

Volquin Momma
Kupfermeister 1650

THE MUMMA SURNAME DNA PROJECT

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INTRODUCTION

This report summarizes the DNA Y-chromosome data that has been obtained for the Mumma Surname DNA Project since its inception in April of 2000 to the present time, more than six years later. This was the first privately funded surname project started with Family Tree DNA shortly after the company was formed and began offering DNA testing services. This data is also available on my web site at <http://www.mumma.org/DNA.htm>.

The MUMMA Surname DNA Project utilizes several unique properties of Y-Chromosome found in the DNA of men to augment and compliment traditional genealogy. First, only males carry the Y-chromosome and it determines whether a person is male or female. The other unique characteristic of the Y-chromosome is the fact it is passed from father to his sons, essentially unaltered or changed, generation after generation. Therefore, a man's Y-chromosome is representative of his male ancestors and thus provides a small window or glimpse of their Y-chromosome "fingerprint" or "signature". As a result, male cousins will also share almost identical DNA Y-chromosome "signatures" since they too share a common male ancestor from whom they received their Y-chromosome. Hence, the DNA from very distant cousins should also match and this is the reason you don't need the DNA from a deceased ancestor to infer their Y-chromosome "signature". There are occasional small mutations (or changes) of the Y-chromosome and it is these mutations that can be used to identify specific branches of a family. At the current state of the technology, the results will not allow the determination of the exact generation two men share a common ancestor, but within a range of generations. Greater precision can be obtained by sampling more men from a family surname.

There are many excellent web pages which discuss and further describe the fundamentals and terminology used in analysis of a man's Y-Chromosome. Instead of repeating much of that information, I refer readers to these sites.

<http://www.familytreedna.com/dna101.html> Family Tree DNA web site tutorial

<http://blairgenealogy.com/dna/dna101.html> Blair DNA Project - DNA 101: Y-Chromosome Testing

<http://www.kerchner.com/dna-information.htm> Kerchner's DNA Testing & Genetic Genealogy Resources Page

http://www.smgf.org/pages/dna_links.jsp An excellent page of links to excellent DNA resource information

Additional information can be found in an excellent book entitled "Trace Your Roots with DNA" written by Megan Smolenyak Smolenyak and Ann Turner in 2004. The results of this Mumma project have also been discussed in a book, "DNA & Genealogy" written by Colleen Fitzpatrick & Andrew Yeiser in 2005.

BACKGROUND AND HISTORY

There were many Mumma surname branches in the United States that could not be connected together through civil or church records. For example, we did not know whether or not the immigrants, Jacob, Leonard and Peter Mumma were brothers, cousins or not related at all. We were not sure from which immigrant various "unconnected" branches descended. They arrived in Philadelphia in 1731, 1732 & 1748 respectively. There were questions as to whether individuals with the Mummey, Moomey surname or the Canadian Mummas descend from a common Mumma ancestor. In addition, the Mumma surname does not exist outside the United States, except for a small isolated group in Estonia. Family traditions and legends suggest a variety of the family origins. Some suggest the progenitors were Swiss Mennonites or from the Alsace-Lorraine region of France and were Huguenots. Other stories suggest that the Mumma family descends from Lucium Mummius, the Roman General who destroyed Corinth in 146 BC. Yet another family tradition suggests the surname originated from one of the ancient kingdoms of Ireland called "Muma". The most likely tradition suggests that the MUMMA spelling is a variation of the surname, MOMMA, which can still be found in Germany today. The Wilhelm Momma family has been documented as living in the Aachen-Stolberg area of Germany (then the Holy Roman Empire) near the intersection of the current German-Belgium-Dutch boarder. This family was first identified in that area around the 1500's and descendants of the Momma family reside there to this day. Unfortunately, there has been little proof or evidence to support these family traditions, all of which probably have some truth in them, but selecting the correct pieces is always difficult. The chart on the next page shows the five major branches of the Momma and Mumma families. The question marks at the top of the Mumma lines indicate the uncertainty of the correct connection to the Momma family.

While researching my own family genealogy, many roadblocks were encountered which prevented identification of specific ancestors. In an attempt circumvent some of these roadblocks, I began collecting and compiling large amounts of family records. Eventually these records were entered into a database that is now available as an on-line searchable database which currently contains over 68,000 Mumma descendants. Many "unconnected" branches or small twigs remain in the database and the use of DNA technology piqued my curiosity as to whether it might possibly be used to determine family connections and guide traditional research. Thus the Mumma Surname DNA Project was conceived. The specific goals for the project were to determine whether or not the various Mumma branches were related and to provide a bank of data that could be used to identify specific branches.

Because of the embryonic state of DNA testing in 2000 for genealogical purposes, it quickly became apparent that it would be desirable to use a testing laboratory associated with a qualified and recognized genetic research team. Data interpretation would obviously need assistance and guidance from genetic scientists. When I began my search of testing companies in April of 2000, there were almost no companies offering genealogical DNA testing services.

My initial search led me to GeneTree, Inc., a company primarily performing DNA testing for paternity cases, but they were expanding their business into DNA testing for genealogical purposes. I felt that GeneTree, who was working in close cooperation with Dr. Scott Woodward at BYU, would be qualified scientifically.

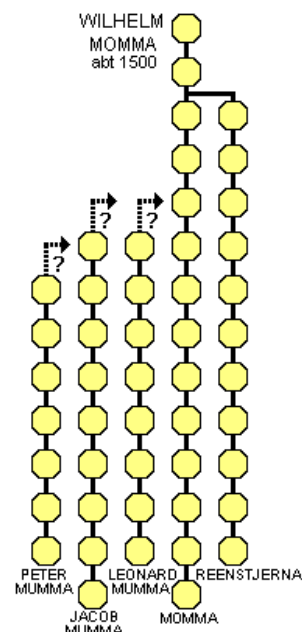
I also found a new startup company by the name of Family Tree DNA, Inc. (FTDNA). This company was founded strictly for the purpose of performing genealogical DNA testing and analysis. They were working closely with Dr. Michael Hammer of the University of Arizona. Dr. Hammer was a highly respected and well published geneticist who had done much research on a variety of Y-chromosome projects.

Contact was also attempted with another new company called "Oxford Ancestors", a British startup company associated with Dr. Bryan Sykes of Oxford University. Dr. Sykes was also investigating the application of DNA testing for genealogical purposes. While Oxford Ancestors described Y-chromosome testing, they were not offering the service at that time.

After discussions with all of these companies, Family Tree DNA was selected as the organization to perform the DNA extraction and analysis for the Mumma Surname Project. This selection was based on a number of factors including, price, the number of "markers" measured (eleven at the time of initial discussions) and the excellent reputation of Dr. Michael Hammer as a respected genetic researcher and scientist.

After selecting FTDNA to perform the DNA analyses, the project goals were refined and e-mail invitations sent to a distribution list of over 500 people associated with the Mumma surname, requesting men with the Mumma surname (or alternate spellings) to participate. The response was extremely positive and the project proceeded swiftly, the details of which are the subject of the remainder of this report.

The Mumma project is still actively gathering additional information with new participants submitting samples for analysis on a regular basis. Project signup can be done at: http://www.mumma.org/dna/dna_signup.htm or through the FTDNA signup link at http://www.familytreedna.com/surname_join.asp?code=J26528



PROJECT OBJECTIVES

The objectives of this project are to answer many of the typical genealogical questions which haunt most family historians and genealogists. The following objectives were established when the project was started in April of 2000. Many of them remain unchanged today.

- Are the American MUMMA and German MOMMA families closely related? Family traditions and legends suggested they were, but no documentation or proof was available.
- Were the original 1731, 1732 & 1748 Mumma immigrants closely related? These immigrants all lived in close proximity to each other in Lancaster County, Pennsylvania, but again no documentation or proof had been found. Intuition suggested they might be brothers or first cousins.
- Are variant surname spellings closely related, including Mumma, Muma, Mummau, Mummah, Mumaugh, Moomaw, Moomau, Moomey, Mumme, Mummey, Reenstierna and Reenstjerna? While the genealogies of many men can be linked together through documentation, there existed many "unconnected" branches and twigs.
- Can DNA "signatures" be determined to uniquely identify specific family branches or trees? Because many "unconnected" family branches exist, it was hoped that DNA testing might provide a tool for identifying to which branch men belonged.
- Can an individual's DNA "fingerprint" be used to connect them to a specific family tree?

In order to achieve many of the project objectives, results from a large number of men were necessary, especially from men whose genealogies were well known and documented. These results would then become the baseline upon which the results from "unconnected" men would be evaluated and compared.

PROJECT RESULTS

These DNA results have been obtained since the year 2000 and are presented below in ten different groupings as an aid in data interpretation. Some of these groups have only recently been created based on the results. In general, the results are grouped according to each person's known progenitor or probable progenitor. Group 1 contains the results of the European participants, namely 2 men with the Momma surname who still live in Germany. The other man in this grouping has the name of Reenstjerna and his ancestors lived in Sweden before migrating to America about 1875. The unusual spelling of his name occurs because several Momma men migrated to Sweden in the late 1500's. They became so important to the economy of Sweden due to their contributions to shipping and mining that the King of Sweden "ennobled" them and gave them the name of "Reenstierna". This branch has used that surname ever since. The connection of these two families is well documented in Swedish and English court records due to lawsuits. Fortunately for genealogists, lawyers can create large mountains of paperwork. Group 2 contains men who are known to have descended from immigrant Jacob Mumma who arrived in America in 1731. Group 3 was created after the 37 marker data was received. Because of a unique result at one marker, their results strongly suggest they too are Jacob descendants, but for whom documentation is lacking. This group will be discussed in more detail in the data interpretation section. Group 4 are men who descended from immigrant Peter Mumma who arrived in 1748 and they also have a unique "signature". Group 5, the largest grouping, are known descendants of immigrant Leonard Mumma who arrived in 1732. Group 6 is another grouping that was created after the 37 marker data became available. From family traditions and the identification of a unique marker, we believe that these men are also descendants of Leonard Mumma, but definite proof is lacking. The remaining groupings are not Mumma descendants, but were included in the project to evaluate similar surname spellings or because of unusual DNA results. Group 7 are primarily men who were unlikely Mumma descendants, were adopted and not expected to match the Mumma family or they are cases of probable infidelity or unknown adoptions. Group 8 contains men with the Mummey surname spelling or shared a similar DNA signature. Group 9 contains the results of 2 men with the Moomey surname who were tested to determine whether or not men with this surname were related to the Mumma family. The final group, Group 10, has two men with the Webb surname and one Moomaw who also matched their DNA signature exactly. The results of each group will be discussed in more detail later.

A brief description of Y-Chromosome testing is given below to help understand some of the terms used in the data table (This description was written by Kevin Blair <http://blairgenealogy.com/dna/dna101.html>).

"The Y-Chromosome has definable segments of DNA with known genetic characteristics. These segments are known as Markers. These markers occur at an identifiable physical location on a chromosome known as a Locus. Each marker is designated by a number (known as DYS#), according to international conventions. You will often find the terms Marker and Locus used interchangeably, but technically the Marker is what is tested and the Locus is where the marker is located on the chromosome.

Although there are several types of markers used in DNA studies, the Y-Chromosome test uses only one type. The marker used is called a Short Tandem Repeat (STR). STRs are short sequences of DNA, (usually 2, 3, 4, or 5 base pairs long), that are repeated numerous times in a head-tail manner. The 16 base pair sequence of "gatagatagatagata" would represent 4 repeats of the sequence "gata". These repeats are referred to as an Allele. The variation of the number of repeats of each marker enables discrimination between individuals."

So, it the repeating patterns of the measured alleles of two people which are compared. If they don't match one to one, then we say a mutation occurred. This allele comparison could be between a father & son, any two men or even a group of men. Mutations occur very rarely and so a comparison of the alleles of closely related men should show few differences. Statistically, a probability can be calculated to determine how close two men are probably related. The total number of mutations or allele differences observed between men is called their genetic distance. A genetic distance of zero means there are no differences in the results being compared and they are probably very closely related.

The first column in the table, "Kit#", is the number FTDNA (Family Tree DNA) assigned to the sample kit. The "M#", is a number that I assigned to each participant, based on the date their sample was received. This was prior to FTDNA assigning kit numbers. The next column, "Surname", is the surname of the participant. The next thirty-seven columns, marked 1 to 37, represent an arbitrary identification marker number assigned to the various loci where the STR repeat values were measured and alleles determined. The DYS# is the specific identification number given to a specific location along the Y-chromosome. DYS markers highlighted in blue have been identified by FTDNA as being markers which they have been observed as mutating faster than average. The row highlighted in yellow just below the DYS names is the "ancestral haplotype" or most likely haplotype of the oldest Momma/Mumma ancestor. (A "haplotype" can be thought of as a person's DNA signature and is simply the series of allele values that were measured.) It is this ancestral haplotype or signature from which the haplotypes of each man have changed or "mutated". The column marked as "Mutate" represents the total number of mutations observed for each man, as compared to the "ancestral haplotype". This number is also referred to as the "genetic distance" of each man from the reference or "ancestral" haplotype. The column marked "HaploGroup" lists the haplogroup to which each individual belongs. Haplogroups identify to which migration group a person's ancient ancestors belonged when they migrated out of Africa to Asia and Europe. The far right hand column is a modified "Henry" reference identification number that has been assigned to all Mumma descendants listed in the Mumma surname database. This database contains over 68,000 descendants or spouses of the Momma or Mumma families. <http://www.mumma.org/databases/mumma/mumma.html> The Henry reference number is a generation identification number which uniquely codes each person based on the number of generations they are removed from the progenitor of their branch. Each number typically represents his birth order at that generation. These numbers are further explained and identified in the notes on the page following the data table.

(Note: A special modified Henry numbering system is used to identify each individual in the chart. The top individual in a particular genealogical tree is given an identifying number. At each new generation an additional digit is added to each descendant and the numeric value added is typically the child's order of birth. 1st child = #1, 2nd child = #2, 9th child = #9, 10th child = #0, 11th child = #a, 12th child = #b, etc. Therefore, a seven digit number means that the person is the sixth generation down from the top individual. If a group of individuals cannot be linked to one of the known Mumma immigrant trees, then that group is assigned a unique "U" number at the beginning of their Henry number. Individuals not listed in the Mumma database have only their surname listed.)

- Henry Ref# beginning with 1 = Descendants of Jacob Mumma - arrived America in 1731 & were primarily Mennonite.
- Henry Ref# beginning with 2 = Descendants of Leonard Mumma - arrived America in 1732 & were Mennonite & Lutheran/Reformed.
- Henry Ref# beginning with 4 = Descendants of Peter Mumma - arrived America in 1748 & were primarily Reformed.
- Henry Ref# beginning with E = Descendants of Wilhelm Momma - b. ~1543 in Germany where the family remains today.
- Henry Ref# beginning with U07 = Descendants of David Muma - b. 1760 in PA, appears in Page Co., VA ~1810.
- Henry Ref# beginning with U21 = Descendants of Jacob Muma - b. ~1750 migrated to Canada ~1800. Known as the Canadian Mumas.
- Henry Ref# beginning with U30 = Descendants of John Mumma - b. bef 1750 migrated to Cumberland County, PA about 1803
- Henry Ref# beginning with U45 = Descendants of Christian Mummer - b. 1768 surnames of Moomau, Moomaugh, Moma
- Henry Ref# beginning with U46 = Descendants of David Mumma - b. ~1790 appears Franklin Co., PA ~1810.
- Henry Ref# beginning with U51 = Descendants of George Mummaugh - b. ~1809 appears in Carroll Co., MD in the 1840 census.
- Henry Ref# beginning with U57 = Descendants of Samuel Mumma - b. ~1822. Appears in Lykens/Wiconisco townships of Dauphin Co.in 1860
- Henry Ref# beginning with U62 = Descendants of John Mumma - b. ~1750 in Lancaster Co. PA, migrated to York Co., ~1780.
- Henry Ref# beginning with U74 = Descendants of Jesse N. Mumma - b. 1833 - resided in Rocky Ridge, MD
- Henry Ref# beginning with U76 = Descendants of Elias Bertram Mumma - b. ~1830 in Lancaster County. His grandmother was a Mumma.

INTERPRETATION OF THE RESULTS

Data interpretation is the most difficult task in evaluating DNA test results. When this surname project was first begun five years ago, there were essentially no results available from other projects to use as comparison or provide guidance as to how often mutations might be observed and when observed, what they meant. Since the primary objective of this project was to determine the relatedness of men with the Mumma surname, the task was reduced to simply gathering the data into a table and noting the number of mutations observed between men with known relationships. This allowed me to estimate how many mutations I might expect between men who are known to share a common ancestor.

It should be noted from the data table that all men do not have the same number of results. Currently, FTDNA offers measurements at 12, 25, 37 and now, 67 marker locations. Initially, only 12 markers were measured for all men. Because of costs, only the DNA of men who were expected to share a common Mumma ancestor had their DNA analyzed at additional marker locations as they became available.

MUMMA/MOMMA Haplotype -

A person's haplotype (which can be thought of as their DNA Y-Chromosome signature) is simply the allele values that have been measured at the different marker locations. There is no specific number of markers or order in which they must be presented. Haplotype comparisons can be made with results from other testing companies as long as the allele values of similar markers are compared.

As observed from the alleles recorded for each man in the data table, there is one allele value at each marker location which is commonly shared by a majority of the men. This can be done for each group of men and a common haplotype determined for each group. The collection of all these commonly shared alleles is often called the "modal" haplotype. This value is used as the reference by which all individual haplotypes are compared. Any allele difference from the modal haplotype is considered as a "mutation". Additionally, a "modal" haplotype can be determined which represents the surname "ancestral" haplotype or the likely haplotype of the oldest common ancestor for that surname.

The MUMMA haplotype was determined by examining the most common allele values that were observed at each marker or locus. When evaluating the 12 and 25 marker data, determining the MUMMA Modal Haplotype was rather simple as it was the most frequently observed allele at each marker. In the case of 12 markers, 32 men had identical haplotypes so these allele values become the MUMMA Modal Haplotype. Examining the 25 marker data shows that 22 men shared an identical haplotype so these allele values became the 25 marker MUMMA modal haplotype. When examining the 37 marker data, 9 men share a common haplotype and it would likely be the MUMMA Modal Haplotype. However, several of the groups did not share this haplotype, including the European Momma men. We would expect that both European and American men would likely share the same haplotype from a common European ancestor. So the large number of participants in Group 5 (immigrant Leonard Mumma descendants) caused a bias of the data. To eliminate this bias, a single haplotype was determined for each of the groups and then the four group haplotypes were examined to determine the likely "ancestral" haplotype. This ancestral haplotype is shared by only 4 men which use both the Momma and Mumma surname spelling. This 37 marker haplotype I have defined as the MOMMA Surname Ancestral Haplotype.

Using this MOMMA Ancestral Haplotype, the results of all men were evaluated and the of mutations determined. The Momma ancestral haplotype is shown in the row near the top of the table and highlighted in yellow. The total number of mutations for each participant are added together and the total is recorded in the column highlighted in yellow and called "MUTATE". This total value is also called a persons "Genetic Distance" by FTDNA. As a visual aid and to make the mutations stand out and become obvious, the cells containing mutations have been colored differently.

Mutations While it would seem rather straight forward to determine the number of mutations between a reference haplotype or that of another man, a complication arises with two specific markers. The first is DYS389ii. DYS389 is a special marker that is composed of two different allele values at the same location. DYS389i is the first allele for this marker, however the second allele measured at DYS389ii includes the DYS389i allele. To accurately determine whether a mutation occurred along the second part of the marker, one needs to compare the values of DYS389ii minus DYS389i. Some laboratories report the second allele value as DYS389b which is DYS389ii-DYS389i. A more detailed explanation can be found at <http://www.roperld.com/Y-Markers.htm>. In the case of the Mumma project, it makes no difference since no mutations have been observed on DYS389i or DYS389ii for all men who share a common Momma ancestor.

The other marker that needs some explanation is DYS464, a highly polymorphic marker. This marker can have up to 7 copies at different locations on the Y-Chromosome, however the normal number of copies are 4 and they are designated as DYS464a-d. In the case of the Mumma project, 5 copies were measured for only one man. FTDNA reports the number of alleles for these copies from low to high. The number of mismatches must be then be evaluated as to whether or not they are a result of the way the data is presented. Further, for this marker, an allele difference of more than one is only counted as a single mutation. I.e. the reporting of allele 17 at DYS464b for one man and allele 14 for another man is only considered to represent a single mutation. This is called the infinite allele model and I have used it for all markers. I believe this is a realistic approach when comparing the results of men who are expected to share a common ancestor. This is how the values represented in the column labeled MUTATE were calculated. Again, a more detailed explanation of DYS464 can be found at the same URL listed in the above paragraph. FTDNA calculates their genetic distances slightly differently in that they treat some markers as an infinite model and other using the stepwise model where an allele difference between a 16 and 18 is counted as two, one step mutations and not as a single, two step mutation. The difference is insignificant in the Mumma project as there is only one instance of a two step mutation for the men who share a recent common ancestor.

Genetic Distance There are several ways to determine the Genetic Distance. Either by comparing a man's haplotype with a known reference, such as the Momma ancestral haplotype discussed above or by comparing mutation differences between 2 men. The two methods yield surprisingly different results and possible interpretations. The data table with all of the results computes the genetic distance for each person against the MOMMA ancestral haplotype, which was defined. Another way to present the data is by comparing the Genetic Distance between any two men. Such a comparison is shown in the table below. The table was created using the Y-Utility tools available at Tim McGee's web site <http://www.mymcgee.com/tools/yutility.html> The genetic distances are shown for 56 closely related men in the Mumma project who have had their DNA analyzed at 37 markers. Each man's kit number is displayed both vertically and horizontally across the top. The intersection of the kit# for the same person has a number 37 recorded. This simply represents the number of markers measured. The first column and row called Modal represents the Momma ancestral haplotype which was the likely original haplotype of each man prior to their haplotypes mutating to their present state.

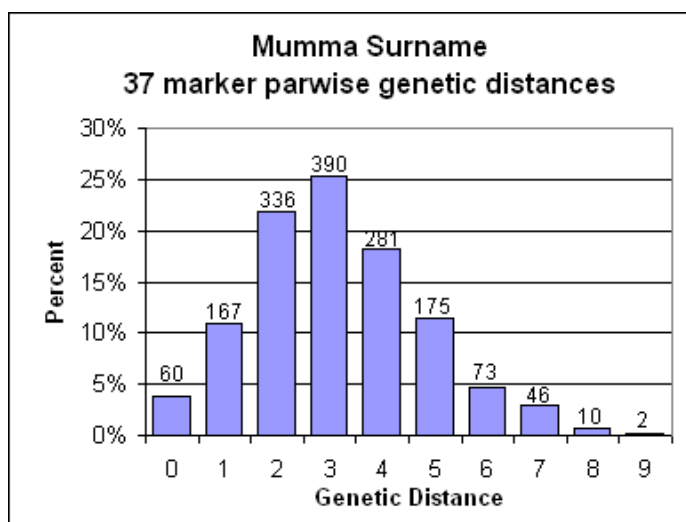
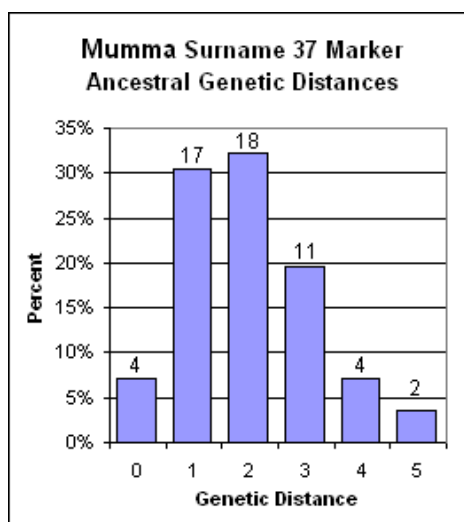
Genetic Distance

ID	M-01	M-02	M-03	M-04	M-05	M-06	M-07	M-08	M-09	M-10	M-11	M-12	M-13	M-14	M-15	M-16	M-17	M-18	M-19	M-21	M-22	M-25	M-26	M-27	M-30	M-31	M-33	M-34	M-35	728	1860	1861	1862	3314	3315	3316	3317	7055	7056	7057	10612	10613	10614	10615	10617	10619	10975	20816	21370	21946	21947	21948	39581	39609	62454																																															
Modal	37	1	1	1	1	3	1	1	2	1	2	0	2	0	1	3	3	4	2	1	3	3	2	1	2	4	3	5	2	0	2	5	1	4	2	1	3	2	2	3	3	0	2	3	3	0	2	7	0	5	6	7	1	0	6	1	2	1	0	6	1	7	1	0	6	1	9	1	0	9	7	5	1	0	8	1	6	2	1	9	4	7	2	1	9	4	8	3	9	5	8	1	3	9	6	0	9	6	2	4	5	4
M-01	1	37	0	0	2	0	2	3	1	1	1	1	0	2	2	3	1	0	2	2	1	0	3	5	2	6	1	1	1	4	0	3	1	2	2	1	3	2	2	1	3	3	3	2	2	1	2	1	3	2	2	3	5	4	0	2																																														
M-02	1	0	37	0	2	0	2	3	1	1	1	1	0	2	2	3	1	0	2	2	1	0	3	5	2	6	1	1	1	4	0	3	1	2	2	1	3	2	2	1	3	3	3	2	2	1	2	1	3	2	2	3	5	4	0	2																																														
M-03	1	0	0	37	2	0	2	3	1	1	1	1	0	2	2	3	1	0	2	2	1	0	3	5	2	6	1	1	1	4	0	3	1	2	2	1	3	2	2	1	3	3	3	2	2	1	2	1	3	2	2	3	5	4	0	2																																														
M-04	3	2	2	2	37	2	4	5	3	3	3	3	2	3	4	4	3	2	0	4	3	2	5	7	4	6	3	3	4	2	3	1	4	4	1	5	4	4	3	5	3	5	4	3	1	4	3	5	3	4	5	6	4	2	4																																															
M-05	1	0	0	0	2	37	2	3	1	1	1	1	0	2	2	3	1	0	2	2	1	0	3	5	2	6	1	1	1	4	0	3	1	2	2	1	3	2	2	1	3	3	3	2	2	1	2	1	3	2	2	3	5	4	0	2																																														
M-06	1	2	2	2	4	2	37	3	2	3	1	1	1	2	4	4	3	2	4	4	3	2	3	5	4	6	3	1	3	6	2	5	3	2	4	3	3	2	4	1	3	3	3	2	2	3	2	2	3	3	4	2	4																																																	
M-07	2	3	3	3	5	3	3	37	3	2	2	4	2	3	5	3	6	4	3	5	3	6	4	3	5	3	6	2	2	4	5	3	4	4	3	5	2	3	4	4	3	4	3	4	3	3	3	3	3	3	3	3	4	3	3																																															
M-08	1	1	1	1	3	1	2	3	37	2	1	2	1	1	3	3	4	2	1	3	3	2	1	3	5	3	6	2	1	2	5	1	4	2	3	2	3	3	3	1	3	3	3	2	2	2	2	3	2	2	3	5	4	1	3																																															
M-09	2	1	1	1	3	1	3	2	2	37	2	2	2	1	3	3	4	2	1	3	3	2	1	4	6	3	6	2	2	3	1	2	2	3	3	2	4	3	3	2	4	4	4	3	3	2	4	4	4	3	3	2	4	6	5	1	3																																													
M-10	0	1	1	1	3	1	1	2	1	2	37	2	0	1	3	3	4	2	1	3	3	2	1	4	6	3	5	2	0	2	5	1	4	2	1	3	2	2	3	2	4	1	3	0	2	2	1	1	2	2	1	2	4	3	1	3																																														
M-11	2	1	1	1	3	1	1	4	2	2	37	2	1	3	3	3	2	2	1	3	3	2	1	4	6	3	7	2	2	2	5	1	4	2	3	3	2	4	1	3	2	4	4	4	3	3	2	4	4	3	2	4	3	3	4	5	1	3																																												
M-12	0	1	1	1	3	1	1	2	1	2	0	2	37	1	3	3	4	2	1	3	3	2	1	2	4	3	5	2	0	2	5	1	4	2	1	3	2	2	3	3	0	2	2	2	1	1	2	1	2	2	1	2	4	3	1	3																																														
M-13	1	0	0	0	2	0	2	3	1	1	1	1	37	2	2	3	1	0	2	2	1	0	3	5	2	6	1	1	1	4	0	3	1	2	2	1	3	2	2	1	3	3	3	2	2	1	2	1	3	2	2	3	5	4	0	2																																														
M-14	3	2	2	2	3	2	4	5	3	3	3	3	2	37	4	5	3	2	3	2	2	5	7	4	7	3	3	3	2	2	4	3	2	5	4	4	3	2	5	4	4	3	5	4	4	4	2	4	5	4	4	5	7	6	2	2																																														
M-15	3	2	2	2	4	2	4	3	3	3	3	3	2	4	37	5	3	2	4	2	3	2	4	6	4	8	1	3	3	6	2	5	3	4	4	3	4	4	4	3	4	4	4	4	4	5	4	4	3	4	4	4	4	6	5	2	2																																													
M-16	4	3	3	3	4	3	3	6	4	4	4	2	4	3	5	37	4	3	4	5	4	3	6	8	5	7	4	4	4	7	3	6	4	5	4	4	6	1	5	4	6	6	6	5	4	4	5	4	6	4	5	6	5	6	3	5																																														
M-17	2	1	1	1	3	1	3	4	2	2	2	2	1	3	3	4	37	1	3	3	2	1	4	6	3	7	2	2	2	5	1	4	2	3	3	2	4	4	3	3	2	4	4	4	4	3	3	2	3	2	4	3	4	6	5	1	3																																													
M-18	1	0	0	0	2	0	2	3	1	1	1	1	0	2	2	3	1	0	2	2	1	0	3	5	2	6	1	1	1	4	0	3	1	2	2	1	3	2	2	1	3	2	2	1	2	1	3	2	2	3	5	4	0	2																																																
M-19	3	2	2	2	0	2	4	5	3	3	3	3	2	3	4	4	3	2	37	4	3	2	5	7	4	6	3	3	4	2	3	1	4	4	1	5	4	4	3	5	3	5	4	3	1	4	3	5	3	4	5	6	4	2	4																																															
M-21	3	2	2	2	4	2	4	3	3	3	3	3	2	3	2	5	3	2	4	37	2	2	4	6	4	8	1	3	3	5	2	4	3	4	2	3	4	4	4	3	4	4	4	3	4	5	5	4	4	3	4	1	4	4	6	5	2	1																																												
M-22	2	1	1	1	3	1	3	4	2	2	2	2	1	2	3	4	2	1	2	3	7	1	4	6	3	7	2	2	2	4	1	3	2	2	4	3	3	2	4	4	3	3	2	4	4	4	3	3	2	3	1	4	3	4	6	5	1	2																																												
M-25	1	0	0	0	2	0	2	3	1	1	1	1	1	0	2	2	3	1	0	2	2	1	0	3	5	2	6	1	1	1	4	0	3	1	2	2	1	3	2	2	1	3	2	2	1	3	2	2	1	3	2	2	3	5	4	0	2																																													
M-26	2	3	3	3	5	3	3	3	4	2	4	2	3	5	4	6	4	3	5	4	4	3	37	2	5	7	3	2	4	7	3	6	4	3	5	4	0	5	5	2	0	4	4	3	3	4	3	4	0	3	3	0	4	3	3	4																																														
M-27	4	5	5	5	7	5	5	5	6	4	6	4	5	7	6	8	6	5	7	6	6	5	2	37	5	7	5	4	6	7	5	8	6	3	7	6	2	7	7	4	2	6	6	5	5	6	5	6	2	5	5	2	6	5	6																																															
M-29	3	2	2	2	4	2	4	5	3	3	3	3	2	4	4	5	3	2	4	4	3	2	5	37	6	3	3	3	4	2	5	3	2	4	3	5	4	4	3	5	5	2	4	3	2	3	5	4	2	5	7	6	2	4																																																
M-30	5	6	6	6	6	6	6	6	6	5	7	5	6	7	8	7	7	6	6	8	7	6	7	6	37	7	5	7	5	6	6	5	4	7	5	7	6	8	5	7	5	7	6	6	5	6	7	7	6	6	7	9	8	6	8																																															
M-31	2	1	1	1	3	1	3	2	2	2	2	2	1	3	1	4	2	1	3	1	2	1	3	5	3	7	37	2	2	5	1	4	2	3	3	2	3	3	3	2	3	4	4	3	3	2	3	4	4	3	3	2	3	3	5	4	1	1																																												
M-32	0	1	1	1	3	1	1	2	1	2	0	2	0	1	3	3	4	2	1	3	3	2	1	2	4	3	5	2	37	2	5	1	4	2	1	3	2	2	3	0	2	2	1	1	2	1	2	1	2	2	1	2	4	3	1	3																																														
M-34	2	1	1	1	3	1	3	4	2	2	2	2	1	3	3	4	2	1	3	3	2	1	4	6	3	7	2	2	37	5	1	4	2	3	3	2	4	3	3	2	4	3	3	2	4	3	3	2	4	3	3	2	4	3	3	4	6	5	1	3																																										
M-35	5	4	4	4	4	6	5	5	3	5	5	5	4	3	6	7	5	4	4	5	4	4	7	7	4	5	5	5	37	4	1	3	4	5	3	7	6	6	5	7	5	7	6	6	3	6	4	7	6	6	7	9	8	4	4																																															
728	1	0	0	0	2	0	2	3	1	1	1	1	0	2	2	3	1	0	2	2	1	0	3	5	2	6	1	1	1	4	0	3	1	2	2	1	3	2	2	1	3	3	3	2	2	1	2	1	3	2	2	3	5	4	0	2																																														
1860	4	3	3	3	3	5	4	4	2	4	4	3	2	5	6	4	3	3	4	3</																																																																																		

Initially focus on just the first two columns, namely ID (Kit #) and "Modal". The Modal column thus lists the genetic distance between each participant and the Momma Ancestral Haplotype. The largest genetic distance observed in this column is 5 recorded for the Reenstjerna participant and also for a descendant of immigrant Leonard. Both of these men are at least 12 generations away from the probable common Momma ancestor so observing 5 mutations is quite possible and likely. The colors on the chart show the criteria FTDNA suggests for the probability of relatedness, namely 5 is the maximum number of mutations they feel are possible and still be closely related. And, to have 5 mutations and still share a common ancestry, the mutations must have occurred on the more "volatile" markers (those that mutate more frequently) and the men must share a common surname. Both of these men satisfy this criteria.

However, if you look at the number of mutations observed between any two men, the greatest Genetic Distance recorded is 9 mutations between Kit# 30, a Reenstjerna, and Kit# 21948, a descendant of immigrant Peter. So, if one was just looking at the genetic distance between these two people, you would conclude that they would not share a recent common ancestor, but we know that is not true. Hence, you must be cautious when comparing the genetic distance between two men and not comparing each man to an ancestral or modal haplotype. All of the men on this chart are known to share a common ancestor within the last 12 generations. And as you look closely you will find a number of instances where genetic distances of 6, 7, 8 & 9 are recorded. This will serve to illustrate the difficulty in determining whether or not two men share a common ancestor in the recent past. The consequences of this large genetic distance will be discussed later. The lack of any color used in a box of this table indicate that the two men are not related, but this is known to be wrong for the case just described for the Mumma project.

Another way of expressing the same genetic distance information is by graphically plotting the percentage of genetic distances between pairs, or simply "pairwise differences". The chart on the left only plots the genetic distance for each man compared to the Momma Ancestral Haplotype. About 35% of the men had 2 mutations. About 90% of the mutations lay between 1 and 3 mutations. If the genetic distance between all pairs of men is plotted (chart on the right), the spread in the genetic distance almost doubles with 25% of the pairs to 3 mutations. This also demonstrates that mutations are expected and it becomes unusual if no mutations are observed.



Relatedness -

The primary purpose of this project is to determine whether two men, or a group of men, share a recent common ancestor and are thus "closely related". I say recent because we all shared a common ancestor many tens of thousands of years ago which is far beyond the genealogical timeframe in which I have interest. The earliest common Momma ancestor has been identified as living in the area of Aachen Germany in the late 1400s to early 1500s. Since that time, about 13-14 generations have occurred. It is highly doubtful that new records will be uncovered which identify any Momma ancestors who lived more than a few generations prior to this time.

Therefore I consider men to share a "recent" common ancestor if that ancestor lived up to 20-30 generations ago. Using the time between generations of 35 years for Momma males, my longest time of interest is about 700-1000 years ago. It is highly unlikely that any documentation will be uncovered that could verify such a common ancestor.

The relatedness of two men therefore depends on their genetic distance. The more mutations observed, the less likely that a man will share a recent common ancestor with another man or a group of men. Criteria for probable relatedness, can be based on observing their genetic distance and comparing it with their known genealogies. An alternate way is to calculate the probability of relatedness the mutation rates of the various loci and genetic distance. Both methods have been used in the Mumma Surname Project.

Relatedness by Observation - Once the genetic distance for each participant was determined, the main question then arises is how the various groups of men are inter-related. When this project began, almost no criteria was available which was backed up with data, especially for a group of men with a common surname. Therefore, I determined a criteria of relatedness by looking at the genetic distance for each man and noted whether or not the men were likely related. For the initial 12 marker data, a simple "relatedness" criteria was developed. All of the men who were likely Mumma\Momma descendants either showed no mutations or at most, 1 mutation. All unrelated men had genetic distances of 3 or more. There was one man thought to be a Mumma descendant, but he had 4 mutations and was thus deemed to not share a recent common ancestor with the Mumma family. So for 12 markers, the criteria was that a man could not have more than 1 mutation and still descend from a common Mumma ancestor. That initial criteria, developed by observation, is still valid after evaluating the results of more than 60 men and is identical to that suggested by FTDNA. The converse, however, is not true. Just because a man has a genetic distance of zero for 12 markers, when compared with the Mumma/Momma modal haplotype, does not necessarily mean he shares a common ancestor. It simply means that he might be closely related, but there is insufficient data to make that determination. If he doesn't match, however, one can say with great certainty that he is NOT related. These tests are wonderful at proving a negative answer.

Similarly, genetic distances were noted with 25 markers for the 56 men who we believe share a recent common ancestor. In this case, there are only two men who had a genetic distance of 3 from the Momma Ancestral Haplotype whereas all of the rest were either exact matches or had 1 or 2 mutations. So, the observations suggested that men with 0, 1 or 2 mutations at 25 markers are very likely to be related and those with 3 mutations can only be considered if those mutations were on the more volatile markers and they share the Mumma/Momma surname. Again, this was the case and it became my criteria for relatedness.

FTDNA has also analyzed a large amount of data and have posted relatedness charts on their web site which can be use to determine the likelihood whether people are related. I have combined their information with my own observations of the Mumma data and developed the following "relatedness chart". The table lists the likelihood of relatedness based on the genetic distance from the Momma ancestral haplotype. As we saw in the prior genetic distance charts, the distances are really only valid when comparing men against a modal or ancestral haplotype.

Relatedness	12 Marker	25 Marker	37 Marker	67 Marker
Closely related – A high likelihood you are VERY closely related	-	0-1	0-2	0-3
Possibly related – Other positive proof needed, i.e. same surname	-	2-3	3-5	4-6
Doubtful of relationship – Very unlikely that the person is related	-	4	6	7
Not Related – This number of mutations preclude a close relationship	3 or more	5 or more	7 or more	8 or more

The results of the Mumma study clearly showed that men which displayed no mutations with a 12 marker test were Mumma descendants. A search of the Y-Search database maintained by FTDNA database and the SMGF database maintained by Sorenson Molecular Genealogy Foundation revealed a combined total of only 52 men out of 41,000 who shared the exact same 12 marker Momma ancestral haplotype. This did not include the 33 men in the Mumma Surname project who share this ancestral haplotype. Further, an examination of the FTDNA RAO (Recent Ancestral Origins) database of 72,289 men, representing 19587 unique haplotypes shows that 98 men share the same haplotype, including the 33 Mumma men. The surnames of the other matching men were quite varied with ancestral origins from many countries. This simply illustrates that even a perfect match of 12 out of

12 markers is sufficient to determine the sharing of a "close" common ancestor. For this reason, the results of a 12 marker test are primarily useful to determine that a man DOES NOT share a close relationship with another man or a surname group.

Similar evaluations of RAO database were done for 25 and 37 markers. In the case of 25 markers, the RAO database contains 35,027 results with 24280 unique haplotypes. there are 43 men who match exactly or are within one mutation of the Momma Ancestral Haplotype. All 43 of these men are part of the Mumma Surname study. Thus, we can conclude with 25 markers, anyone with a maximum of 1 mutation will very likely share a recent common ancestor with the Mumma family. However, in the case of Kit# M-30 (Reenstjerna), he and another Mumma in the project had a genetic distance 5 between them, yet an examination of the RAO revealed a man with a genetic distance of 1 from him, but is not related. This suggests that even 25 markers are insufficient to make definitive statements and conclusions about relatedness.

For 37 markers, the RAO database contains 20,015 DNA results with 17,869 unique haplotypes. 37 men are within 2 mutations of the Momma Ancestral Haplotype for 37 markers. Again, all of the 37 men within 2 mutations are part of the Mumma Surname Project. Of interest, the fellow in the RAO who matched Kit# M-30 by 1 mutation at 25 markers did not match him within 4 mutations at 37 markers.

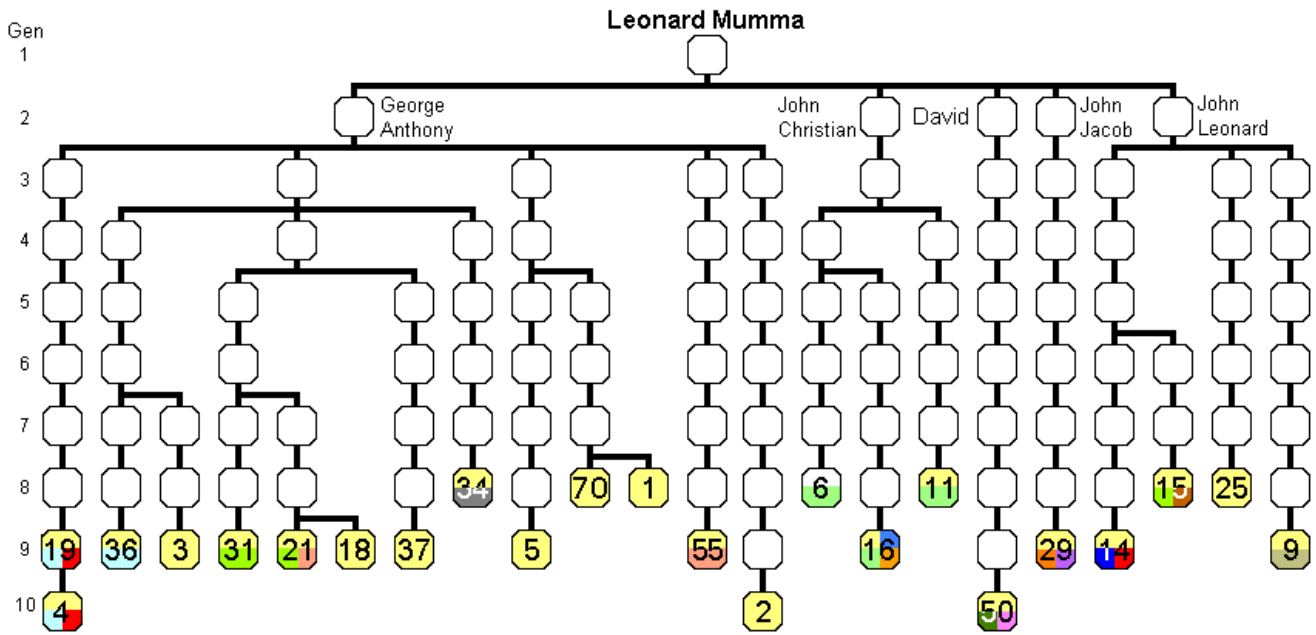
The column for 67 markers has been developed from the results of 10 men that have been received. Only 7 mutations were observed and of those 7, one man's results contained 4 mutations. His results are being re-evaluated. These data certainly suggest the last 30 markers are not highly volatile, at least for the Mumma project.

Mutation Rates -

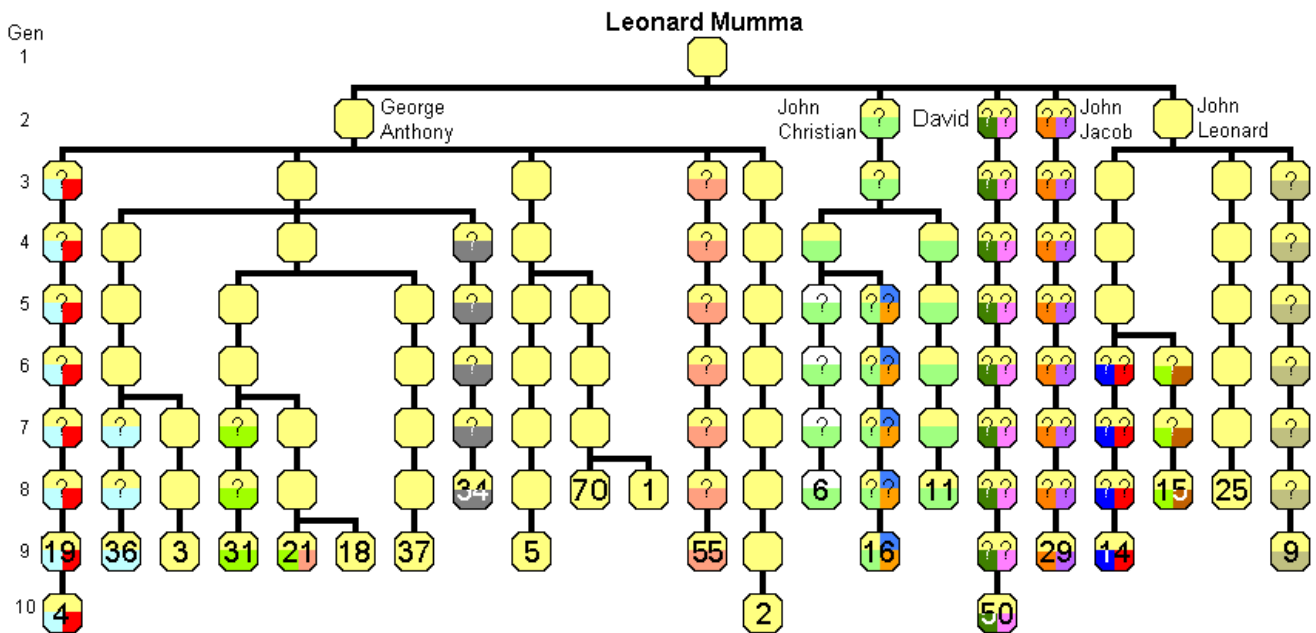
The number of mutations that one expects to observe at any marker is dependent of the mutation rate for each particular marker. Some mutate frequently whereas others have much lower mutation rates. A European study of father-son pairs recorded an average mutation rate of 0.0037 using 15 loci. Another study of 9 loci showed an average mutation rate of 0.0021 (about 1 mutation in 500 births).

I determined mutation rates for the Mumma Surname project so that project specific rates could be used to predict relatedness and the probability that two people share a common ancestor in the past. In order to determine such rates accurately, it is necessary to determine the number of mutations and to know how often there was an opportunity for a mutation to occur, i.e. a birth. To illustrate how this is done, we will look at the descendants of immigrant Leonard Mumma. The genealogies for these men are well known so the exact number of births, or "opportunities for mutations" to occur, could be determined exactly. Care must also be exercised to insure that "shared" mutations are not counted twice or other mutations missed.

As an aid in this process, I created a descendant chart for immigrant Leonard (shown on the next page) for whom we have the greatest amount of DNA data and genealogical pedigrees. 23 men and their interrelationships are shown in the descendant chart below. For this chart, the participants are shown at the bottom of each descendant line and are given different colors to denote their specific mutations when compared to the Momma ancestral haplotype. In general, the same color represents the same mutation at a specific marker. If there are multiple colors in a box, then that man's results showed multiple mutations and the number of mutations could be thought of as their genetic distance from the Momma ancestral haplotype shown in yellow in the data table at the beginning of this report.

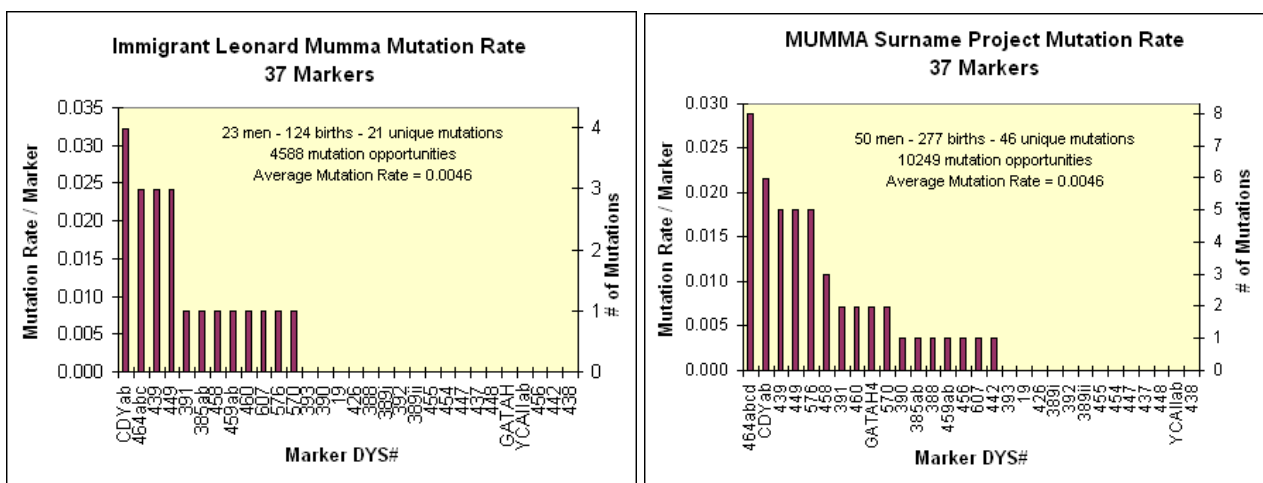


There is one haplotype, denoted by the solid yellow color, which is shared by 8 men. This represents a single mutation at DYS570 for all Leonard descendants. For these men, this was their only mutation which must have been passed down to them from Leonard, the common ancestor in this chart. Since this haplotype is found in two branches of two of Leonard's sons, then Leonard also must have had this haplotype. Hence, all of the boxes above the ones marked in solid yellow can be colored yellow. After that, the remaining boxes are shaded with that persons mutation colors. Then the boxes above those with multiple colors are colored until a solid yellow box is encountered. We know no mutations could have occurred above this intersection or his close cousin would also have shared that mutation.



The boxes which contain question marks indicate that there is insufficient information to determine at what exact generation the mutation(s) took place. The mutation could have occurred with that persons birth or several generations above.

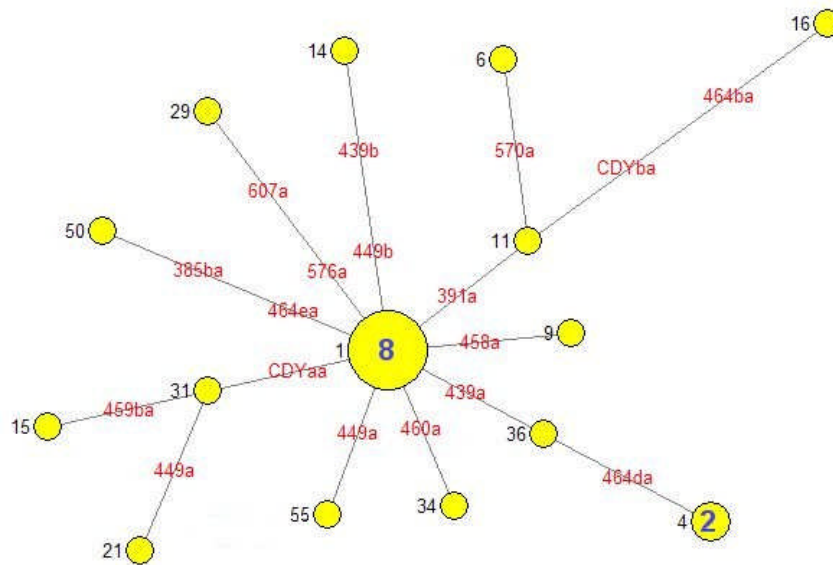
By counting the number of boxes which represent births and counting the number of single event mutations, a simple calculation can be made of the average mutation rate for the descendants of Leonard Mumma. In this case of 23 men, 21 mutations resulted from 124 births for 37 markers. This calculates to an average mutation rate of 0.0046. This information is shown graphically below. Rates calculated for just the 12 and 25 marker results are 0.0034 and 0.0042, respectively. Similar descendant charts were created and calculations performed for all of the groupings of Mumma men for which I had known genealogies. The resulting data was then combined to create an overall mutation rate specific to the Mumma Surname Project. The overall rates determined from 50 men with 46 unique mutations from 277 births (10249 mutation opportunities) were 0.0030 for 12 markers, 0.0039 for 25 markers and 0.0046 again for 37 markers. These rates are higher than that determined from prior European studies, but very similar and consistent to rates determined by other surname projects and FTDNA. Since these rates are derived from the actual Mumma data, they are used in all calculations requiring a mutation rate. Both DYS464abcde and CDYab had the highest number of mutations and mutation rates. It is interesting that the mutation rate remained the same when the mutations from the known genealogies of the other immigrants were combined.



Cladograms

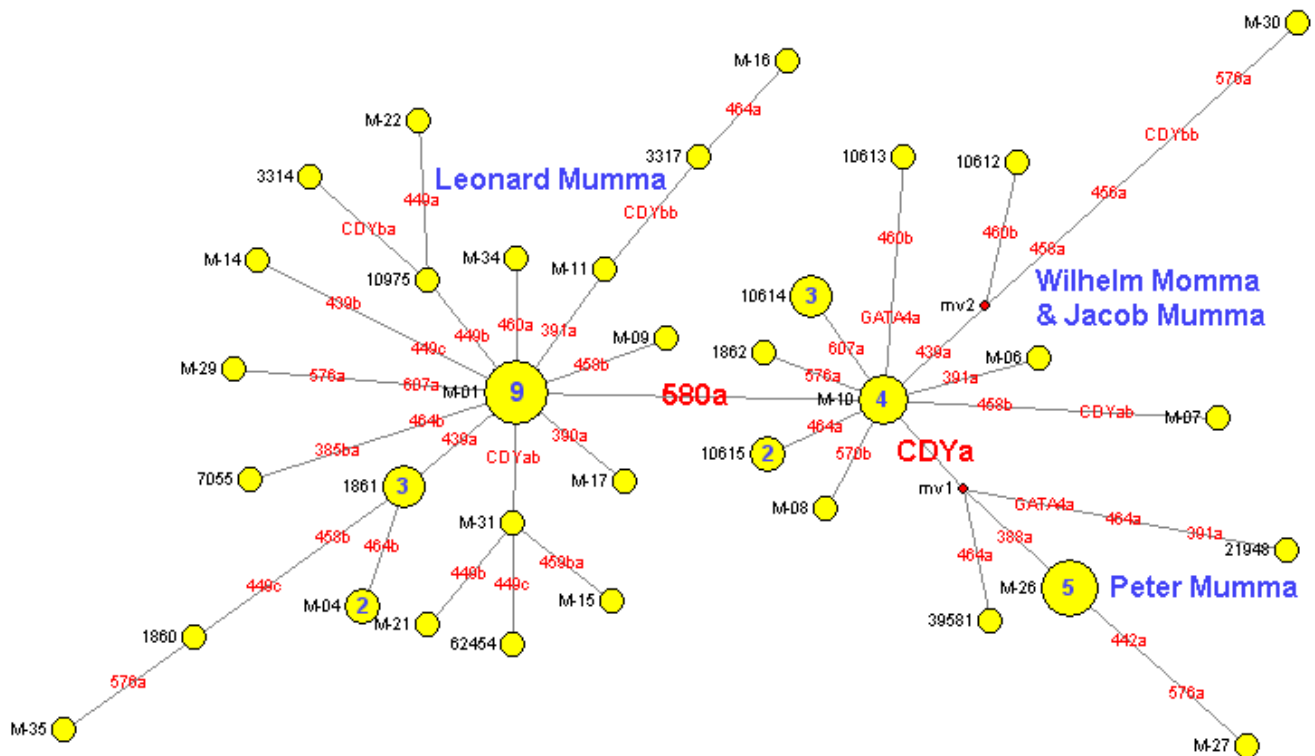
An alternate way of viewing the same information about the mutations of the descendants of immigrant Leonard is to create a Cladogram. These charts determine an interconnection of all the haplotypes using the minimal number of mutations (rule of parsimony). It may or may not accurately depict ancestor-descendant relationships that a genuine phylogenetic tree would show, but It is useful, however, for evaluating potential relationships.

The chart was created for Leonard's descendants using a free phylogenetic network software program offered by Fluxus Engineering <http://www.fluxus-engineering.com/sharenet.htm>. This program determines the simplest configuration which has the least number of interconnections or mutations. For these charts I used the Reduced Median algorithm with a Reduction Threshold of 1. In the chart shown below, the yellow circle in the center represents the same 8 men who share the same haplotype which is the "modal" haplotype for immigrant Leonard. Radiating out from the central circle are spokes which connect to smaller circles. These circles are men whose haplotype is different from the modal haplotype by one or more mutations. The DYS number, shown in red, represents a specific marker or locus location which mutated.. The black number beside each circle represents that same Mumma project number shown in Leonard Mumma pedigree chart shown earlier. The Mumma project numbers are shown because they take up less space than their corresponding FTDNA kit#. The only thing that is misleading with this method is it can, and does, understate the number of mutations. This can occur when 2 men on different parts of the descendant tree undergo a mutation of the same locus, but it is not a mutation which they share. This style of charting nicely identifies the "modal" haplotype and the mutations which radiate away from that haplotype. The advantage of viewing the information in a descendant chart is you can see if any inconsistent mutations occur.



Another chart was created in which all 56 Mumma men listed in the data table, groups 1 to 6, are included. These are men who are all closely related. Again the yellow circles represent identical haplotypes and the interconnections between them represent mutations. In this chart we can now see the separation of the data into several branches developing of immigrants Leonard, Peter and Jacob. These results show that immigrant Jacob closely matches the haplotypes of Wilhelm Momma who is the likely generator of all these men.

For clarity, only the DYS numbers for two of the mutations are shown in red. The size of the circles are proportional to the number of haplotypes they represent. The black numbers are one of kit numbers the circle represents. This chart nicely shows immigrant Jacob and the European Momma/Reenstierna families are separated by single mutations at DYS570 or CDY_a.



Mumma Family Time Span Per Generation -

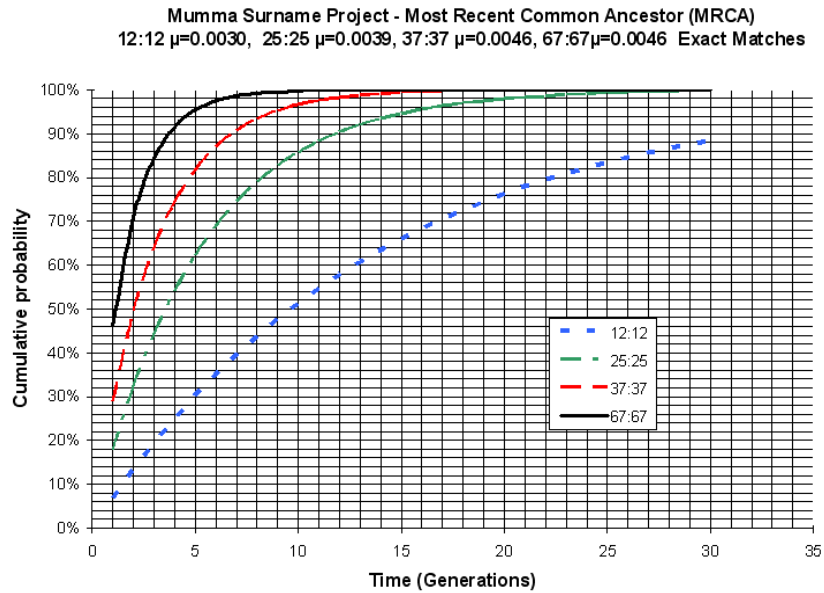
So how long a time period is a generation? This number is useful in estimating how many years in the past a common ancestor probably lived. Geneticists often suggest 15 to 25 years as the number of years per generation, but this number substantially understates the value for a several reasons. This number appears to be the time for the "first birth" for a female and does not closely determine an average time for the birth all of her children. For example, if we simply assume a woman's child bearing period was typically from age 20 to 45, the median child would be around 12 years after marriage. Assuming a typical marriage age of 19-20 years, then the median child would be born when the woman was about 31-32 years of age. Another reason is the typical male married somewhat later than females, likely around age 25 so the average time from the father's birth to the average time when the median child was born would be somewhat longer, say around 35 years of age. To verify these assumptions, I determined the average male generation time span men with the Mumma surname to be 31 years of age (over a period of 250 years) and for the Momma/Reenstjerna families of Europe, the time increases to an average of 36 years during a time span of 410 years. A published paper by Tremby & Vézina, American Journal of Human Genetics 66:651-658, 2000 reached similar conclusions. In their study where they determined an "Intergenerational Interval" of 34.4 years for men from family reconstruction. Thus an average time period of 35 years between male generations is a reasonable value to use for the Mumma surname project.

Most Recent Common Ancestor (MRCA)

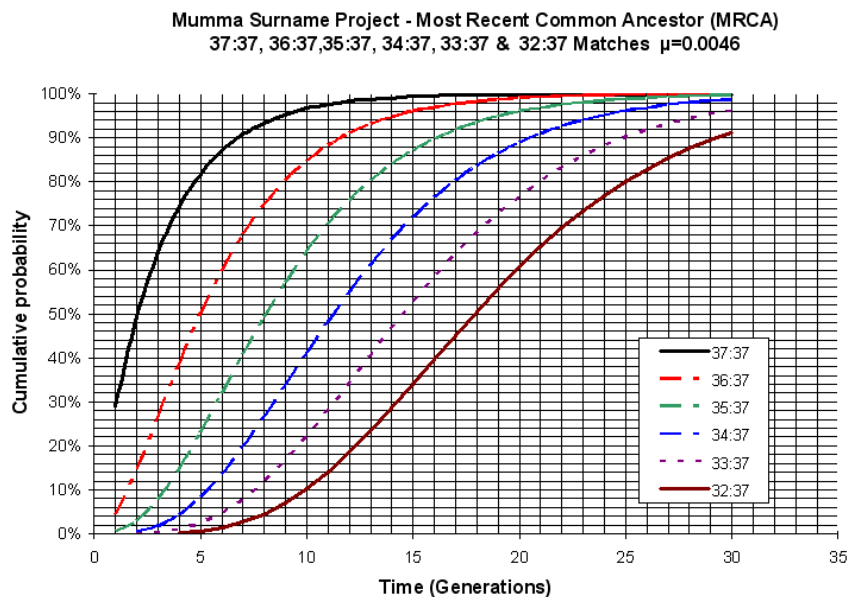
Of course, most people want to know the amount of time in generations or years to when two people share a common ancestor. Now that we have calculated mutation rates for the Mumma Surname project and the average number of years or time span between Momma/Mumma male generations, we can apply statistics to calculate the likely amount of time to a common ancestor based on the number of markers measured and number of mutations observed. The Most Recent Common Ancestor (MRCA) is defined as the closest direct paternal ancestor that two males have in common (such as a grandfather or g-g-g-grandfather) and TMRCA is the amount of time, in generation or years, to reach that common ancestor. In general, the closer the match in haplotypes between two individuals, the shorter the time back to a most recent common ancestor.

A research paper published in 2000 by Dr. Bruce Walsh of the University of Arizona "Estimating the Time to the Most Recent Common Ancestor for the Y-chromosome or Mitochondrial DNA for a pair of Individuals" addresses this subject. A more simplified discussion of this paper, MRCA and its implications written in layman terms can be viewed on this his web site at <http://nitro.biosci.arizona.edu/ftdna/TMRCA.html> Behind his calculations are several variables, namely how fast the various loci mutate and that any change in a marker is treated as a single mutation (infinite allele model).

A handy MRCA calculator is available on the web site maintained by Barbara Good & Suzanne Hallstrom at <http://www.moseswalker.com/mrca/calculator.asp> Using mutation rates determined for this project, the following graph show the probability of a man sharing a common ancestor against the number of generations. The graph shows the effect of using more markers at 12, 25, 37 and 67 markers. It becomes rather apparent that the 12 marker test does not adequately determine whether or not two men share a recent common ancestor.



This next graph plots the cumulative probabilities for an exact match of 37 markers and the effect of up to 5 mutations. The number of generations for a man sharing a common ancestor with a 90% probability decreases from 6.9 generations for exact 37:37 matches to 29.5 generations with 5 mutations or a 32:37 marker match. This clearly shows that statistically, you would not expect Kit# M-35 and Kit# 21948 to share a recent common ancestor since both men use the Mumma surname, but first one has a genetic distance of 5 mutations to the Momma ancestral haplotype and the other one has a genetic distance of 4 mutation. Between them they have a genetic distance of 9. This demonstrates that the MRCA can provide general guidance about mutations and relatedness, it cannot determine exactly when mutations will occur.

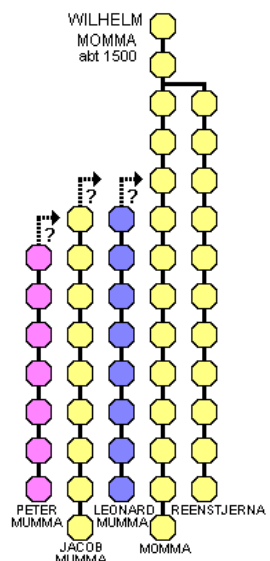


The time scale of the graphs can be changed to years by multiplying the number of generations by 35, the average number of years determined for the Mumma/Momma family. The total number of years to 35 generations is 1335 years.

Calculating the Time to Most Recent Common Ancestor is based on probability and is not an exact science. The calculation will determine the most likely time that a common ancestor might have lived, but there will always be a degree of uncertainty. For this reason, it is better to think of TMRCA as a range of time rather than a point in time. One would expect that two individuals share who 35 out of 36 markers, they would share a more recent common ancestor than two individuals who share 32 out of 36 markers. That is generally true, however there are several examples in this study where men who have almost no genetic distance between them are more distantly related than some who exhibit larger genetic distances. These graphs nicely demonstrate, however, why the likelihood of sharing a recent common ancestor diminishes dramatically as the number of mutations increase.

Discussion of Results Within Groups -

Initially, the results were arranged and grouped according to each person's likely progenitor. There were separate groupings for the three immigrant descendants, a group for the unattached descendants and finally a group of men who were clearly not Momma/Mumma descendants. What immediately became evident when the 37 marker data was received was all of the descendants of Leonard Mumma had allele 16 at DYS570. The descendants from immigrant Jacob Mumma and Peter Mumma had allele 17 at DYS570 as well as the Momma/Reenstjerna men from Germany/Sweden. So I concluded that allele 16 at DYS570 for immigrant Leonard and his descendants became a distinguishing "identifier" allele for his descendants. The Momma descendant chart at the right visually shows the descendants of Immigrant Leonard in blue according to their allele value at DYS570 and Immigrant Peter's descendants are shown in purple for their allele 35 at CDY_a. We know the German Mommas and Swedish Reenstjernas connect at the top of the chart to a Wilhelm Momma. The connection of the Mumma immigrants is unknown and exact connection points can not be determined as yet, hence question marks. These fortuitous mutations at DYS570 and CDY_a were a stroke of luck and good fortune. Something that I had hoped for, but didn't expect to observe.



Based on these observations, the original groupings were slightly re-arranged according to known progenitors and their identifying alleles. Group 1 represents men whose direct ancestry can be traced in Europe. Group 2 represent the known descendants of immigrant Jacob Mumma who arrived in 1731. Group 3 are men who we feel are likely Jacob descendants because they have allele 17 at DYS570, but lack written documentation. Group 4 are descendants of immigrant Peter Mumma who arrived in America in 1749. This group uniquely have allele 35 at CDY_a. Group 5, the largest grouping, are known descendants of immigrant Leonard Mumma who arrived in 1732 and they have allele 16 at DYS570, except for one known descendant. Group 6 are men who likely descend from immigrant Leonard, based on the fact they too had allele 16 at DYS570. Group 7 are the results of men who were probably not Mumma descendants or who have been shown to not be Mumma descendants from their DNA results.

Discussion of Group 1 Results - European Momma & Reenstjerna

The results obtained from the two German Momma participants show a perfect match to the MUMMA haplotype. Obviously this suggests that we should probably say that the MUMMA families of America descend from the MOMMA family of Germany since the Momma family is older than any of the Mumma families. While we can't clearly say at what specific generation the two families share a common ancestor, at least we know they do link together in the not too distant past. The earliest would be eight generations ago from known documentation. Also of interest is the fact that the Reenstjerna participant only differed by one digit from the MOMMA haplotype clearly suggesting that these two families share a common ancestor. This unusual surname spelling occurred in 1669 when two Momma brothers were ennobled by the King of Sweden for their great contributions to that country's economy and were allowed thereafter to use the surname of Reenstierna. The genealogies of both these

families are well documented and these participants share a common ancestor 12-13 generations ago. Again we see consistency in the data and the analysis.

Discussion of Group 2 Results - Immigrant Jacob Mumma

Only five descendants of immigrant Jacob have participated. Jacob's DNA modal haplotype closely matches the ancestral haplotype that has been identified for the Momma family. There is nothing that is particularly unusual about their genealogies or their results, other than the 4 mutations observed for Kit#1862 for markers 37-67.

Discussion of Group 3 Results - Probable Immigrant Jacob Mumma

The men in this grouping are probably immigrant Jacob descendants because they too have allele 17 at DYS 570. Because Jacob was a strong Mennonite, few baptismal or other church type records exist making this branch the hardest to identify genealogically.

The first three men, Kit#s 10614, 10519 and 21946, descend from a John Mumma who appears in Cumberland County, PA around 1800, but we know he was born prior to 1750. There is strong evidence that he lived in the Hershey area of Dauphin county prior to his migration to Cumberland County. These three men share an unusual allele 14 at DYS 607 which helps identify this branch.

Kit#s M-08, 7056 and 21370 use the surnames of Moomau and Moma. Other surnames in this branch include Moomaugh. They descend from a Christian "Mummer", b. 1768 and first appeared in Augusta County, Virginia in the late 1700s.

The final man, Kit# M-32, has the surname of Mumah. He was initially thought to be a descendant of Peter Mumma, but his DNA does not match that of Peter, but does match the DNA signature of Jacob so he was relocated to Group 3.

Discussion of Group 4 Results - Immigrant Peter Mumma

When this project was first begun, there were few descendants identified for immigrant Peter. There were a few men who were thought to be Peter descendants from family traditions, but again no proof. The DNA results, however showed an interesting haplotype pattern. All of the eight men have allele 35 at CDYa. No men from any of the other groupings have this allele at CDYa and this becomes the defining allele for descendants of Peter Mumma. This is an extremely fortuitous mutation. Also, the results show a "defining" allele for the descendants of Peter's eldest son, John. The six participants who are descendants of this son share allele 13 at DYS388 whereas the descendants of Peter's other sons do not exhibit this allele. They descend from his other sons. It is interesting that both of these two men exhibit allele 14 at DYS464b, raising the question as to whether they could be from the same son of Peter. That question remains to be answered.

About the time the results were extended to 37 markers, new documentation was discovered which showed that the four men who were previously listed in "unconnected" branches were really Peter descendants and they were regrouped with Peter accordingly. This is when Peter's defining allele at CDYa became apparent. One problem was identified at that time, however. Participant M-32, a man with the Mumah surname was attached to the Peter group, however he did not have allele 35 at CDYa. His documentation was re-examined and little evidence was found to support his being a Peter descendant. He came from an area of Lancaster County, PA where both immigrant Peter and immigrant Jacob descendants were living. His great grandmother was a known Jacob descendant. In addition, he had allele 17 at DYS570, the defining allele for Jacob descendants. As a result of these facts, participant M-32 was disconnected from the immigrant Peter (Grouping 4) and placed in the "unconnected" Grouping 3 with other men who have allele 17 at DYS570 and are believed to be Jacob descendants.

An interesting result was obtained from a man with the surname of Bell. After receiving his 12 marker results, he contacted me, saying he had an exact 12 marker match with participant M-26, a Muma. Initially I was not particularly excited since there are a number of men with different surnames who match the MUMMA haplotype

for the first 12 markers. Then he related the story that his great grandfather was a traveling salesman in Ohio who was "robbed & murdered" before he could marry his great grandmother. She was pregnant with his grandfather at that time. His great grandmother eventually married a man named Bell, who adopted the "illegitimate" boy, thus the Bell surname. Soon after the marriage, the family moved to New York from Ohio. Their family oral tradition claimed his "murdered" great grandfather's name was "Elmer Maumau", but there was uncertainty of the exact spelling because no written records have been found for his birth or the "murder". For many years he has been curious as to his true "genetic" surname and he decided to submit a DNA sample to FTDNA for analysis. After hearing his story and the surname of "Maumau", I became more interested. The Mumma surname is often spelled incorrectly. I found an Elmer Mumma from the same region of Ohio, but this Elmer had not been "murdered" and he married and raised a family. It didn't appear as if he was a candidate. Then the results were received for the remaining 37 markers. His haplotype matched the results of three immigrant Peter Mumma participants exactly, 37 out of 37 markers. Thus I concluded with confidence that the true "genetic" surname of Kit# 20816 is MUMMA, but uncertain of the connection. The facts and results were presented to one of the great grandchildren of Elmer Mumma and they revealed that he was a "traveling salesman", was living in the same area of Ohio and was not married at the time Mr. Bell's grandfather was conceived. After comparing all of the facts and even family photographs, we concluded that Elmer Mumma was the genetic father of Mr. Bell's illegitimate grandfather. We suspect that the family "wanted to murder" Elmer Mumma for not marrying the daughter. The descendants of both the natural and illegitimate families have now met via the Internet and have exchanged pictures and stories. I consider the likelihood of anyone blindly finding their "genetic" surname in a DNA surname database is like finding a needle in a haystack. Previously I have been asked by people whether a person should submit their DNA sample as a way to find their genetic ancestors and I would always say they were throwing their money away. Now I have to rethink and rephrase my answer.

Discussion of Group 5 Results - Immigrant Leonard Mumma

For this group I will discuss their results using each participant's Mumma "M" number, the same one used in the descendant charts presented in the Mutation Rate section.

When this project was first begun, a Christian Mumma was attached as the grandson of immigrant Jacob Mumma and two of his descendants were listed in Group #2. Upon receiving the 37 marker results, the allele values of these descendants stood out as being very questionable. The father-son results, #19 and #4 both had allele 16 at DYS570 and not the expected allele 17 for other descendants of immigrant Jacob. This raised a number of questions as to the validity of their results or their lineage. A request was made for the laboratory to re-verify their results and insure there was not a laboratory induced error. The laboratory confirmed their original scoring. I personally re-examined the genealogies for these men and the documentation revealed there was possible doubt in their pedigrees. It turns out both immigrants Jacob & Leonard had grandsons named Christian, both about the same age and both living in the same township of Lancaster County, PA. No verifiable documentation could be found to support the attachment of these Christian descendants to immigrant Jacob or Leonard. A search of the Lancaster County Mennonite Society library revealed a Mumma descendant chart created by one of their respected researchers. In this chart he commented that he was uncertain as to which immigrant this Christian Mumma descended. He thought it could be either Jacob or Leonard and there was no compelling evidence either way. The DNA evidence now clearly supports the reattachment of this Christian Mumma as a descendant of immigrant Leonard. This "reattachment" appears as the first two entries in Group 5 with the surname of Mummau. Their haplotypes are consistent with the other men in this grouping. Thus DNA data provided guidance for connecting men to specific branches and another project goal was achieved. While the proof is not 100% that the reattachment is correct, at least there is a rational basis for making the change.

A careful examination of this chart shows several sets of mutations which are perplexing and appear to be questionable. The first questionable result is between two brothers, #21 and #18. In the 25 marker data, #21 only had one mutation and I thought that it was unique to have observed a mutation between brothers. Now, however, with two different mutations (a genetic distance of 2), I become suspicious of the data since the probability of observing two mutations between brothers diminishes to 4% or 1 every 25 times. While this is possible, I become skeptical when such unusual events are observed. FTDNA re-verified the scoring of his data and the results were correct. I discussed this issue with the brothers and both indicated there are no "hidden" family secrets, as far as

anyone knows. There is a separation of 20 years between the births of the brothers which may be a small factor. I still consider this result as questionable. If #18 also had a "green" mutation (CDYa), then the data becomes consistent and believable since the "green" mutation could have occurred at a number of generations above all 3 men which includes their cousin, #31.

The next troublesome combination is between #14 and #15 who are 2nd cousins, once removed. The one cousin had two mutations and the other one also had two mutations, but at different markers. In this case, there are 4 mutations which occur within 7 conception events. The probability of observing this sequence is about 2.5%. What is interesting is these two men were tested because some unusual facts surround their ancestry which made them question whether they were 2nd cousins, once removed or not. I personally reviewed their documentation and feel the relationship is extremely solid and correct. Obviously these tests only cloud the issue even more. I guess the Mumma project is just lucky at observing events which occur very rarely.

Another unusual event is the mutation of #6. He has a mutation at DYS391, common to the other two men in this branch, but he had allele 17 at DYS 570 which is normally found only in "non-Leonard" participants. The only explanation for this must be that a mutation reversal occurred allele at DYS570. Some where above immigrant Leonard, the allele changed from a 17 to 16 and then changed back to a 17 within a few generation of #6.

Other than these few unusual results, the 23 Leonard Mumma results has been excellent and contributed greatly to the understanding and confidence in using DNA testing to assist in determining family connections.

Discussion of Group 6 results - Probable Immigrant Leonard Mumma

Men are placed in this group if they have allele 16 at DYS 570, the same as men with known family connections to immigrant Leonard Mumma. In addition, the family traditions of several of them point to a Leonard connection, but are lacking proof. The first three Muma men, Kit#s M-13, M-17 and M-18 are descendants of Jacob Muma who migrated to Canada about 1800. I call this group the "Canadian Muma family". I have rarely seen this family use an alternate spelling. We have been unable to connect this branch to immigrant Leonard.

Kit# 10617, a Mumma, is from the Rocky Ridge area of Frederick County, Maryland. His ancestor first appeared in this area of Maryland about 1833. A possible link has been identified for this small branch, but proof is lacking.

The surname of Kit# 3315 is Mewmaw, a rather unusual and uncommon way of spelling the name. There are strong feelings this branch connects to a David Mumma, the son of George Anthony Mumma, the son of immigrant Leonard Mumma.

Kit#s M-35 and 1860 are descendants of a David Mumma who appears in Fulton County in the early 1800's. The DNA signature and birth age strongly suggest the connection of this branch is to George Anthony Mumma's eldest son, Christian Mumma.

The ancestor of Kit# 3314 appears in Carroll County, Maryland around 1800. No potential connection has been identified.

The ancestor of Kit# 3317 is well documented as a John Mumma who appears in Lancaster County, PA around 1750 in Hempfield County and migrates to York County about 1790. He was the founder of "Mummasburg", a small town in Adams County, PA. Through an adoption, this participant uses the surname of Stevenson.

The final participant of this group is Kit# 62454. His ancestor likely connects as the eldest son of a John Mumaw who was born about 1790 in Lancaster County, then migrated and remained in Luzerne Co., PA. Additional testing will be necessary to verify this connection.

Discussion of Group 7 Results - Participants Unconnected to the Momma/Mumma Family

Group 7 contains data for five men who were generally not expected to be Mumma descendants. Some of their surnames are spelled and are phonetically close to Mumma, but no documented proof existed to either confirm or deny they shared a common Mumma ancestry. In such cases, a simple 12 marker analysis has proved to be sufficient to make that determination.

One fellow, Kit# M-20 with the MUMA surname spelling was not expected to be in this group. This Muma family group migrated to Canada shortly after the Revolutionary War. They were likely "Loyalists" sympathetic to the King of England to whom they, or their ancestors, pledged an oath of allegiance. The results of three Canadian Muma men had allele 16 at DYS 570 and were placed in Group 6 as unconnected Leonard descendants. kit# M-20 had a genetic distance of 6 for the first 12 markers and was judged to not be a Mumma descendant. This was a surprise to the participant and was the the first case in this project of a non-paternity event resulting from either an adoption, rape or infidelity.

The grandfather of Kit# 7054 was known to be adopted, but the surname of the genetic father was unknown. Out of curiosity he submitted his DNA sample in the outside chance that this might have been an adoption within the Mumma family. His results rule this out as he does not even belong to the R1b haplogroup.

Kit# M-23, a man from Estonia with the Mumma surname was included to satisfy my curiosity. The Mumma surname spelling is almost never found outside the United States where it originated. After an extensive world wide search, I discovered a small family group living in Estonia who used the Mumma surname spelling. Contact was made and one fellow agreed to supply his DNA. The results show that in spite of sharing a common surname spelling, there is no recent connection between Mumma family of Estonia and the Mumma families of America.

The Mumme spelling is still found in Germany today and a participant with this surname was included to determine whether or not there was a possible relationship with the Momma family. Again the results show this family surname is likely not related. These were people whom we felt, before the testing began, did not likely share a common ancestry with the MOMMA/MUMMA families. The results confirm the supposition. In all cases, the genetic distance from the MOMMA ancestral haplotype was 22 for the 25 marker analysis.

I was contacted by a fellow whose surname was Garbutt. In tracing his lineage, he uncovered an 1894 marriage entry for his grandfather in the records of Schuylkill County, PA which listed his grandfather's name as William J. Mummy, b. 1872 in PA. William was adopted by the Garbutt family and he used that surname in his later life. The family moved from Schuylkill County to Lykens/Wiconisco townships of neighboring Dauphin County. Mr. Garbutt submitted his DNA hoping to identify whether his "Mummy" grandfather descended from the Mumma or Mummey families. Again to my surprise, his results did not closely match the Momma ancestral haplotype, the Mummey modal haplotype, nor anyone else in this project. His ancestry remains unknown. There are no exact 12 marker matches in the entire FTDNA database of over 77,000 samples.

Discussion of Group 8 Results - Mumma-Mummey Surname:

When the project was first begun, several men with the Mummey surname were included. I had a strong feeling that the Mummey surname and the Mumma surname were probably closely related. The results, however, proved this to be an incorrect assumption. Not only did their results not match the Mumma surname haplotype, but they did not match each other. The origins of both men were from the Schuylkill County area of Pennsylvania. Since they did not match the Mumma haplotype, they were originally assigned to group 7, the "Non-Mumma" grouping.

Recently a fellow from an "unattached" branch with the Mumma spelling submitted his DNA sample (Kit #25944) for analysis. Much to my surprise, he did not match the Mumma haplotype, but he did match the haplotype of one of the Mummey men. A review of his genealogy shows he descends from Samuel Mumma who first appeared in Lykens/Wiconisco townships of Dauphin County in the 1860s. He and his family were enumerated in the 1860 census under the surname of "MUMY", but after the 1860 census, the surname spelling of

MUMMA was always used. He used this surname when he served in the Civil war and all of his descendants have used it since that time.

Additional men with the Mummey surname were solicited to participate and their results are shown in the Group 8 results shown below. One participant is known to have descended from Samuel Mummy, the eldest known Mummey originating in Northampton county around 1710. This Samuel is recorded as having purchased land in Bucks County in 1738. While there is no documented connection between all of these men, the results clearly show they share the same "genetic" surname. Their origins are from nearby Schuylkill, Columbia, Northampton and Northumberland counties, Pennsylvania.

In this table, a Mummey surname modal haplotype was determined and these alleles are shown in the yellow boxes. The values in the red boxes represent the genetic distances compared to the Mummey modal haplotype, hence mutations. I believe all of these men descend from a common ancestor as they are exactly a genetic distance of 1 from the Mummey modal haplotype.

GROUP 8 - Participants with the Mummey surname or share a similar haplotype																													
Test =>	Y-STR12												Y-STR25																
Marker #	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25				
DYS # [Green DYS # = faster mutations]	3	3	1	3	3	3	4	3	4	3	3	3	4	4	4	4	4	4	4	4	4	4	4	4	4	4	MUTATE	HG AR PO LU OP	Oldest Ancestor
KIT# SURNAME	13	24	14	10	11	14	12	12	13	13	13	30	17	9	10	11	11	25	14	19	29	15	15	16	17	0	<==	Mummey Haplotype	
21944 Mumma	13	24	14	10	11	14	12	12	13	13	13	30	17	9	10	11	11	25	14	19	29	15	15	16	16	1	R1b1	U57-19111 Lykens, PA	
M-33 Mummey	13	24	14	10	11	14	12	12	13	13	13	30	17	9	10	11	11	26	14	19	29	15	15	16	17	1	R1b1	Mummey – Ringtown, PA	
49643 Mummy	13	24	14	10	11	14	12	12	13	13	13	30	17	9	10	11	11	25	14	19	29	15	15	15	17	1	R1b1	Mummy – Pottsville, PA	
49817 Mummey	13	24	14	10	11	14	12	12	13	13	13	30	17	9	10	11	11	25	14	19	28	15	15	16	17	1	R1b1	Mummey- Northampton	
5350 Mummey	13	22	15	9	13	14	11	13	11	12	11	29	17	9	9	11	11	24	16	21	31	12	13	14	14	24	G2	Mummey- Columbia Co	

The reasons why the DNA from #5350 does not match the other men is puzzling and an explanation is not known. A possible explanation would be that one of his ancestors may have been adopted, or an ancestor simply changed their name, or a illegitimate birth occurred due rape or an unknown affair.

From the analysis of the Y-chromosome STR data obtained from the Mummey participants, a Mummey surname ancestral haplotype has been identified. Since one of them is known to have descended from Samuel Mummy, the eldest known Mummey, I conclude that all of these four men likely share a recent common ancestry and it is likely that Samuel Mummy is that common ancestor.

Again DNA testing demonstrated that it is a reliable tool to distinguish whether men share a common ancestry.

Discussion of Group 9 Results - Moomey Surname

The results of the two Moomey surname participants are reported in Group 9. These men were included in the original testing to determine whether the Moomey surname was a variant spelling of Moomaw, a variant of Mumma. I thought there was a high likelihood that these two surnames would be closely related. The results show that both men match each other, but do not closely match the Mumma surname haplotype and are not closely related.

Discussion of Group 10 Results - Moomaw-Mumaw-Webb

While assisting other researchers trace an unconnected Moomaw/Mumaw branch in Shenandoah County, Virginia, it was discovered that a possible link to the main Mumma tree was through a female whose maiden name was Mumaw, but for whom no husband could be identified. It was unclear whether this was a case of Mumaw cousins marrying or possibly a case of an illegitimate birth. To better understand the connection, a descendant of this branch was sought, found and a sample of his DNA analyzed. That participant is Kit# 720. Needless to say, the lack of similarity between his results and that of the MUMMA modal haplotypes was striking and clearly showed his father was not a Mumma/Mumaw/Moomaw. Additional record searches revealed one entry in the 1850 census of Virginia of a child with the correct age and the mother's age was correct, but the boy's surname was listed as "Webb" and he was living with a family named Fadeley. Further detective work revealed that the maiden name of the female married to Mr. Fadeley was "Mumaw". Speculating that a man with the Webb surname may have been his father, a message was posted on the Shenandoah County, Virginia GenWeb bulletin board, asking whether anyone was familiar with the Webb families living in that area at that time. The known evidence was described and an inquiry made whether any males with the Webb surname would be willing to volunteer their DNA for analysis. An immediate response was received from a Webb researcher who was interested in assisting. In addition, this researcher had a copy of a Will written by a Mr. Webb in which he left substantial money to his housekeeper, an Anna Mumaw, if she "continued to serve him as she had in the past". This was an unusual bequeath as it represented a large amount of money to leave to a housekeeper. His wife was still living, but they were separated. Mr. Webb died just prior to the 1850 census. Now we had clues and evidence as to the likely male ancestor of participant Kit#720. Two Webb participants were located, including a known descendant of the suspect Mr. Webb, the likely father of Anna Mumaw's son.

Since we only wanted to determine whether the haplotype from the Webb men matched Kit# 720, a simple 12 marker test was used. The results are compared below and are conclusive. The MUMMA modal haplotype is again shown with yellow shading and the values which match the MUMMA modal haplotype appear as white boxes. Kit# 720 clearly shares the Webb surname haplotype, not the MUMMA modal haplotype. (Mumaw & Moomaw are alternate surname spellings of Mumma). There was a perfect match of all 12 markers for both Webb participants showing that they too descend from a common Webb ancestor in the recent past. This is an excellent example showing the power of Y-chromosome testing to confirm or deny genealogical relationships. Since his mother was a Mumaw descendant, the descendants of this branch still share a Mumma ancestry, but through the maternal side.

GROUP 10 - Participants with the WEBB surname or share a similar haplotype															
Test =>	-----Y-STR12----->														
Marker #	1	2	3	4	5	6	7	8	9	10	11	12			
Marker	3	3	1	3	3	3	4	3	4	3	3	3	M	H A R P O L U P	
DYS #	9	9	9	9	8	8	2	8	3	8	9	8	U		
[Green DYS # = faster mutations]	3	0	*	1	5	5	6	8	9	9	2	9	A		
KIT# SURNAME	13	25	14	11	11	14	12	12	13	13	13	29	0	<===	Mumma Modal Haplotype
720 Moomaw	14	22	14	10	13	13	11	14	12	13	11	29	14	R1b1	292481221(Webb)
1857 Webb	14	22	14	10	13	13	11	14	12	13	11	29	14	R1b1	Webb surname
1858 Webb	14	22	14	10	13	13	11	14	12	13	11	29	14	R1b1	Webb surname

MSY1 DATA

After the initial 12 marker data was received in late 2000, It became apparent additional markers would be needed in order to use the DNA results to separate various branches of the Mumma\Momma families. I contacted Dr. Jobling at the University of Leicester and requested his laboratory provide additional analyses of 4 men from the Mumma surname project. He graciously agreed to perform an analysis of 17 markers, many of which were different than those provided by FTDNA. In addition to analyzing 17 markers of the Y-STR, Dr. Jobling and Ms. Turi King also performed an analysis of the highly polymorphic marker, MSY1. I was interested in this marker because it was one used in the historic DNA analysis of the President Jefferson - Sally Hemings case . In that project, it was considered to be useful in uncovering small differences in similar samples and I thought it might be ideal for the Mumma project.

The numeric allele values determined for MSY1 were:

M-01 No data obtained - (this was frustrating since these would have been my results)
M-07 (1)17 (3)41 (4)2 (3)2 (4)16 - (Richard M. MUMMA of America)
M-12 (1)17 (3)41 (4)1 (3)3 (4)16 - (Udo MOMMA of Germany)
M-30 (1)17 (3)41 (4)3 (3)1 (4)16 - (Frederick R. REENSTJERNA of Sweden)

Graphically, the results are displayed as:



Since no commercial laboratories are currently providing analysis of this marker, there is little other data by which to compare these results and a technical description of the measurement is beyond the scope of this report. Dr. Jobling's comments were that "the results show there is little variation of the Y-chromosome for these three DNA samples".

HAPLOGROUPS

Haplogroups are generally not considered to be useful in surname studies since haplogroups track the ancient migrations of man and not recent ancestries. For this project, it has been determined that this surname belongs to the most common haplogroup found in Western Europe called R1b. The following description of Haplogroups is provided on the FTDNA web site.

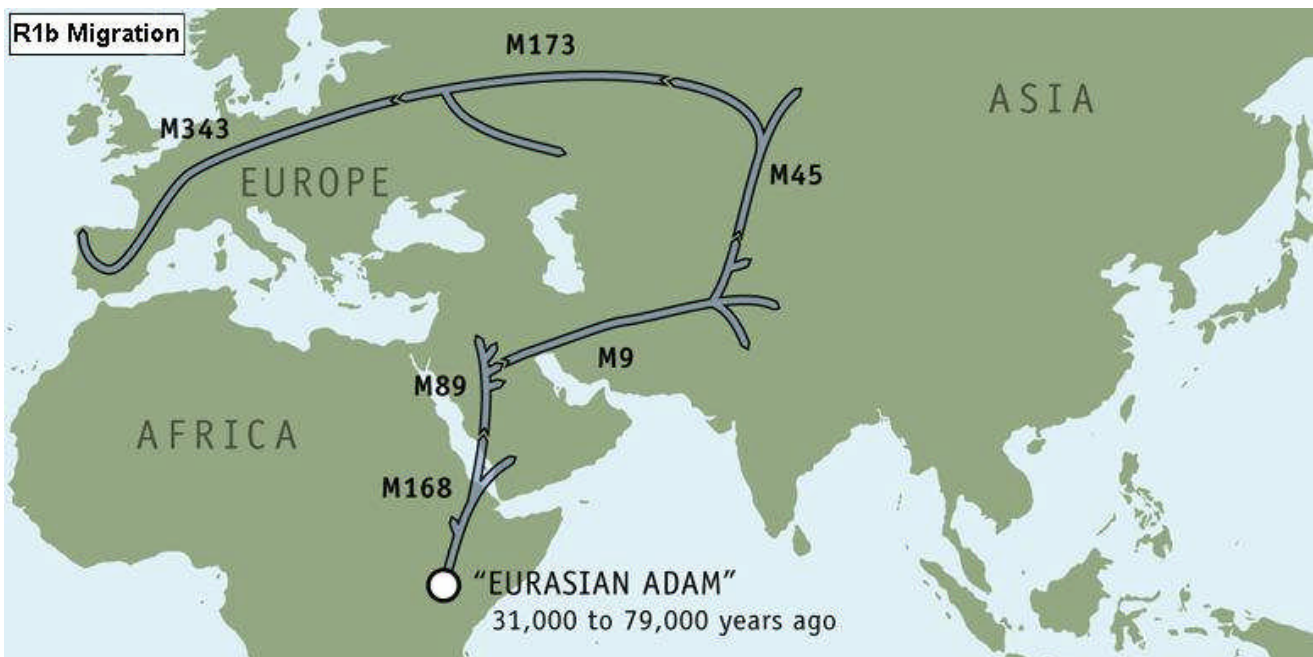
*"Haplogroups are clusters of Haplotypes (expressed as exact or near exact 12 or 25 marker matches) that are in a tight proximity to each other. Expressed another way Haplotypes are subsets of a Haplogroup. Think of the Haplotypes as the leaves of a tree, and the Haplogroups as the limbs of a tree...in fact the Haplogroups are the limbs of the tree of Homo Sapien-Sapien—our unique branch of humanity. The Haplogroups have been crafted into what is called a Phylogenetic network, and the male version can be seen here:
<http://www.familytreedna.com/haplotree.html>.*

Please note that people in different Haplogroups cannot be related within many thousands of years, and that each male test result provides a prediction of the Haplogroup currently about 90% of the time. In general the following rule of thumb may be used:"

Haplogroup Designations

- R1b Western Europe
- R1a Eastern Europe
- I Nordic
- J2 Semitic
- E3b Semitic
- Q3 Native American
- G India or Pakistan

All of the men who share a close common ancestry with the Mumma family descend from haplogroup R1b and some have even been further refined as R1b1. Some non-Mumma participants are from other haplogroups. The haplogroup determination was made by SNP testing of my DNA. R1b (determined by the M343 marker) is the most common haplogroup (70%) in Western Europe. The migration path is shown in the following map. This map is from the Genographic Project in which I participated. Because the time frame of the R1b haplogroup migration began around 31,000 years ago, I have not focused much attention to Haplogroups and this area of "anthrogenealogy".



PROJECT HISTORICAL TIMELINE

The project timeline is recorded below for historical interest:

- 15 Nov 1998 - E-mail messages were exchanged with Udo Momma of Germany discussing the possibility of using DNA analysis to trace ancestors and the possibility of using this technique to verify the Mumma/Momma family connection. No commercial laboratories could be found at that time to perform DNA analysis for private individuals.
- Early 2000 - A newspaper article is published about Dr. Sykes analyses of the DNA from men with the Sykes surname which produced interesting results He announces plans to create a company called Oxford Ancestors to perform DNA analyses for genealogical research.
- 10 April, 2000 - Contact was made with David Roper regarding a DNA testing program he was proposing to conduct. He was not aware of any commercial testing companies available at that time who offered Y-chromosome analysis for surname investigations. Most companies only performed DNA analyses for paternity determination and civil cases.
- 10-17 April, 2000 - An intensive Internet search found two companies, FTDNA and GeneTree, who were beginning to offer DNA testing services. Discussions were held with both companies regarding the DNA analysis of a large group of Mumma participants.
- April 17, 2000 - The Mumma DNA surname project was formally launched and males with the Mumma surname (or spelling variants) were actively solicited by letter, e-mail and telephone calls.
- June 2000 - 27 men volunteered to participate in this project with most funding their own analytical costs. Test kits were distributed to men living in America, Canada, Germany and Estonia.
- 7 July 2000 - 26 DNA samples were returned and sent as a group to FTDNA for DNA extraction and analysis. This was the first Surname Project created at FTDNA.
- 20 Sept 2000 - The initial results were received and in the short span of 6 months, the project progressed from a concept and dream to the receipt of analytical results for the 26 participants.
- February 2001 - Because few mutations were observed from the 12 marker results, four men were selected to be tested at additional loci to assist in identifying specific family branches. Testing services were solicited from several DNA laboratories including Dr. Jobling at the University of Leicester in England, Dr. Woodward with the Microbiology Department at BYU and from Dr. Hammer of the University of Arizona through FTDNA.
- July 2001 - Dr. Mark Jobling's laboratory at the University of Leicester in England completed an analysis of 19 markers of four Mumma participants. A meeting was held with Dr. Jobling in England to receive and discuss the results.
- October 2001 - FTDNA completed their analysis of an additional 13 unnamed markers for a total of 25.
- December 2001 - A contract with Dr. Woodward at BYU was cancelled due to lack of performance on their part as they were unable to provide the requested DNA analysis.
- March 2002 - FTDNA expanded the number of markers they were measuring and offering to 25.
- April 2002 - FTDNA revealed the DYS nomenclature for all of the loci they measure and the data was now reported in allele/repeat values. Full disclosure of the results was finally being made.
- January 2003 - A total of 45 men have provided their DNA for the Mumma project.
- January 2004 - FTDNA expands the number of markers 37. All men, whose 25 marker analysis showed they were likely Mumma descendants, were analyzed at the additional loci. 55 men have submitted DNA samples for the Mumma Surname DNA Project and their results have been received and analyzed.
- January 2005 - A total of 62 men have provided their DNA for the Mumma project.
- June 2006 - FTDNA expands the number of markers available for analysis to 67. As of this time, 73 men have participated in the Mumma project. Results have been received for 10 men who have had 67 markers analyzed.

SUMMARY AND CONCLUSIONS

The data obtained from the additional markers in the 37 marker analysis has proved to be very beneficial to the Mumma Surname DNA Project. While a few issues and concerns have been identified, a much better haplotype mapping is being generated for the Mumma family. The initial project objectives have been met and in several cases, exceeded.

- *Are the American MUMMA and German MOMMA families closely related?* - The answer to this question is YES. There are exact 37/37 matches between these two surname groups, suggesting they share a recent common ancestor. The 67 marker data shows several men were within one mutation of each other, 66/67 matches further confirming the families are closely related.
- *Were the original 1731, 1732 & 1748 Mumma immigrants closely related?* - YES, the data clearly shows that the original immigrants were closely related. Because of mutational differences at specific loci, I conclude it is doubtful they were brothers.
- *Are variant surname spellings related - Muma, Mummau, Mummah, Mumaugh, Moomaw, Moomau, Moomey, Mumme, Mummey & Reenstjerna?* In some cases the surname groups are closely related, but other surnames such as Mumme, Mummey and Moomey do not descend from the same genetic tree. In addition, cases of surname spelling errors between the Mumma & Mummey families were uncovered.
- *Can DNA "fingerprints" be determined to uniquely identify specific family branches or trees?* YES, specific DNA signatures have been determined which are unique to specific immigrants and even particular branches.
- *Can an individual's DNA "fingerprint" be used to connect them to a specific family tree?* YES, specific DNA signatures have allowed us to correctly identify a man with the Bell surname to a specific branch of the Mumma family which was later confirmed with documentation. In another case, it was determined that a man with the Mumma surname genetically descends from the Mummey surname family.

From the results I conclude that 37 markers are sufficient to identify whether men are Mumma/Momma descendants and in some cases, even which immigrant. There are two key markers which define from which immigrant a person descends. They are DYS 570 and CDYa which are only analyzed by FTDNA. Other surname projects may identify "key" mutations at other marker locations. The 67 marker analysis has not demonstrated any particular usefulness for this project, but the results might be different for different surname projects.

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