

Analysis of the Dillman DNA Project Results
(an update of the discussion at 2004 Mega Reunion)
Version 1.0

Written by: G. Andrew Stillman
Draft Reviewed by: Earl Dillman, Toby Hurley, Frank Dillman

April 15, 2005

SUMMARY

Since there has been much new information available regarding DNA testing and test results following the 2004 DFA Mega Reunion, it is good to bring it all together so that people have an opportunity to review it and draw their own conclusions.

While this document focuses its attention on the Hans Georg/Andrew Dillmann lines, the other lines are also discussed towards the end.

The Hans Georg/Andrew Dillmann family tree has evolved through the use of DNA testing. Long held traditions are being reassessed and re-evaluated. While it has been shown that Hans George Dillmann could be the father of George Stillman, Andrew Dillman and Georg Michael Dillman, we cannot yet discard the Andrew Dillman Sr. scenario.

Following the 2004 Mega Reunion, we now have 37 marker test results for 6 more participants from the Hans Georg/Andrew Dillmann grouping for a total of 10. Also, Family Tree DNA has issued updated marker mutation rates which show that mutations occur much more frequently than originally expected.

Another area that we need to focus on is an analysis of the Y-chromosome Haplogroup. It turns out that both the Haplogroup and the Dillman surname are quite rare.

Additional analysis of mutations and expected number of mutations for the newest DNA results continues to indicate that Hans Georg Dillmann is the probable common ancestor of the test participants in the G2 Haplogroup.

Based solely on DNA results, a simulated family tree was constructed to minimize the number of mutations. This alternate or experimental tree, however, does not fit with documentary evidence and must be rejected as a possibility.

A wish list has been developed for potential future test participants for the G2 Haplogroup cluster.

Terms that appear in **bold** can be found in the [Glossary](#) at the back. Links to online glossaries have been shown for those wishing to view other definitions.

2004 DFA MEGA REUNION

Prior to the 2004 DFA Mega Reunion, there were two alternative views on the origin of Andrew Dillman (born 1751/1753) who married Barbara Roush. There were those who had found evidence that Andrew Dillman, born in 1753 was the son of Hans Georg Dillmann and Margaretha Murr. On the other hand, the predominant viewpoint based on long held traditions and research published by earlier genealogists, was that Andrew was born in 1751 and was the son of Andrew Dillmann. This is depicted in Figure 1.

The startling DNA test result matches between Earl Dillman and Andrew Stillman led to the realization that Andrew Stillman's earliest Stillman ancestor, George Stillman, could be none other than Georg Adam Dillman, son of Hans Georg Dillmann. Documentary evidence of British Army records for the 84th Regiment indicate that Georg Dillman was taken prisoner by the British Army in 1776 and sworn in to the 84th Regiment in September 1776. George "Stillman" was later mustered out of the Regiment in October 1783 in Nova Scotia. The surname change seems to have originated in the Regiment.

The objective here is not to go over this information again, but to recognize that this linkage was the trigger in the reassessment of thinking about the origins of Andrew Dillman, born in 1751/1753. (More information on this linkage can be found at www.dillmanfamilyassociation.org/connection.html)

Andrew Stillman's presentation demonstrated, by analyzing the mutations, that it was possible for Hans Georg to be the common ancestor of Georg Adam Dillman (aka George Stillman), Andrew Dillman, and Georg Michael Dillman. Dr. Freed's presentation corroborated this using the concept of "expected number of mutations". The premise was that if the actual number of mutations exceeded the expected number of mutations the hypothesis could not be supported. The hypothesis was that Hans Georg Dillmann was the common ancestor of the three branches (4 DNA test participants). The results were that the actual number of mutations was **less than** the expected number. This resulted in the updated family tree as shown in Figure 2.

It needs to be reiterated that although it was shown that it is **POSSIBLE** that Hans Georg Dillmann was the ancestor of all three branches, DNA testing *to date* cannot irrefutably prove this to be true. For instance, it is possible that there could have been three different but very closely related fathers for the branches of the Dillman family being currently examined. This is because the mutation rate for the DNA markers being used is very low, on average 0.0058 (or every 172 generations)¹. The markers can be passed on for generations with no changes. It is possible that at the time of the birth of Andrew Dillman, there were several male Dillmanns with the same DNA profile in Pennsylvania. Andrew Dillmann, born circa 1706 is still a candidate to be the father of Andrew Dillmann born 1751. At this point, we can't discard that scenario. Later on, I will outline possible ways to pin this down.

¹ 1st International Conference on Genetic Genealogy for Family Tree DNA Group Administrators. Houston, October 30, 2004.

Dillman Family Tree as it was historically believed (pre DNA)

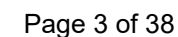
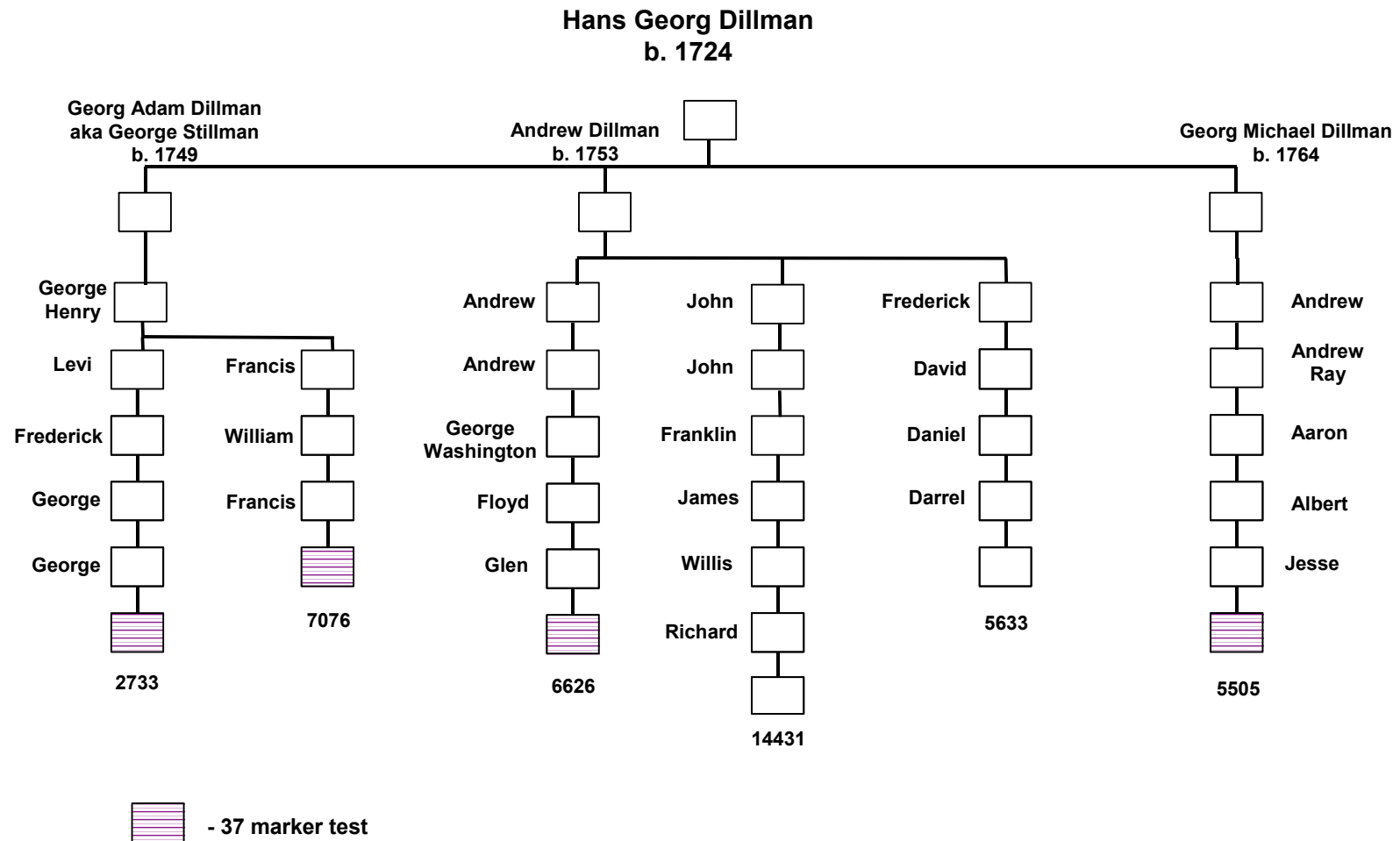


Figure 2.

Dillman Family Tree from paper trail/DNA



SUBSEQUENT TO THE 2004 MEGA REUNION

The Georg Dillman/George Stillman link has been further substantiated following the reunion by research by Maryellen Canfora who found land records for Nova Scotia, Canada wherein George is referred to as George Dillman. Other Nova Scotia land records for 2 of George's sons, Edward and Andrew also use the Dillman surname, sometimes interchangeably within the same transaction. The surname of one of George's daughter's was listed as Dillman on her marriage record.

Other analysis has indicated that Georg Dillman was not the only member of the Pennsylvania Rifles to have been taken prisoner and sworn into the 84th Regiment. There were approximately 6 others recognizable by name.

Finally, as of April 14, 2005 we have received high resolution test results for 6 additional participants (5 Dillmans and 1 Stillman). Results for a 7th participant indicated that he actually belonged to another Dillman group.

Before looking at these results, we should discuss three concepts, namely, Haplogroups, Surname frequency, and updated marker mutation rates. As can be seen, in the span of a few months, there have been many interesting developments. (Two additional topics, Multi-Copy Markers and Marker Value Frequencies, are discussed in [Appendix 1](#) and [Appendix 2](#) for more advanced readers).

HAPLOGROUPS

To date, the Dillman DNA project has focused on the DNA test for Short Tandem Repeats "**STRs**", which describes the number of repeats at a particular marker (or locus). "13" is an example of an STR value for marker DYS 393. It is also interesting and necessary to consider what the Haplogroup tells us as it sets the framework for analyzing the results.

First we need a definition for Haplogroup. A Haplogroup is used to describe groups of humans through long-term migration histories. A Haplogroup is recognized by a specific set of **SNP** (single nucleotide polymorphisms) markers that are either present or not. Haplogroups, inherently, are useful mainly for "deep ancestry", that is, events that happened thousands and tens of thousands of years ago. (More information can be viewed using the following link: www.familytreedna.com/hap_explain.html) However, we can also make use of Haplogroups for general comments on the studies focused more on genealogical timeframes.

A haplotype is the actual marker results for an individual test participant. Loosely, a haplogroup is a collection of related haplotypes. Haplotypes define individuals. Haplogroups are more generic versions of the DNA test results that we see in Frank's charts. Haplogroups only take into account a subset of information. Because they are less specific, they encompass more people, making them more akin to "tribes" rather than just family groups, but people who are nonetheless related. The common ancestor for people belonging to a Haplogroup is much further back in time, such as thousands or tens of thousands of years ago.

Haplogroups are also referred to as clades and are organized into a family tree, which shows how each of them branched off from the parent Haplogroups. This family tree can be viewed at: www.familytreedna.com/haplotree.html . There is also a consortium responsible for the naming of the different Haplogroups and sub-Haplogroups (or clades and subclades). Haplogroup G consists of the sub-Haplogroups of G1, G2, and G2a. I will refer to Haplogroups and sub-Haplogroups simply as Haplogroups. For now, it is only important to note that names follow a letter, number, letter, and number sequence as with G2a, R1b1, etc. (Confusingly, mitochondrial DNA clans also use a similar nomenclature)

Haplogroup G2

The most common cluster of Dillman DNA results has a predicted Haplogroup of G2. This value is “predicted” since the actual test to determine precisely which Haplogroup the DNA belongs to has not been undertaken for most participants. I requested a Haplogroup test on my own DNA and the results came back as G2 on December 15, 2004. Family Tree DNA has stated that the predicted results only occasionally differ from the actual results. My results confirm that G2 is the correct Haplogroup for this cluster.

It is very fortunate for this study that the Haplogroup is G2. This is fortunate because G is a rare Haplogroup. According to the “Y Haplogroup G website”, which can be found at home.comcast.net/~whitathey/indexg.htm, only about 1-2% of European men today belong to this group. The location where Haplogroup G is most prevalent is in the Caucasus region where the Haplogroup peaks at 30%. Also, about 10% of Turkish men belong to this group. Please refer to the maps located at: www.scs.uiuc.edu/~mcdonald/WorldHaplogroupsMaps.pdf for distribution of Haplogroups. Haplogroup G is only visible in the pie charts for Italy (IT), Turkey (TU), Georgia-Armenia (GE), and Persia (PE) and does not even register on the scale for Germany (GM). These results are based on random tests done on populations to determine migration patterns. Different groups may be over or under represented in the sample, hence in the future when more testing is done, the percentages could change somewhat.

Haplogroup G came into being somewhere around 30,000-35,000 years ago in an area that incorporates the Middle East as far east as the Himalayan foothills. It is thought that the members of Haplogroup G were part of the group of people who were among the first in the fertile crescent to switch from hunter-gatherer societies to farming in the Neolithic era. They later migrated to Europe via Turkey and along the Mediterranean coast and brought agriculture with them around 6-8,000 years ago. Also Haplogroups E, I and J were part of this same general migration and those Haplogroups are more common than G.

Among other Pennsylvania German DNA Surname projects, Haplogroup G2 is also rare. This can be seen at the following website for the Kerchner Surname project:

www.kerchner.com/kerchdna.htm

(scroll down 1/3 of the page to the 12 marker panel. Haplogroup is on the far right hand side of the chart). There are no Gs in the Kerchner project. R1b is the most common followed by E, I, and J. Looking at another surname project organized by Charles Kerchner for the Laudenslager surname, we can see more interesting results:

www.kerchner.com/laudendna.htm

(scroll down almost to half the page to the 12 marker panel). This is a smaller project and it consists solely of R1b.

Haplogroup G2 is very uncommon, even among early German settlers of Pennsylvania.

Haplogroup R1b

Haplogroup R represents a full 55% of today's European men. R, and its sub-Haplogroup, R1b (also known as the Atlantic Modal Haplogroup or "AMH") has been so successful, that people with different surnames will often match on the Haplogroup and on the low and medium resolution DNA marker tests and still are unrelated in genealogical time. A rule of thumb outlined by Chris Pommery in "DNA and Family History" suggests that surname studies for the R1b haplogroup would require about 50 participants before being able to draw meaningful conclusions. This number refers to low resolution tests.

Looking again at the Haplogroup distributions maps, it can be seen that R1b, for example, makes up approximately 25% of the male population in Norway, 40% in Germany, and up to 75% in Scotland.

www.scs.uiuc.edu/~mcdonald/WorldHaplogroupsMaps.pdf

Haplogroup R came into being about 35,000-40,000 years ago. The R1b sub-clade is somewhat younger. The first humans to populate Europe following the last glacial period were from the R1b Haplogroup. Some researchers also believe that they were present in Iberia 30,000 and were the people who are credited with the cave paintings in this area. R1b were hunter-gatherers who followed big game into Europe as the ice retreated. Their arrival in Europe ahead of other groups accounts for the high concentration in modern European males. If you are interested in this Haplogroup, please be aware that many researchers are beginning to refer to R1b as R1b3 or R1b3*.

Haplogroup I, I1c

Haplogroup I represents about 18% of European males with a range of 10-15% of southern Europeans (Italy, Spain, Portugal) and as much as 35-40% of Nordic (Sweden, Norway, Iceland) men (and oddly about 25% of Iranian men). This group developed its distinguishing mutation sometime about 20,000. Because of its predominance in Europe, researchers believe that it arose in Europe from Middle Eastern peoples.

I1c is predominantly a Northwest European group, there is a "southern" variety that appears along the Mediterranean coast.

Haplogroup J2

Haplogroup J probably represents around 10% of European males. It can be found as high as 50% in modern Middle Eastern men, 25% of Turkish men, and about 15% of Italian men. There are also concentrations of less than 10% in Iran and southern India.

Haplogroup J originated in the Middle East or northern Ethiopia and spread along the fertile crescent. J2 spread into Europe about 7,000-9,000 along with Haplogroups G, I, and E, bringing farming to Europe. J2 also spread eastward into India. J1 remained in the Middle East and spread south into northern Africa.

SURNAME FREQUENCY

One aspect of any study is to consider how rare or common a particular surname is. Should we be dealing with a common surname, then perfect DNA matches at low and medium resolution tests (i.e., 12 and 25 marker tests) are less meaningful. The more people who share a common surname, the greater the chance that they will match at the 12 or 25 marker tests but not share a common ancestor in “genealogical time”. This is even more so for people who share a common Haplogroup, like R1b.

Again, the Dillman DNA project is fortunate. According to the 1990 US Census, the Dillman surname makes up a slim 0.002% of the total population of 245 million. This translates into 4,900 individuals with this surname (men, women and children). Assuming a 50/50 split of men to women, there are 2,450 potential DNA participants. The ranking of the surname is 7098th. (There are considerably more Wong's, with about 61,250 people)

Interestingly enough, the Stillman surname is more common than Dillman. It makes up 0.003% of the 1990 US population for a total of 7,350 individuals. The surname ranking is 4739th. (One of the first Stillman's to colonize America was a George Stileman – later Stillman - in 1685. He is an ancestor of George Bush: www.stillman.org/bushq.htm)

Not surprisingly, the top 5 names are Smith, Johnson, Williams, Jones, and Brown. This data can be viewed at:

www.census.gov/genealogy/names/dist.all.last

Smith alone had a frequency of 1.006%, or 503 times more common than Dillman (total number of people with this surname would be 2.5 million).

The pertinent information here is that in the Dillman DNA Project, the cluster of results being used for analysis is from a very rare Haplogroup and a very rare surname. Hence, there is greater confidence in the matches and conclusions drawn from a smaller sample size.

UPDATED MARKER MUTATION RATES

At the 1st International Conference on Genetic Genealogy for Family Tree DNA Group Administrators in Houston in October 2004, Family Tree DNA released a portion of their findings from a study of mutation rates for individual markers. The study was based on a more comprehensive dataset than what had been used in the past. Submissions of data came from Surname Project Group Administrators who voluntarily submitted family trees and results. Their findings indicate that the mutation rate for individual markers is actually higher than previous estimates of 0.002 gathered from population studies. While individual marker results were not released at that time, the average mutation rate was disclosed to be 0.0058 (almost 3 times faster).

A more granular breakdown was provided by Family Tree DNA by “panel” of markers. The mutation rate for markers 1-12 was determined to be 0.00399, for markers 13-25 it was 0.00481, while the rate for markers 26-37 was given as 0.00748.

Individual marker mutation rates have been independently calculated by Doug McDonald using a smaller dataset than that available to Family Tree DNA. His rates were strictly calculated for Haplogroups R1a and R1b and are only shown here for information purposes. They can't be used in the Dillman DNA Project, as they are Haplogroup specific. (It is unknown at present if mutation rates vary by Haplogroup, but this is an area that Family Tree DNA is investigating.) The source data can be found at: archiver.rootsweb.com/th/read/GENEALOGY-DNA/2004-11/1101600544

Figure 3. Doug McDonald's Individual Marker Mutation Rates

Marker		Rate	Marker		Rate	Marker		Rate
1	393	0.0014	13	458	0.0095	26	460	0.0065
2	390	0.006	14	459 - a	0.0025	27	GATA H4	0.0075
3	19	0.0025	15	459 - b	0.0025	28	YCA II - a	0.004
4	391	0.0059	16	455	0.0007	29	YCA II - b	0.004
5	385 - a	0.005	17	454	0.0007	30	456	0.01
6	385 - b	0.005	18	447	0.0075	31	607	0.0095
7	426	0.0007	19	437	0.0027	32	576	0.015
8	388	0.0018	20	448	0.004	33	570	0.014
9	439	0.008	21	449	0.015	34	CDY - a	0.017
10	389-I	0.0035	22	464 - a	0.0063	35	CDY - b	0.017
11	392	0.002	23	464 - b	0.0063	36	442	0.006
12	389-II	0.0052	24	464 - c	0.0063	37	438	0.002
			25	464 - d	0.0063			

According to Doug's calculations, the mutation rate for CDY is 0.017, which is approximately 3 times faster than average rate of 0.0058. It is also more than 8 times faster than the "old" average rate of 0.0002. **CDY, from this study, is the fastest mutating marker of all 37.** Clearly the mutations found in the Dillman DNA project are in the group of fastest mutating markers (458, 449, 456, 607, 576, 570, and CDY).

Also for comparison, Figure 4 shows the mutation rates calculated solely from the Dillman DNA Project for the Hans Georg/Andrew Dillman Cluster. The highlighted row indicates the average mutation rate for the project, which is 0.0037. The Dillman DNA Project mutation rate is below FTDna's average mutation rate of 0.0058. Since the sample size is so small, there is less confidence that the numbers are statistically meaningful. Hence, it is necessary to also consider the level of uncertainty. This is depicted in the final 2 columns in the chart. The last column is calculated based on the level of uncertainty and it shows a range of possible values that are statistically possible for the calculated mutation rates. For instance, the rate of 0.0037 could really be between 0.0004 and 0.0069. This range is known as a 95% confidence interval, meaning that we can be confident 95% of the time that the true mutation rate for the

Dillman DNA project lies between these two numbers. The more participants we have, the smaller this range of possible values will be.

The other rates shown in Figure 4 are just for interest. Since the sample size is so small, it is not useful to compare the individual marker mutation rates to those from Doug McDonald or the panel rates. For instance, there were no mutations found in the first 25 markers, so the mutation rate for these two panels is 0.

Figure 4. Mutation Rates from Dillman DNA Project.

#	Description	Transmission Events	Markers	Mutations ¹	Mutation Rate ²	Statistical Uncertainty ³ (Std Deviation)	Possible Range in Values for Mutation Rate ⁴ (95% Confidence Interval in Mutation Rate)
1	8 participants ⁵ markers 1-37	47	37	6	0.0035	0.0014	0.0006 - 0.0063
2	8 participants ⁵ markers 1-12	47	12	0	0.0000	0.0000	0.0000 - 0.0000
3	8 participants ⁵ markers 13-25	47	13	0	0.0000	0.0000	0.0000 - 0.0000
4	8 participants ⁵ markers 26-37	47	12	6	0.0106	0.0043	0.0020 - 0.0193
5	8 participants ⁵ markers 1-25	47	25	0	0.0000	0.0000	0.0000 - 0.0000
6	CDY-b only - 8 participants ⁵	47	1	2	0.0426	0.0301	0.0000 - 0.1027
7	576 only - 8 participants ⁵	47	1	3	0.0638	0.0369	0.0000 - 0.1375
8	CDY-b AND 576 - 8 participants ⁵	47	2	5	0.0532	0.0238	0.0056 - 0.1008

NOTES:

1) Participants 2733 and 7076 share the SAME mutation at CDY-b. The mutation came from a common ancestor.

2) **Mutation Rate** is calculated as the number of **Mutations** divided by the product of **Transmission Events** and number of **Markers**.

3) Similar formula as for the **Mutation Rate** except the square root of the **Mutations** is used instead. The simple formula used is adequate for low frequency events such as mutations. This is also known as Standard Deviation.

4) **95% Confidence Interval for the Mutation Rate** is calculated by subtracting and adding 2 **Standard Deviations** from the calculated **Mutation Rate**.

5) The 8 participants are: 29019, 2733, 7076, 6626, 14431, 5633, 5505, 24701. See Figure 5 for family tree chart.

ADDITIONAL HIGH RESOLUTION TEST RESULTS

Now, we have 37 marker test results for participants 5633, 14431, 22978, 24701, 25672, and 29019 in addition to the 4 sets of results discussed at the Mega Reunion. Although we don't have paper trail links for 22978 and 25672, we can certainly make some observations and suggestions for future research for people investigating these lines.

The actual test results can be seen at: www.frankdillman.com/dnalist.htm

I have created some family tree charts using a summary of the data found in the above noted test result table. In my charts, I am only interested in the mutations. It is much easier to concentrate on these, as there are so few of them. I will use them to analyze the mutations and also to calculate the Expected Number of Mutations.

Analysis of Mutations

Before turning to Figure 5, I should make some general comments. I am showing only the 10 participants for Haplogroup G2 (another Stillman participant has no results). The other participants are not related in a genealogical timeframe. The R1b group will be discussed separately at the end of this document. 4 of the Haplogroup G2 participants results were available at the 2004 Mega Reunion, 6 more are now available.

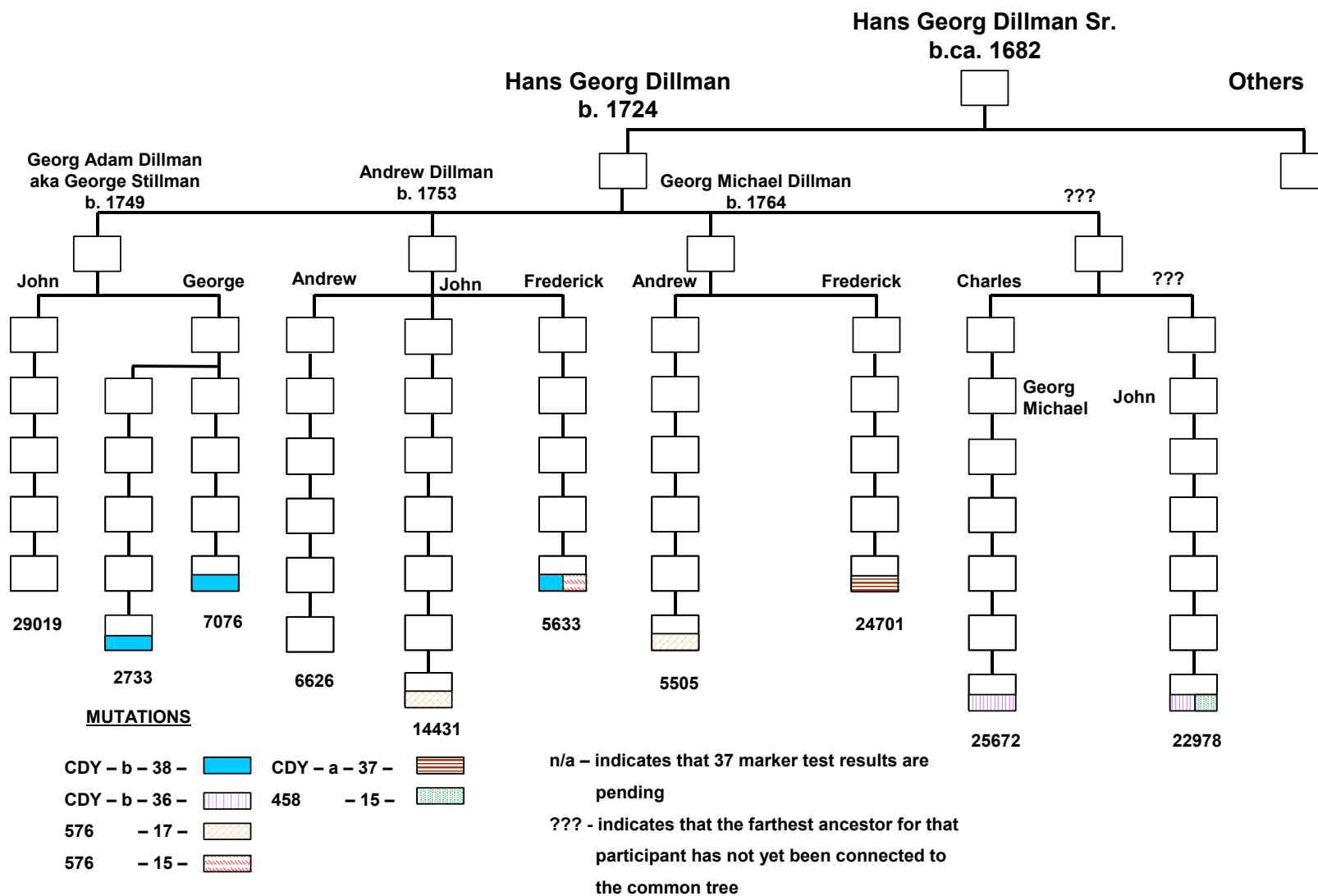
Using standard genetic guidelines, I am using boxes to indicate males (circles for females). For the most part, I have included names only for the first 3 generations to keep the chart relatively simple and yet make the tree recognizable.

The DNA profile for 6626 remains as the most likely candidate for the profile of the common ancestor, shown here as Hans Georg Dillmann. This profile is then referred to as the Ancestral Haplotype. Mutations will be measured relative to the values contained in the Ancestral Haplotype. I have used 6 colours/patterns to indicate the 6 different mutation varieties from the most likely profile that we have so far encountered.

Other projects often look at something called the modal haplotype, which is simply the most common set of DNA results. The most common results can be biased by oversampling of a particular branch. For instance, the Stillman branch, with 3 participants, may have 3 sets of the same results. In that case, the Stillman DNA results would be the modal haplotype. Alternately, 14431 and 5505 also share the same results and could be the modal haplotype. However, I think it is more interesting to use the results of the most likely profile for the common ancestor as the base from which to measure the mutations.

Figure 5.

Dillman Family Tree from DNA and paper trail



Since I don't know how participants 22978 and 25672 fit in, I have placed them at the right hand side of the chart with ??? at the box where I have linked them temporarily. From their common mutation, it would appear that they are more closely connected to each other than to the other lines on the chart. This box could represent one generation or several. Based on birth year for their earliest known ancestors, the box may indeed represent only one generation. The box may also not belong at this level, but could descend from a brother or cousin of Hans Georg.

If we start tracing the mutations up the tree, we can attempt to establish where the mutations may have first taken place. This can assist in finding markers that may be used to readily assign future participants to appropriate branches, without knowing the documentation of their lines. For instance, on the Stillman branch, we can see that the CDY – b mutation (value of 38 versus that of the base profile value of 37), could have begun at the first common ancestor for 2733 and 7076, namely George Stillman, son of Georg Adam Dillman (aka George Stillman). In Figure 5, I have indicated this with a blue section all the way up to George Stillman as we can be sure that since two branches had the same mutation that it is the profile of their common ancestor. From the results of 29019 who does not share this mutation, it is clear that this mutation originated with George Stillman, son of Georg Adam Dillman.

We can follow the same process for the other mutations and lines. For 14431, the mutation could have started all the way back with John. At this point we cannot determine the exact generation where the mutation began. Likewise with 5633 and his two mutations. These mutations could have crept in anywhere back to Frederick. It is extremely unlikely that both mutations occurred in the same generation, and there are several possibilities for the source of each. Had there only been one transmission event (generation) from Frederick to 5633, the number of mutations would be suspect. As it is, there are enough generations to be candidates for the source of the mutations and it is physically possible to have two mutations in just a short time span even though the probability of this occurring is small. I will revisit this case when looking at the Expected Number of Mutations.

With 5505, the mutation could have entered the line anywhere back to Georg Michael himself. For 24701, his mutation may have originated with Frederick. However, it is very unlikely that both mutations began with George Michael's son. It is also extremely unlikely that George Michael had either of these mutations. Further testing on cousins more closely related to 5505 or 24701 can clarify where these mutations arose.

Finally, looking at the results for 25672 and 22978, they share a mutation on CDY-b where they have a value of 36 rather than 37. Their results are more similar to each other than to the other participants. Hence, they are probably more closely related. Given that their earliest known ancestors, Georg Michael and John were both born in Kentucky about 4 years apart, they could potentially be brothers. (Georg was born in 1810 and John in 1814). I am showing this possible relationship in Figure 6. Knowing this could help focus research efforts in this area and could provide additional clues to the researchers of these two branches.

Results for 29019

The results for 29019 are very important for the project. First, they permit us to conclude that he does indeed belong to the Stillman family line. Although there were no

birth/baptism records, there is documentary evidence that he held land close to George Stillman and later his family and the family of a confirmed son of George relocated to another area together. Using the logic that there were no other males in Nova Scotia with a similar DNA profile, Georg Adam Dillman/George Stillman was the only possible father. Further, since the results for 29019 are a perfect match to those of 6626, the conclusion that 6626 and 29019 share a common ancestor is very strongly supported.

The results for 29019 also allow us to triangulate on the DNA profiles for 2 key people. The first is Georg Adam Dillman/George Stillman. 29019 results differ from those of the other two descendants of George Stillman, 2733 and 7076 by one marker. As the results for 29019 match those of 6626, it can be deduced that the DNA profile for Georg Adam Dillman/George Stillman is the same as that of 29019. Therefore Georg Adam Dillman/George Stillman had no mutation. He passed a mutation to his son, George but not to his son, John.

The second person whose DNA profile can now be conclusively confirmed is Hans Georg Dillmann himself. Prior to these results, the DNA profile for 6626 was deduced to be the Haplotype of Hans Georg since it was an intermediate profile between participants 2733, 7076 on one side and 5505 on the other. Now that we know the profile of his son, Georg Adam and that of his son, Andrew and that they are identical, we know that Hans Georg must have had the same DNA profile. It is statistically improbable for someone to pass along the same mutation to 2 sons due to the low mutation rates. That marker value would have to be the same as the one contained in Hans Georg's Y-chromosome.

Other remarks

Figure 6 provides a bit of discomfort in one respect. This has to do with the independent appearance of the CDY –b 38 mutation in the Stillman line AND in participant 5633's results. Also, mutation 576 – 17 appears to have arisen independently in participant 14431's results and in participant 5505's result. I will look into this further in the section on Family Tree Based on DNA.

Conrad Dillman

Before moving on to the Expected Number of Mutations analysis, I also wanted to draw attention to the chart in Figure 7. In Figure 7, I am displaying the children of Hans Georg Dillmann and Margaretha Murr from the research of Barbara Jensen. Instead of formatting the tree so the children are evenly spaced, I have deliberately squeezed them together. I left Georg Adam, Andrew, and Georg Michael in the same positions as they were in Figures 5 and 6. I placed the daughters in between in order of birth (except Margaretha as I wanted to keep Georg Adam where he was). If you turn back to Figure 6 then to Figure 7, it is clear that the only son who is "unaccounted" for in the DNA study, is Conrad. Coincidentally, and this is pure coincidence (not science or documentary research), the only unconnected lines we have for this group are participants 22978 and 25672. The link for these participants into the Dillmann family of Hans Georg could be through Conrad. I am not saying that this is the case, but this is a possibility that should be investigated by the researchers of these two participants trees. However, it may be that this potential link with Conrad Dillman may not fit with the facts.

Another possibility is that these participants descend from close relatives of Hans Georg, possibly his brothers or first cousins.

Figure 6.

Dillman Family Tree from DNA and paper trail

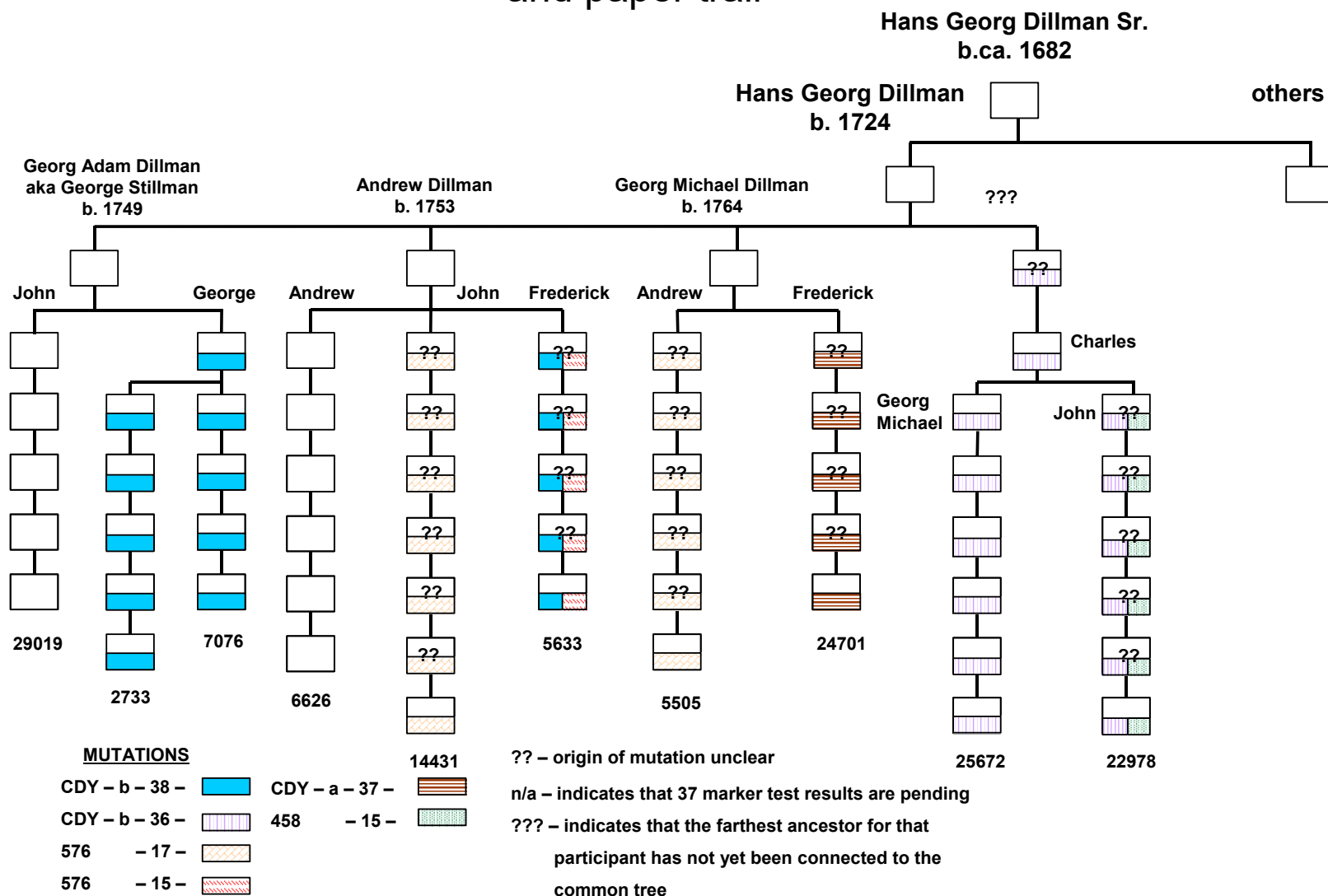
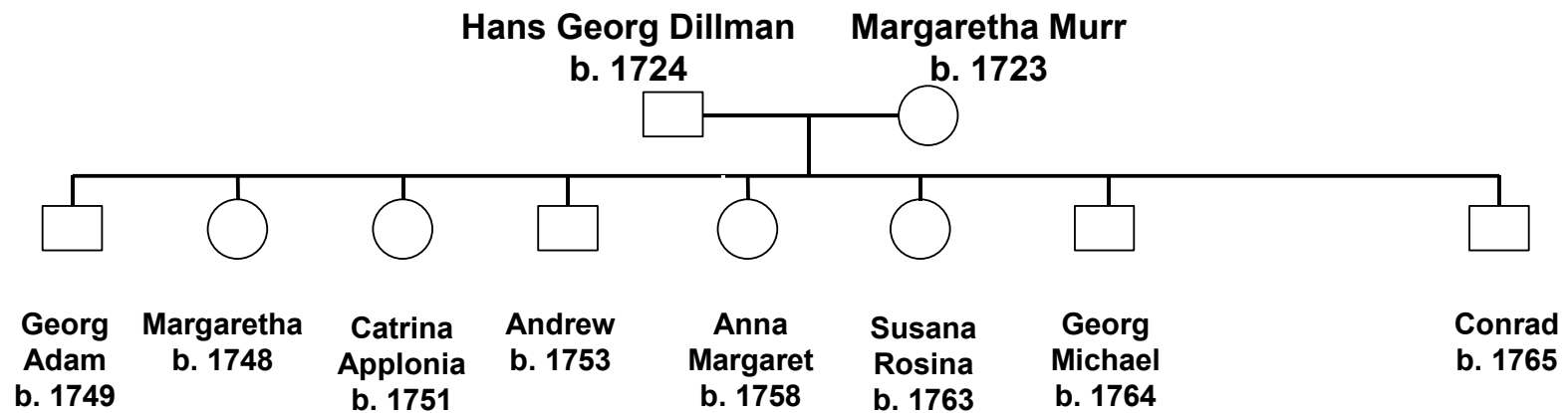


Figure 7.

Dillman Family Tree from B. Jensen



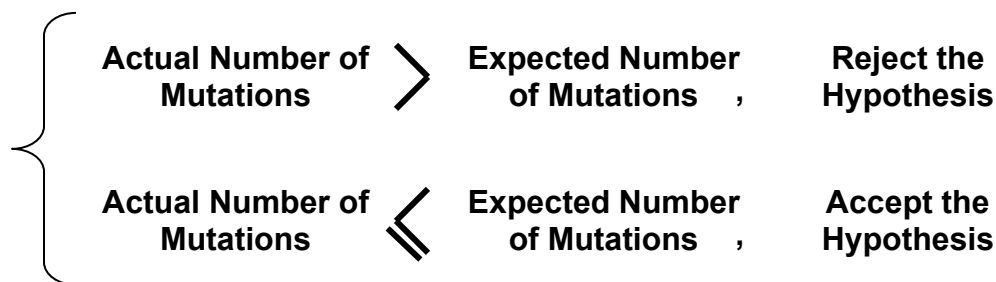
Expected Number of Mutations

Looking now at the Expected Number of Mutations versus the Actual/Observed Number of Mutations, we should explicitly set out the testing criteria. The first item we need to have is a hypothesis to test. The manner in which we test the hypothesis is to use the formula provided by Dr. James Freed in his presentation to the Dillman Family Association at the 2004 Mega Reunion. The formula for Expected Number of Mutations has been given as:

$$\left(\begin{array}{c} \text{Number of} \\ \text{Transmission} \\ \text{Events} \end{array} \right) \times \left(\begin{array}{c} \text{Number of} \\ \text{Markers} \\ \text{Tested} \end{array} \right) \times \left(\begin{array}{c} \text{Average} \\ \text{Marker} \\ \text{Mutation Rate} \end{array} \right)$$

Transmission events are the number of father-son events, that is, where the DNA markers are transmitted from one generation to the next.

And finally, we need rules for evaluating the results. A rule should be simple and easy to understand and implement. For now, we should continue to use the rule that if the Actual Number of Mutations is greater than the Expected Number of Mutations, then we have to reject the hypothesis. Alternately, if the Actual Number of Mutations is less than or equal the Expected Number of Mutations, then we can safely accept the hypothesis. These rules are shown diagrammatically below:



The next 2 paragraphs can be safely ignored by most readers. It is here for completeness only....

I don't want to make things more complicated than they need to be, however, I feel it is important to mention that these two simple rules do have some drawbacks. Firstly, what if the Actual Number of Mutations were fractionally higher than the Expected Number, do we still reject the hypothesis? And since mutations are random events and the mutation rate is an *average*, some mutations will happen faster than the average rate, some slower. If we have a situation where the mutations happen faster than average, we may have a higher Actual Number than the Expected number would lead us to believe the hypothesis is acceptable even though the rule would tell us to reject it. Hence, there should be a range of values above the Expected Number that should still allow us to accept the hypothesis. At present, there is no acceptable way to define this range.

Also, on the other end, if the Actual Number of Mutations is 0 or small relative to the Expected Number of Mutations, we may not be considering an adequate number of transmission events (generations) to the common ancestor, making the common ancestor appear closer in time to the participants than may actually be the case. Alternately, there may not be enough participants in the study.

I think it is acceptable to round the results of the Expected Number of Mutations calculation since either there is a mutation or there isn't. There is no such thing as a partial mutation. That being said, in the table below, I have left 1 decimal place so everyone can see the potential effect of rounding.

The table below looks at 8 different situations. According to the rules laid out above, I would accept all 8 hypotheses. Let's examine the first hypothesis (H1) closely. The participants listed are the 8 for whom we have been able to link directly to Hans Georg Dillman and the hypothesis is whether it is possible that all 8 share a common ancestor in Hans Georg.

Figure 8.

Hypothesis	Participants	Actual Number of Mutations	Transmission Events	Markers	Avg. Mutation Rate	Expected Number of Mutations	Accept/Reject Hypothesis
H1	29019, 2733, 7076, 6626, 14431, 5633, 5505, 24701	6	47	37	0.0058	10.1	Accept
H2	6626, 5633, 14431	3	18	37	0.0058	3.9	Accept
H3	6626, 5633	2	11	37	0.0058	2.4	Accept
H4	6626, 14431	1	13	37	0.0058	2.8	Accept
H5	5633, 14431	3	12	37	0.0058	2.6	?
H6	5505, 24701	2	11	37	0.0058	2.4	Accept
H7	22978, 25672	1/3*	12	37	0.0058	2.6	Accept
H8	29019, 2733, 7076, 6626, 14431, 5633, 5505, 24701, 22978, 25672	9	61	37	0.0058	13.1	Accept

H1 - Hans Georg Dillmann is the common ancestor for these lines

H2 - Andrew Dillman is the common ancestor for these lines

H3 - Andrew Dillman is the common ancestor for these lines

H4 - Andrew Dillman is the common ancestor for these lines

H5 - Andrew Dillman is the common ancestor for these lines

H6 - George Michael Dillman is the common ancestor for these lines

H7 - Charles Dillman is the common ancestor for these lines

H8 - Hans Georg Dillmann is the common ancestor for these lines

* - Note that when considering these two lines, there is only 1 mutation between them.

However, to keep the counting consistent relative to the assumed DNA profile of Hans Georg we can also consider there to be 3 mutations.

We can see that there are 6 mutations (from Figure 5) and 47 father-son transmissions. Using the formula above produces an Expected Number of Mutations of 10.1, or 10 when we round the number. We have seen there are only 6 mutations versus an expected number of 10. Therefore, we can accept the hypothesis that Hans Georg is indeed the common ancestor. This confirms the earlier conclusion that Georg Adam, Andrew, and Georg Michael were brothers.

H2 to H5 deals solely with the Andrew Dillman line. Since we have a variety of DNA test results here, it is interesting to study this line further. With the exception of H5 where I have placed a question mark in the column for Accept or Reject the Hypothesis, all the tests were conclusively "Accept". When we make use of rounding, and round the Expected Number from 2.6 to 3 for H5, we again have to "Accept" the hypothesis. Even if we did not round the results, I would suggest that through the use of logic, we would still be required to "Accept" the results. It would not be physically possible for all three

participants in H2 to be deemed to be descendants of Andrew Dillman and then have every combination of pairs produce a result of accepting the hypothesis except for H5. That just would not be logical and would defy documentary evidence.

Similarly, with H6 there are 2 mutations within these 2 lines. The expected number of mutations works out to be 2.4, or 2 with rounding. We have observed 2 mutations so we accept that George Michael is the common ancestor.

H8 is also an interesting case. This hypothesis tests if all 10 participants, documented or not, could descend from Hans Georg Dillman. The result was that we must accept the hypothesis (perhaps more accurately, that we cannot reject the hypothesis).

This leads us to another technicality in hypothesis testing. This technicality is that that by accepting a hypothesis, we are not necessarily proving something to be true. We are merely saying that we don't have enough evidence to reject the hypothesis. This is a negative test.

This ties in to what I was referring to in the section on the review of the DNA presentations from the 2004 Mega Reunion. We have not proven that Hans Georg Dillman is definitely and conclusively the common ancestor, but we have proven that it is possible for him to be the common ancestor.

FAMILY TREE BASED ON DNA

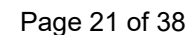
Taking this discussion a step further, I have constructed an alternate family tree to the one in Figures 5 and 6 for the sake of argument. This alternate tree is based only on minimizing the mutations found in the DNA results and the chart is shown in Figure 9. (At this point I should apologize to anyone who may be offended by my redrawing the family tree in this simulation exercise which may have resulted in some grossly incorrect branches. However, the purpose of this discussion is to demonstrate that other trees can also result in hypotheses that are shown to be possible based on analysis relying strictly on DNA test results).

Since the results for participant 5633 are intriguingly similar to those of participants 2733 and 7076, I have left them connected under Hans Georg Dillmann on the left hand side of the tree. The tradition of an elderly Andrew Dillmann signing up for the Revolutionary War with several of his sons is strongly entrenched in the family history and in earlier published genealogies. With one of these sons also being an Andrew Dillman, born in 1751, I opted to also show this Andrew on the right hand side of the chart. Since the test results for participants 6626 and 14431 were a bit different from those of their distant cousin 5633, I have placed them under this Andrew.

Participant 5505 was not 100% confident of his line of descent from Georg Michael Dillman. As his results were identical to those 14431, I have placed his lineage onto this branch. I have also placed participants 22978 and 25672 under this Andrew to reduce the number of mutations (had I placed them under Hans Georg, somewhere along the line there would have to have a 2 step mutation on marker CDY-b)

After these changes, if we focus on the line on the left up to and including Hans Georg, it is now possible that the mutation of CDY – b - 38 may have been present in Hans Georg with a reversion of the mutation on the John Stillman line. Other than John Stillman, all the tested participants in this line share this same mutation. Also, this pushes back the common ancestor of all participants by at least one generation.

Dillman Family Tree from DNA only



Below I have recreated most of the hypothesis testing results. H3-H5 are not applicable based on the alternate tree. H6 would show no change so it has been left out. I have relabeled the hypotheses with a lower case letter to distinguish them from the first set of hypotheses.

Figure 10.

Hypothesis	Participants	Actual Number of Mutations	Transmission Events	Markers	Avg. Mutation Rate	Expected Number of Mutations	Accept/Reject Hypothesis
H1a	29019, 2733, 7076, 5633	2	22	37	0.0058	4.7	Accept
H2a	6626, 14431, 5505	1	19	37	0.0058	4.1	Accept
H7a	6626, 14431, 5505, 22978, 25672	3	34	37	0.0058	7.3	Accept
H7b	29019, 2733, 7076, 5633, 6626, 14431, 5505, 24701, 22978, 25672	8	64	37	0.0058	13.7	Accept

H1a - Hans Georg Dillmann is the common ancestor for these lines

H2a - Andrew Dillman is the common ancestor for these lines

H7a - Andrew Dillmann Sr. is the common ancestor for these lines

H7b - All participants descend from a common ancestor through either the Hans Georg or the Andrew Dillmann Sr. lines

** - Note that when considering this line, there is only 1 mutation between them.

However, to keep the counting consistent, we can also consider there to be 3 mutations.

While all the hypotheses are accepted and the number of mutations is minimized, there are clearly several problems with this alternate tree. The first problem is that it is necessary in this case for Hans Georg and Andrew Dillmann Sr. to be closely related. This does not seem to have ever popped up in family tradition and is certainly very speculative.

The second problem is that there is no documentary evidence to indicate that 5505 descends from Andrew Dillman Jr, born in 1751. In fact, there does not appear to be evidence to date of the existence of two Andrew Dillmans (one born in 1751 and the other born in 1753) producing offspring although both sides suggest that both Andrew Dillmans married Barbara Roush. Obviously in this case, there can only have been one Andrew Dillman who married Barbara Roush. Perhaps the other Andrew Dillman did not survive to adulthood or moved away.

Another issue is that the CDY mutation carried by participant 5633 could have developed independently of the same mutation carried by the Stillman branch. Likewise for the 576 mutation for participants 14431 and 5505. There are other projects where the same mutation has developed in different branches. An example is the Mumma Surname Project, which incidentally was FTDna's first surname project and can be located at: www.mumma.org/DNA.htm (scroll down to almost the bottom). It could be that both lines inherited a region for a particular marker that is unstable from the common ancestor.

There are several things to remember from this section. The first is that it is possible to construct alternate family trees that would be consistent with the DNA results. The second is that these trees can generate more problems/discrepancies than the ones they are remedying. And lastly, although the Hans Georg Dillman tree may cause a reassessment of the Andrew Dillmann Sr. tradition, it does provide a better fit between both documentary evidence AND DNA testing.

Future Testing For G2 Cluster

For future testing of the G2 cluster, I would suggest the following prioritization (shown in the list below).

We have seen that stronger results from hypothesis tests come when we are able to reject the hypothesis. Hence to conclusively be able to discard the Andrew Dillmann Sr. tradition, it would be necessary to find a documented descendant of this Andrew Dillmann Sr. through other sons (Conrad – b. 1730, Christian b. 1732, John b. 1734, Michael b. 1736, Anthony b. 1738 or William b 1740) who because of their birth dates cannot be confused with sons of Hans Georg Dillman. The test results could indicate that this line has a very different DNA profile than the Hans Georg line.

Documented male descendants of Conrad, born 1765, son of Hans Georg Dillman would be a great benefit to the Dillman DNA Project. It would be ideal to get the DNA for the final son of Hans Georg. It would also be very useful in comparing with the results for 22978 and 25672.

Also, it would be interesting to have participants from Germany who relate to either of the Hans Georg or the Andrew Sr. lines.

I think that at this point in the study, we can continue to derive useful information in testing both documented and undocumented male Dillmans. Naturally having documented lines would be valuable, but with the rarity of the haplogroup and the surname, we can still draw meaningful conclusions.

Potential Test Participants Wish List

- 1) Descendants of Andrew Dillmann Sr. sons (other than Andrew and Georg Michael)
- 2) Descendants of Conrad Dillman, born 1765, son of Hans Georg
- 3) German descendants related to Hans Georg
- 4) German descendants related to Andrew Sr.
- 5) Any other Dillman, documented or undocumented

Concluding Remarks For G2 Cluster

The conclusion drawn from analyzing the 4 sets of 37 marker results at the 2004 Mega reunion was that it is possible that Hans Georg Dillmann was the father for Georg Adam Dillman/George Stillman, Andrew Dillman and Georg Michael Dillman. With the addition of 6 more 37 marker tests, that conclusion is even more strongly supported. As each new test result comes in, we find that the conclusion remains the same. Each new test continues to shed light on the DNA profiles of our ancestors.

Discussion of the R1b Cluster, Group 1

The Haplogroup for this Group has been confirmed by Family Tree DNA.

Until recently, there weren't enough participants in this group to proceed with more detailed analysis. Previously, there had been only 2 set of 37 marker results and those participants had no documentation to link up their family trees. Also, the 4 participants in this group do not know who their common ancestor was. Hence, we can't yet identify this group by the common ancestor's name.

Participant 29650's lineage linked his line to a brother of Hans Georg Dillmann. However, his DNA results were quite surprising. They were a perfect match with 1 of the 2 Group 1 participants (27114). Clearly they share a common ancestor. There are 2 possible alternatives to explain these results. The first is that the lineage of 29650 is not correct, that is, his ancestor may not have been the brother of Hans Georg Dillmann. The second alternative is that there was a "non-paternity" event. That is, it is possible that Hans Georg Dillmann's mother had a child with someone other than Hans Georg Dillmann Sr. and this child was raised with the surname Dillmann.

In consultation with June Riccio, we have been able to connect participant 10463 into the same tree as 29650. 29650 and 10463 are 3rd cousins once removed. Please refer to Figure 11, a version of which is also available on the DDNA website.

Participant 5945 has not been able to document his line back. However, it seems very likely that his furthest back ancestor was the grandson of Peter Dillman, b. 1781, who was the son of Anthony Dillman. Since 5945 has a mutation that the other 3 participants with 37 marker results don't have, it is possible that DNA testing may help provide the missing link.

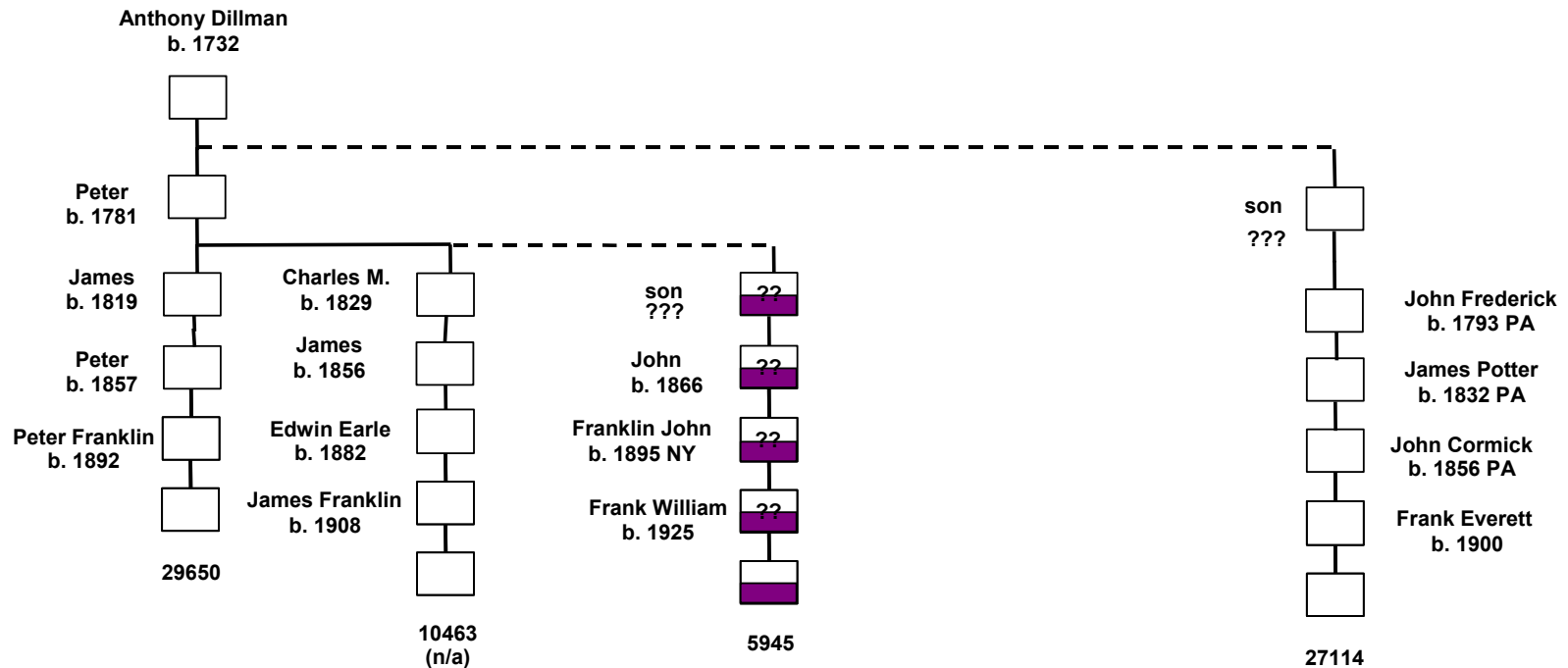
Further testing for this Group should focus on male descendants of Elmer Dillman. Elmer Dillman's father, George Dillman b. ca. 1812, is the son of Peter Dillman, 1781, in Figure 11. George Dillman is also known to have had a son, John. It is possible then that George Dillman is the ancestor who would connect 5945 to the Anthony Dillman lineage. If Elmer's descendants share the same mutation as 5945, it would be possible to conclude that the John Dillman, b. 1866 and Elmer were brothers.

Currently, it is not possible to analyze mutations as there have been no mutations in the documented lineages and the 2 other lineages are not yet conclusively linked.

Please refer to the earlier section on Haplogroups for a discussion on the origins of R1b.

Figure 11.

Possible family tree for the R1b cluster



MUTATIONS

576 - 19 -

?? – origin of mutation is unclear

n/a – indicates that 37 marker test results are pending

??? – indicates that the farthest ancestor for that participant has not yet been connected to the common tree

Discussion of the I Cluster

This cluster descending from Christopher Dillman have been confirmed as being in Haplogroup I.

As DNA testing for genealogical purposes is still a relatively new field, much of the available information is presented and discussed on the Rootsweb Genealogical-DNA maillist. There are several renowned scientists who regularly contribute to the knowledge being circulated in this medium. The list's expert on the Haplogroup I uses markers 392,392 to discriminate the subclade of I1c from I1a and I1b. When the marker values are 12,15, as in the case with the Dillman I cluster, the Haplogroup can be distinguished clearly as I1c.

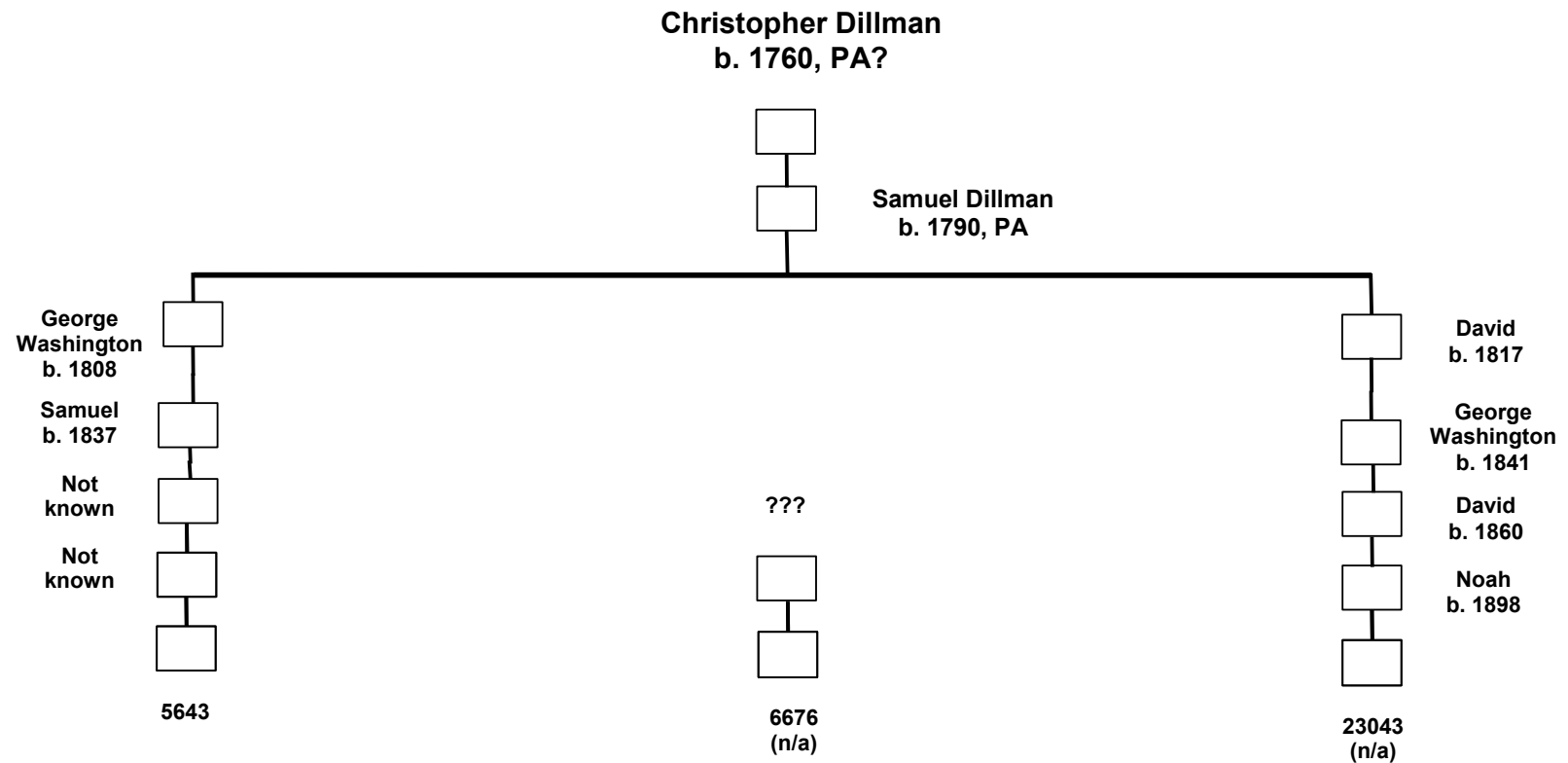
Other representative markers for I1c are 459a and 459b with values of 8,9. These values for 459a and 459b further break I1c into a "southern" variety that made their way along the Mediterranean rather than the "northern" route along the Baltic. Again, this marker values for this I cluster in the DDNA have the values 8 and 9.

Please refer to the earlier section on Haplogroups for a discussion on the origins of I1c.

A family chart appears in Figure 12 for this cluster. The 3 participants in this cluster do not all have 37 marker results. Also, participant 6676 has not provided his lineage. Hence, it is not possible to do conduct further analysis at the present.

Figure 12.

Family tree from paper trail for the I cluster



n/a – indicates that 37 marker test results are pending
??? – indicates that the farthest ancestor for that participant has not yet been connected to the common tree

Discussion of the R1b Cluster, Group 4

Please refer to the Haplogroup discussion for information on the Haplogroup R1b.

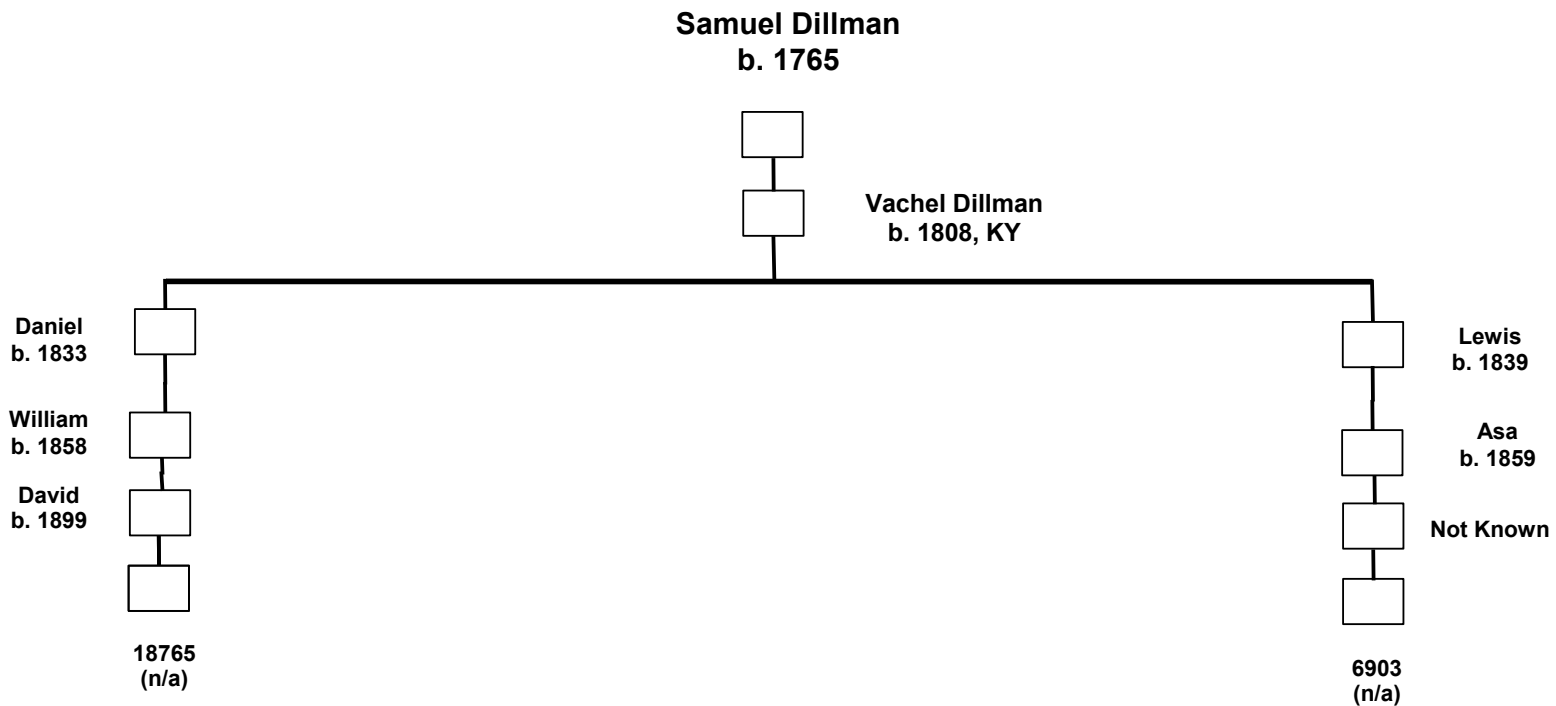
This line has marker values that are different enough from the R1b Cluster, Group 1 to distinguish it as a separate family. Looking at the 25 marker results there are 8 markers where the values differ from those of Group 1. Of those, 1 marker is off by 3 and another marker is off by 2. Clearly, these are not close relatives to Group 1.

Again, the 2 participants in this group do not have the same level of DNA testing so it is difficult to draw any conclusions at this point.

A family chart follows in Figure 13.

Figure 13.

Family tree from paper trail for the R1b cluster, Group 4



n/a – indicates that 37 marker test results are pending
??? – indicates that the farthest ancestor for that participant has not yet been connected to the common tree

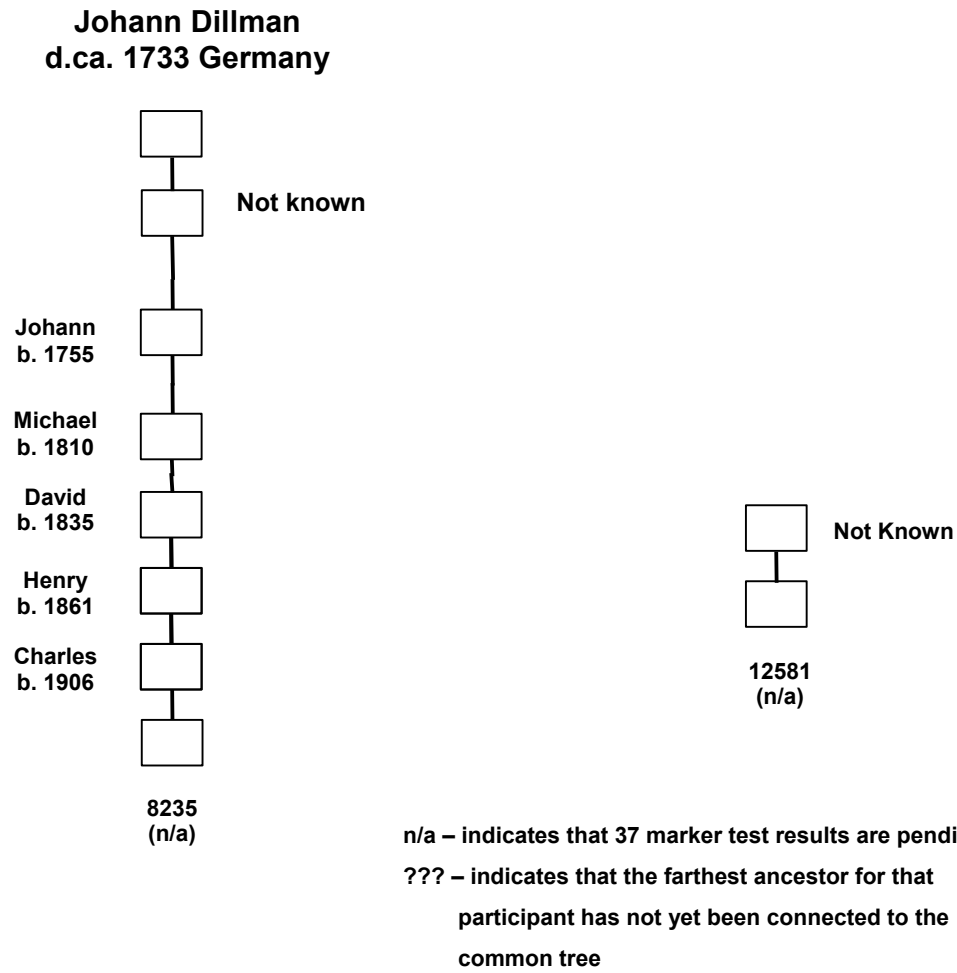
Discussion of the Johann Dillman Cluster

A family chart follows in Figure 14 for this cluster. It is very difficult to predict Haplogroups with only 12 marker tests, as is the case for this cluster. However, an initial indication using a web based Haplogroup predictor seems to say that this cluster may belong to Haplogroup I. Again, with only 12 markers, this is not certain. It is possible that this cluster's Haplogroup may turn out to be J or E.

There can be no analysis done on this cluster since there is only 1 participant who has provided a lineage and existing test results are only at the 12 marker level.

Figure 14.

Family tree from paper trail for the Johann Dillman cluster



Discussion of the J2 Cluster

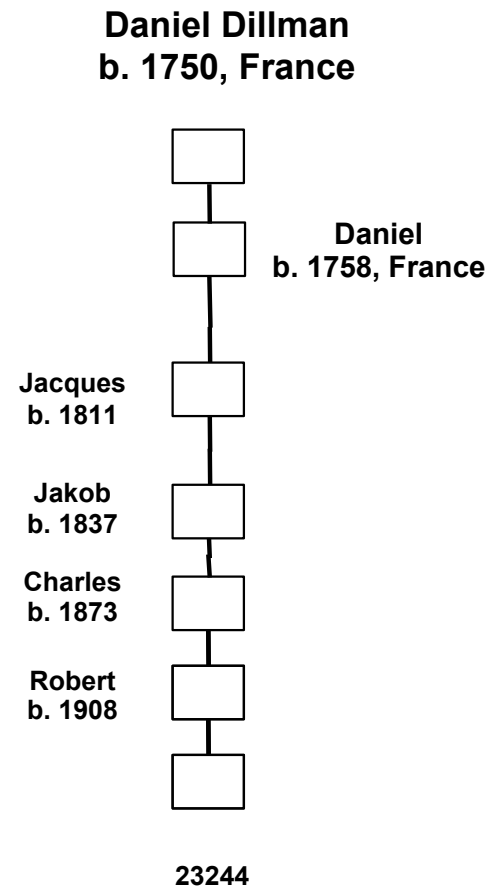
A family chart follows in Figure 15 for this cluster.

Please refer to the Haplogroup section for a discussion of the J2 haplogroup.

As there is only 1 participant in this cluster, very little analysis can be currently completed.

Figure 15.

Family tree from paper trail for the J2 cluster



APPENDIX 1: MULTI-COPY MARKERS

A multi-copy marker is a special marker, which will often copy itself in at least one other location on the Y-chromosome. For instance, CDY is a multi-copy marker as there are 2 versions of it, i.e., CDY a and CDY b. Other examples include markers 385, 459, 464 (usually 4 copies), and YCA2. The DNA testing process **CANNOT** distinguish which copy they are measuring. Hence, results are *always* reported in ascending order.

This can be seen readily with marker 464. The values of STRs returned are 12, 13, 13, 14. Hence, FTDNA (and other testing companies) will report the values as follows:

KIT	4	4	4	4
	6	6	6	6
	4	4	4	4
	a	b	c	d
2733	12	13	13	14

The results may actually be more like:

KIT	4	4	4	4
	6	6	6	6
	4	4	4	4
	a	b	c	d
2733	13	14	12	13

With present testing equipment and processes, there is no way to tell which is the actual value for any of the individual copies.

It is important to keep this in mind since one of the mutations in the G2 cluster of the Dillman DNA Surname Project involves the multi-copy marker, CDY. The mutation on CDY for participant 5633 may not be the same as for participants 2733 and 7076 or vice versa. The results may actually be reversed (and then would be two mutations one on CDY – a and the other on CDY – b) in the reporting of the locations since the testing company cannot distinguish one from the other.

APPENDIX 2: MARKER VALUE FREQUENCIES FOR G2 CLUSTER'S DEDUCED ANCESTRAL HAPLOTYPE

Marker		Value for DAH ¹	Frequency ²	Marker		Value for DAH ¹	Frequency ²	Marker		Value for DAH ¹	Frequency ²
1	393	14	11%	13	458	15	18%	26	460	11	57%*
2	390	22	12%	14	459 - a	9	22%	27	GATA H4	12	53%*
3	19	16	20%	15	459 - b	9		28	YCA II - a	20	2%
4	391	10	50%*	16	455	11	83%*	29	YCA II - b	20	
5	385 - a	14	4%	17	454	11	94%*	30	456	15	35%*
6	385 - b	14		18	447	23	14%	31	607	13	N/A
7	426	11	35%	19	437	16	17%	32	576	16	N/A
8	388	13	9%	20	448	21	9%	33	570	18	N/A
9	439	11	34%	21	449	29	32%*	34	CDY - a	36	N/A
10	389-I	13	62%*	22	464 - a	12	N/A	35	CDY - b	37	
11	392	11	32%	23	464 - b	13		36	442	11	19%
12	389-II	31	N/A	24	464 - c	13		37	438	10	29%
				25	464 - d	14					

NOTES:

1) DAH - Deduced Ancestral Haplotype. These are the estimated marker values for the Common Ancestor, in this case, Hans Georg Dillman.

2) The value frequency is as determined by the Sorenson Molecular Genealogy Foundation. This can be seen on their website: <http://smgf.org:8081/pubgen/site23.jsp>. Please note that they don't use the same markers as Family Tree DNA, hence some of the frequencies are not available.

* - This is the value with the highest frequency for this particular marker.

GLOSSARY

SNPs or Single Nucleotide Polymorphisms – are variations in the bases (A, G, T, C) at specific locations on the chromosome that occur very infrequently. These changes can be used to track humans geographically back in time. SNPs are used to identify Haplogroups.

STRs or Short Tandem Repeats – each marker contains a series of bases A, C, G, and T in a seemingly random pattern. Within the segments of bases, there are often patterns that repeat themselves. For instance, if the following were the bases contained in hypothetical Marker named XYZ-3:

ACTAGGAT**CATACATACATACATACAT**AGTGAGC

it can be seen that part of the segment is repeated several times. That is, the bases **CATA** are repeated several times. **CATA** is a short tandem repeat. The marker value (or allele) for this marker would be 5 since **CATA** is repeated 5 times in this segment of DNA.

For terms not defined here, please refer to the bottom of Page 2 of the handout provided by Dr. James Freed at the 2004 DFA Mega Reunion:

<http://www.dillmanfamilyassociation.org/PDF/DrFreedHandout.pdf>

Another excellent glossary by Charles Kerchner can be found at (Charles has recently published a book on Genetic Genealogy Definitions so this link may be removed at some point):

<http://www.kerchner.com/glossary.htm>

Reference List

1st International Conference on Genetic Genealogy for Family Tree DNA Group Administrators.
Houston, October 30, 2004

freepages.genealogy.rootsweb.com/~dgarvey/DNA/Underhill_2003.html

home.comcast.net/~whitathey/haplogroups.htm

Pomery, Chris. DNA and Family History: How Genetic Testing Can Advance Your Genealogical Research. Dunburn Press, 2004. ISBN 1-55002-536-8

RootsWeb Genealogy-DNA list archives

www.census.gov

www.dillmanfamilyassociation.org

www.familytreedna.com

www.frankdillman.com

www.kerchner.com

www.mumma.org

www.scs.uiuc.edu/~mcdonald/WorldHaplogroupsMaps.pdf

www.smgf.org

www.stillman.org