further into the past were closed, DNA may be the means to re-open those doors.

References

1. Champion I (1979). Markham. Markham Historical Society. pages 16, 63, 134, 135, 168, 209.

2. Haacke EM, (1999). Haacke, Quantz and Baetijer: Some Stories and Some Facts. *Berczy Settlers Gazette* 6: 2; 5-6.

3. Andre J (1971). Infant Toronto as Simcoe's Folly. pages 27, 30, 40, 45, 53-54, 88, 110, 159, Appendix 3.

4. Ontario Archives H. bundle, #76.

5. Pomery C (2004). DNA and Family History. The Dundurn Group, Toronto, Ontario, pages 63, 71.

6. Peterson records photocopy of original church records of Bethesda Evangelical Lutheran Church, Markham twp York co Ontario in possession of Ruth Burkholder.

7. History of Fulton County, Illinois, Peoria, Chas. C. Chapman & Co., 1879.

8. Commemorative biographical record of the county of York, Ontario: containing biographical sketches of prominent and representative citizens and many of the early settled families. J.H. Beers & Co., Toronto, Ontario: 1907: pages 620,621.

9. Wolfenbuettel archival material, Wolfenbuettel, Germany.

10. St. James Cathedral church records, page 2.

11. George Haacke family bible records.

12. Smolenyak M and Turner A. Trace your roots with DNA Holzbring Publishers.

13. Shawker TH (2004). Unlocking your genetic history. Rutledge Hill Press, Nashville, TN.

14. Roderick TH, (2000). The Y-chromosome in Genealogical research: From their Ys a Father Knows His Own Son. NGSQ June; pages 122-43.

15. Haacke EM, (1986). Research in Brunswick Brings New Problems. Western Reserve Historical Society Bulletin, 4: 4; 27,32 and 5: 1; 5.

16. Naturalization records for Heinrich Haacke's son William Haacke of Dayton, Ohio.

17. If there are n sites, m generations and r people, the probability of s mutations is given by:
$P(s) = ({}^{t}{}_{s})p^{t-s}q^{s}$ where $t = nmr$, q is the probability of change in a single allele and $p = 1-q$. In the Haacke family example given here, the probability of no change is very small. This in turn would suggest that q is very small. Currently, it is believed that the chance for change in one allele is roughly 0.004 (it actually changes from locus to locus within a factor of 2 or so from this value). This is not impossible given that q value, but it is highly unlikely. This author's experience suggests that families remain very stable. If one assumes that this can happen 50% of the time over 40 independent generational nodes as in this study, then q would be more like 0.0004. If this is a rare event in only the Haacke family that happens just once in 100 times, then q would be 0.00267. Defining the number of generations to reach a 50% chance of seeing a change as a super-generation and taking 30 years per generation, then a super-generation would be somewhere between 180 and 1200 years using these two q values. Therefore, the Dayton, Ohio family may be related with John Haacke of Toronto as early as the 1750s or perhaps even centuries earlier given that they already show two changes. Although a daunting prospect, it is also an exciting prospect that people could find close relationships easily dating back hundreds if not a 1000 years. Clearly, if in over 41 cases there are no changes in the DNA, then having 13 changes indicates that there is no close connection between this line and the other Haackes.

About the author

The author E. Mark Haacke is a third great-grandson of George Haacke, son of John Haacke and Hannah Adams. He is a Professor of Radiology and Biomedical Engineering at Wayne State University where he focuses on research in Magnetic Resonance Imaging. He has written a number of genealogical articles on the Haacke and Rittenhouse families. He was President of the Rittenhouse Family Association from 1988 to 1996 and edited their newsletter for 15 years. He is currently the senior editor of the Haacke Family Herald.

Responsibility

The conclusions drawn from this data are the sole responsibility of the author and reflect the author's assessment of the data. The author's mathematical analysis uses a forward binomial approach with *a priori* information rather than a Bayesian approach which assumes no other prior knowledge except an estimated mutation rate. The author's analysis also makes it possible to estimate mutation rates based on forward data in a fashion similar to that which is done in the literature.

Acknowledgements

The data for this study were obtained from Relative Genetics and from DNA Heritage. We would like to thank them for their congeniality and continued availability for discussion.

Table 1: The descendants of Johann Haacke

This table shows the results of a DNA analysis for the descendants of four of John Haacke's sons. The date after each name is the birth year of the individual.

FIRST	SECOND	THIRD	FOURTH	FIFTH	SIXTH	SEVENTH	EIGHTH
Johann 1775							
Haacke	David 1801	John 1854	Vivan 1899	David 1929	Kenneth*	Aaron	
Haacke	Henry 1810	David 1844	Henry*** 1879	Albert** 1924	James** 1948	Jeffrey** 1976	
				Frank 1914	Wally*		
Haacke	George 1810	John David 1856	John D. II 1883	Roy 1913	George 1940	Steven* 1965	
		George 1843	Lawrence 1871	Carl 1911	Lorne* 1943		
			Andrew 1880	Charles 1916	Charles 1938	Scott* 1956	
		William 1849	William 1866	Harry 1893	Ewart* 1920	Mark* 1951	Bryon* 1981
Hickey	Edward 1816	Nathaniel 1867	John 1891	Keith* 1927	Randy* 1954		
		Edward 1856	Charles 1875	Walter 1899	Charles 1927	Tim* 1958	

Table 2: Comparison of DNA haplotypes of related and unrelated families

	Clan 1	Clan 2	Clan 3	Clan 4	Clan 5	Clan 6a
DYS385a	11	11	11	12	16	11
DYS385b	14	14	14	15	18	15
DYS388	12	12	12	15	12	12
DYS389	14	14	13	14	13	13
DYS389II	30	30	29	30	31	29
DYS390	24	24	24	22	24	21
DYS391	11	11	11	10	11	11
DYS392	13	13	13	11	11	13
DYS393	13	13	14	13	13	13
DYS394	14	14	14	15	14	14
DYS426	12	12	12	11	11	12
DYS437	14	15	14	14	14	15
DYS438	12	12	12	10	10	12
DYS439	12	12	12	12	13	12
DYS447	26	25	26	26	26	25
DYS454	11	11	11	11	11	11
DYS455	11	12	11	11	11	11
DYS460	11	11	11	10	9	11
DYS461****	12	12	12	12	13	10
DYS462	11	11	11	12	12	11
GGAAT1B07	10	10	10	11	12	7
YCAIIa	19	19	19	20	17	19
YCAIIb	21	23	21	21	21	23
Y-GATA-A10	13	13	13	14	14	12
Y-GATA-C4	23	23	23	21	21	25
Y-GATA-H4	12	12	12	11	12	12
DYS441	13	13	13			13
DYS442	12	12	12			12
DYS444	12	12	12			12
DYS445	12	12	12			12
DYS446	13	13	13			14
DYS448	19	19	19			19
DYS449	29	29	29			29
DYS452	10	11	10			11
DYS456	16	15	16			16
DYS458	16	17	16			16
DYS459a	9	8	9			9
DYS459b	10	9	10			10
DYS463	22	23	22			23
DYS464a	15	13	15			15
DYS464b	15	13	15			15
DYS464c	16	15	16			17
DYS464d	17	17	17			18

***Clan 1: Keith Hickey, Randy Hickey, Lorne Haacke, Kenneth Haacke, Wally Haacke, Steven Haacke, Martin Haacke, Tim Hickey, Ewart Haacke, Mark Haacke, Bryon Haacke all descendants of Johann Haacke from Toronto

**Clan 2: Jeffrey Haacke, James Haacke, Albert Haacke one branch of the Montana group

Clan 3: Joe Haacke of the Dayton, Ohio group

Clan 4: Don Haacke of the Salt Lake City group

Clan 5: Dan Haacke of the Winnipeg, Manitoba, Canada group from England

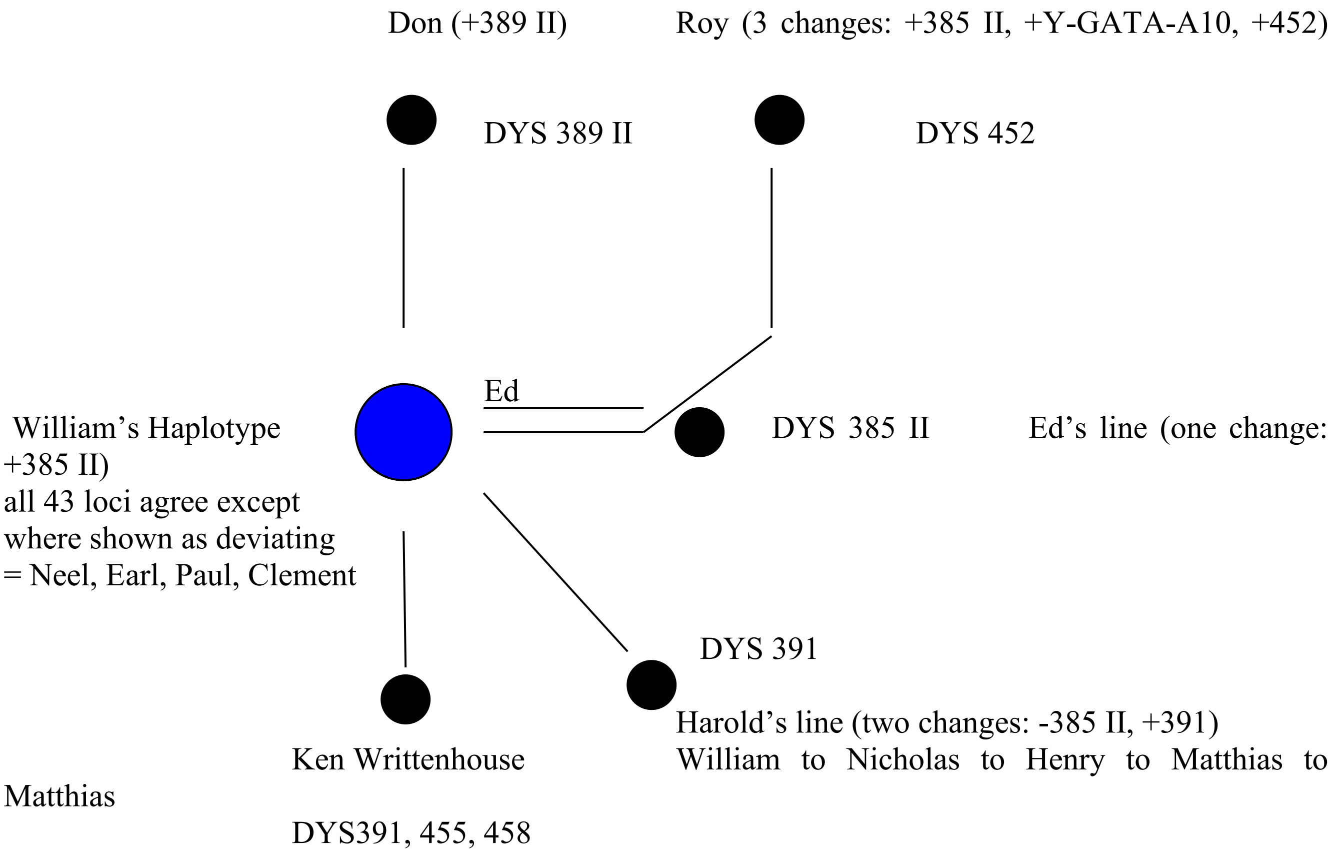
Clan 6: Members of the Rittenhouse family.

****DYS461 was incremented by one over the original reported values prior to June, 2004 to be in conformity with the national standards associated with the counting of the number of repetitions at this site.

The fact that both DYS389 and 389II both change, comes from the change in DYS389 which is then reflected in the total represented by DYS389II and is considered just a single change (despite both numbers appearing to be different).

Appendix I

CORE 43 Loci ●
Haplotype for the William Rittenhouse Line in the USA and Canada
Variations or deviations in a given loci are shown with a black dot.
Four people from two lines back to Nicholas have the same DNA even after 10 generations!
Two people have only one deviation, one has two and two others have three.



Using a probability of 43 x 0.0004 x 45 nodes (1 from wm to nich, 1 from nich to henry plus 3x7 for his kids and one from nich to wm plus 3x7 for his kids = 45) gives w = 0.774

Using exp(w) gives (1,0.774, 0.3,0.077) for changes that are (0,1,2,3) these scale to the following expected ratios of the number of changes after these 10 generations:

No changes	13 or for only 6 people we expect roughly	3 we have	2
One change	10	2	2
Two changes	4	1	0
Three changes	1	0	2
Total number of people	28	6	6

This can be updated when the lines for Neel and Earl are added. We need more numbers of different family lines to participate to improve the statitstics. But we do know 2 zero changes will become 4 putting this more in line with the expected numbers.

William 1644
I

Nicholas 1666
II

Henry 1700 — William 1691
III

IV	Matthias	Nicholas	William 1723	Isaac 1725	John 1742	Nicholas (385b change)
V	Matthias	Samuel	William 1774	Peter 1770	Michael 1768	Martin
VI		John Smith	Joshua 1802	Isaac 1795	John Fretz 1800	Martin D
VII		Levi	John Bell 1840	Charles 1836	Moses 1846	Amos
VIII		Wm W	Harvey 1873	Wm 1865	Edward 1872	Jesse
IX		Fred L	Donald 1910 1911	Clement 1911	Harold 1906	Amos
X	Harold 385b,391	Ken Dean	Paul zero	Wm C 1948 zero	Edward 1934 385b	Junior (Roy) 385b, 452, YGA10
XI		Ken Ray				
XII		Ken Ray 391,455,458				

Two other lines, Neel and Earl also have no changes.

Appendix II

More details. Currently it is believed the values of these loci change with a probability of 0.004. However, our results suggest a much smaller value. This impacts the out of Africa theory considerably.

Let us look at the forward probabilities for the first two scenarios. They are easy to approximate. The chances of having one deviant site in 12 loci for one generation is $12p^{11}q$ where q is the probability for a single site to change and $p = 1-q$ the probability of no change. The chances for two changes over 22 sites is $21*11\ p^{20}q^{2}$ again. In fact, the chances of no changes occurring in 12 loci is simply p^{12} or roughly 19 in 20 in this example and in 22 it is p^{22}, or roughly 9 in 10, again for one generation using $q = 0.004$. The table below shows the new probability for change for a given generation as u for no change and v for one change and z for two changes.

		n = 12		n = 22		
		no chg	one chg	no chg	one ch	two chg
		u	v	u	v	z
Scenario 1	$q = 0.004$	.953	.04593	.923	.08155	.0034
Scenario 2	$q = 0.0004$	.9952	.00478	.9912	.00873	$3.67 * 10^{-5}$

Now testing over 5 generations, with 8 people, raises the probabilities for change dramatically. Basically, it increases the smaller probabilities for a single change by a factor of nearly 40. The relative probabilities between a single change and two changes is then u and 20v respectively. For the first scenario, this means that the ratio is 0.953 to 20*.04593 or 1.04 to 1. That is the chances of seeing one change are as big as seeing no changes. For the second scenario, this means that the ratio is 0.923 to 20*.08155 or 1 to 1.77. That is the chances of seeing one change are now almost twice that of seeing none.

Let's put all of this together. If we have n sites, m generations and r people within a given generation (and they need not all be in a given generation but then the formula becomes a little more complicated), the probability to see s changes is:

$P(s) = ({}^{t}{}_{s})p^{t-s}q^{s}$

where $t = nmr$.

One can also ask the question another way regarding the choice of q. If we have the case where no changes have taken place, what values of q are consistent with this result to within say a 1% probability?

If $P(0) = 0.99$ for a given value of t then we can find what value of q is consistent with this. Likewise, of we assume that we just got a rare result, of $P(0) = 0.01$, then this will give a larger result for q.

These results limit q to be between 0.0004 and 0.004 based on the Haacke table.

The Rittenhouse family data in Table 2 which goes back to William Rittenhouse born in 1644 show how well the DNA loci results remain stable over 380 years.

Following the above discussion, we can write out the first four terms of the rather large binomial expansion for the number of changes as follows:

$P(0) = p^t$, $P(1) = tp^{t-1}q$, $P(2) = t(t-1)p^{t-2}q^2$, $P(3) = t(t-1)(t-2)p^{t-3}q^3/6$

Since $(p+q)^t = 1$ we can write

$1 = P(0) + P(1) + P(2) + P(3) + \dots$

$1 = p^{t-3}(p^3 + tp^2q + t(t-1)pq^2/2 + t(t-1)(t-2)q^3/6) + \dots$

Now it turns out that q is very small (as will be shown below) so that we can approximate p as unity and t, t-1 and t-2 are all roughly t when t is a large number. Therefore, for these relative terms in the brackets we find 1 for no change, tq for one change, $(tq)^2$ for two changes, and $(tq)^3$ for three changes.

Setting w = tq we obtain an important expression for predicting q given t and w.

We refer to this as extracting q from the relative weightings of the number of changes.
This is a simple formula that can be used to understand the results in any family after many generations and tested over many people. The expression in brackets now becomes our measure of the relative weightings for the number of changes

$1 + w + w^2/2 + w^3/6 + \dots$

(this is just the Taylor series expansion of the exponential exp(w)).

Differences in number of loci for the Rittenhouse family

No. of changes	zero changes	1 change	2 changes	3 changes
occurrences	3	1	2	1
normalized	1	1/3	2/3	1/3
prediction	1	w	$w^2/2$	$w^3/6$

These numbers are not large enough to draw statistical conclusions yet. But as a demonstration, take $w^2/2 = 2/3$, this implies w = 1.155. Now take $w^3/6 = 1/3$, this implies w = 1.260. In principle, all these predictions should give the same result. Clearly, w = 1/3 is not in agreement. One might imagine that with a larger population base that the number of single changes would increase to 3 or 4 and that would imply (from the single change column only) that w = 1 or w = 1.33.

For now, taking w = 1, and using w = tq, we find q = w/t. In the Rittenhouse case, t = nmr = 26*10*7=1820 and we find that an estimate for q = 0.00055.

Conclusions
The field of DNA analysis continues to mature. The ability to extract meaningful information from both a family's history and genetically will benefit from studies of families that have records over several hundred years. Care must be taken in drawing conclusions based on a small number of subjects until a given family has been carefully analyzed over many generations.

Appendix III: An impetus for the need to do mitochondrial studies in tracking the female side

The success of this investigation has recently pointed to another avenue to solve a question on the female side of the family that still has impact on tracing the family of John Haacke. There is an article written in the Chapman History of 18xx as part of the centennial of the United States that states he was from Markham Ontario and his mother was from New York City. (Unfortunately it doesn't say where his father was from.) This family believes that they were distantly related to the Adams' Presidents. (A fact I have never proved.) However, just recently an exciting find from a book in 1907 from Toronto, Canada replicates this story from a line I was until then totally unaware of. It was of course from a daughter of John and Hannah. The story comes from a family named Hutty from Yorkville in Toronto. The fact that these two stories are in such excellent agreement with each other and from two families who probably had not been in contact with each other for generations, lends credence to the material. Still, I have no proof that these Huttys are related. Unless, that is there is a means to follow the female side all the way from Hannah Adams to today. This is a direction we are now pursuing with the hopes of connecting yet another branch to the Haacke family. So clearly, having both male and female tools available for tracking a single family can play an important role in validating family relationships.