

Mega Reunion Aug 2008

What DNA Tells Us

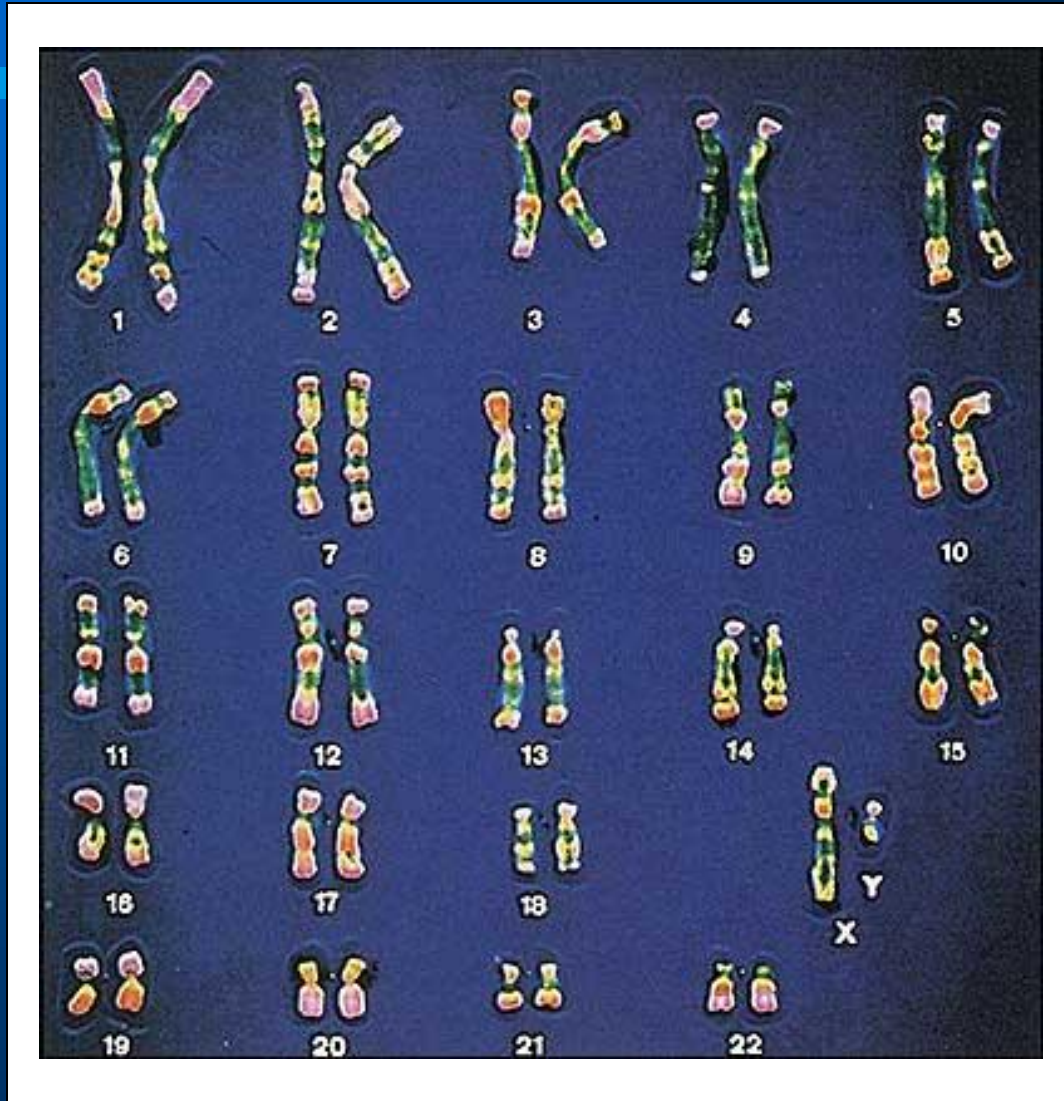
Andrew Stillman

Agenda

- DNA Review
- Results Michael Dhyllmann
- Updated Results Elias Dillmann
- Recent Events
- Conclusions



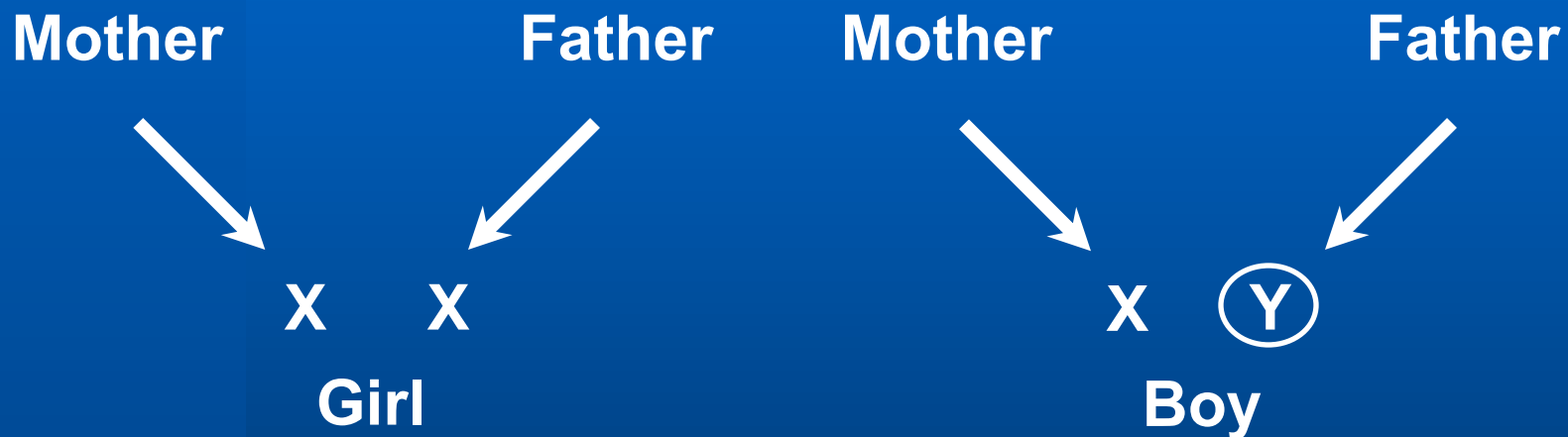
DNA Review



DFA Mega Reunion Aug 2008



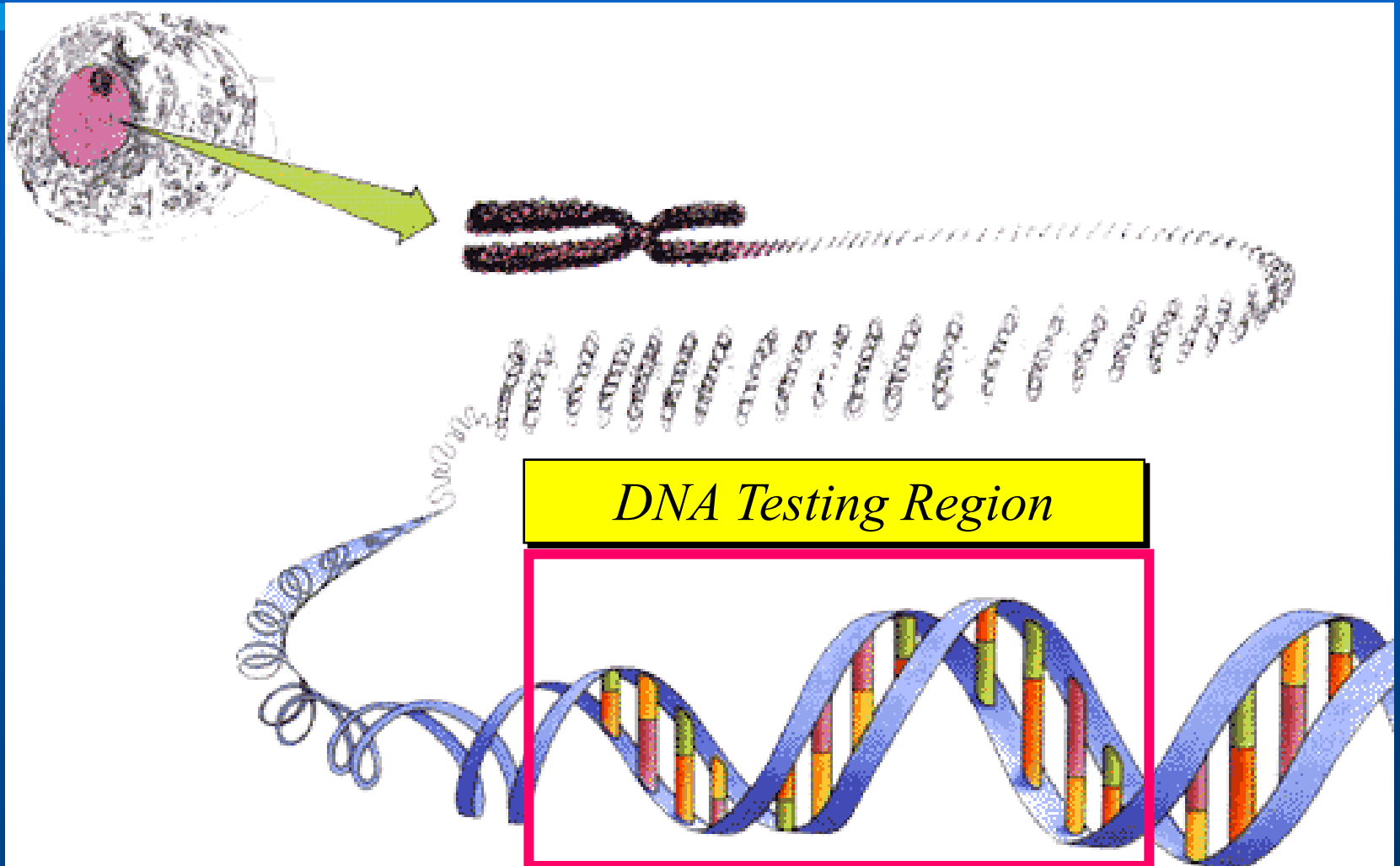
DNA Review



- DNA testing focuses on the Y-chromosome



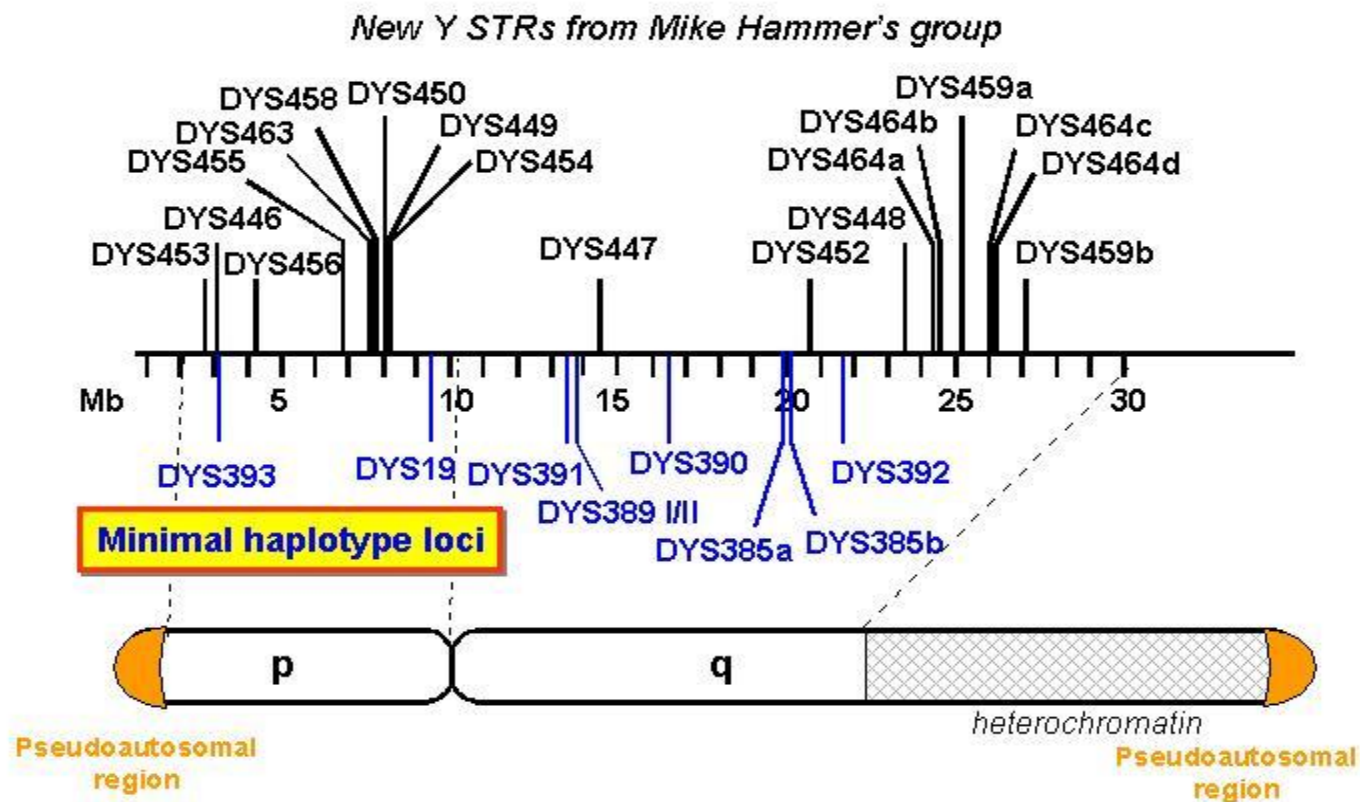
DNA Review





DNA Review

Y STR Positions along Y Chromosome





DNA Review

**Marker Values – number of repeated patterns,
i.e. 'TCTA'**

	1	2	3	4	5	6	7	8	9	
CTGTCTG	TCTA	TCTA	TCTA	TCTA	TCTA	TCTA	TCTA	TCTA	TCTA	TCTGCC

**If this were a marker, it would have a value of
'9'.**



DNA Review

Haplotype – set of marker results for an individual
(mutation = diff. number of repeats)

Haplogroup – collection of related haplotypes sharing a specific mutation
(mutation = diff. letter - 'A','C','G','T')

Mutation – an inheritable change in DNA sequence – a variance from the norm

DNA Results

I D	Y S e a r c h	H a p l o	G r o u p	A n c e s t o r	3 9 3	3 9 0	1 9	3 9 1	3 8 5 a	3 8 5 b	4 2 6	3 8 8	4 3 9	3 8 9 I	3 9 2	3 8 9 II	4 5 8	4 5 9 a	4 5 9 b	4 5 5	4 5 4	4 4 7	4 3 7	4 4 8	4 4 9	4 6 4 a	4 6 4 b	4 6 4 c	4 6 4 d	4 6 0	G A T A H 4	Y C A 2 a	Y C A 2 b	4 5 6	6 0 7	5 7 6		
23244		J2	6	Daniel (France)	12	24	15	10	14	17	11	15	12	12	11	29	16	8	9	11	11	26	16	19	29	13	15	15	19	12	10	19	20	13	13	20		
8235		I	5	Johann Nicolaus (Germany)	13	23	15	10	13	15	11	12	11	13	13	29																						
12581		I	5		13	23	15	10	13	15	11	12	11	13	13	29																						
6903		R1b1	4	Samuel	13	24	14	10	11	13	12	12	12	13	13	29																						
18765		R1b1	4	Samuel	13	24	14	10	11	14	12	12	12	13	13	29	19	9	10	11	11	25	15	19	27	15	15	17	17									
52186		R1b1	4	John Tillman (LA)	13	25	14	10	11	14	12	12	12	13	13	29																						
5495	PJ64P	R1b1	1	George W. (PA)	13	24	14	11	12	14	12	12	12	13	13	30	18	9	10	11	11	26	15	19	30	14	15	15	17	11	11	19	23	16	16	19		
27114		R1b1	1	John Frederick (PA) - DAH	13	24	14	11	12	14	12	12	12	13	13	30	18	9	10	11	11	26	15	19	30	14	15	15	17	11	11	19	23	16	16	20		
29650		R1b1	1	Anthony (PA) - DAH	13	24	14	11	12	14	12	12	12	13	13	30	18	9	10	11	11	26	15	19	30	14	15	15	17	11	11	19	23	16	16	20		
10463		R1b1	1	Anthony (PA) - DAH	13	24	14	11	12	14	12	12	12	13	13	30	18	9	10	11	11	26	15	19	30	14	15	15	17	11	11	19	23	16	16	20		
43562		R1b1	1	Elmer (PA)	13	24	14	11	12	14	12	12	12	13	13	30	18	9	10	11	11	26	15	19	29	14	15	15	17	10	11	19	23	16	16	20		
55729		R1b1	1	Joseph (PA)	13	24	14	11	12	14	12	12	12	13	13	30	18	9	10	11	11	26	15	19	30	14	15	15	17	11	11	19	23	16	16	20		
5505	ZV9GE	G2*	2	Hans George(Germany)	14	22	16	10	14	14	11	13	11	13	11	31	15	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	17		
14431	WGD8X	G2	2	Andrew (PA)	14	22	16	10	14	14	11	13	11	13	11	31	15	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	17		
2733	N3C5J	G2	2	George Stillman (Canada)	14	22	16	10	14	14	11	13	11	13	11	31	15	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	16		
7076	445D8	G2	2	George Stillman (Canada)	14	22	16	10	14	14	11	13	11	13	11	31	15	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	16		
5633		G2	2	Andrew (PA)	14	22	16	10	14	14	11	13	11	13	11	31	15	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	15		
6626		G2	2	Andrew (PA) - DAH	14	22	16	10	14	14	11	13	11	13	11	31	15	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	16		
29019	RYRRT	G2	2	John Stillman (Canada)- DAH	14	22	16	10	14	14	11	13	11	13	11	31	15	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	16		
48630		G2*	2	Andrew (IA) - DAH	14	22	16	10	14	14	11	13	11	13	11	31	15	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	16		
24701		G2	2	Hans George (Germany)	14	22	16	10	14	14	11	13	11	13	11	31	15	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	16		
25672		G2	2	Charles	14	22	16	10	14	14	11	13	11	13	11	31	15	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	16		
22978		G2	2	John (KY)	14	22	16	10	14	14	11	13	11	13	11	31	16	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	16		
34763		G2	2	David T. Stillman (Canada)	14	22	16	10	14	14	11	13	11	13	11	31	15	9	9	11	11	23	16	21	29	12	13	13	14	11	12	20	20	15	13	16		
5843	8V9ND	I	3	Christopher (PA?)	15	23	12	10	15	15	11	13	12	13	12	31	16	8	9	11	11	26	15	20	30	11	15	15	15	11	11	19	21	14	14	16		
55841					15	23	12	10	15	15	11	13	12	13	12	31	16	8	9	11	11	26	15	20	30	11	15	15	15									
6676		I	3		15	23	12	10	15	15	11	13	12	13	12	31																						
23043		I	3	Christopher	15	23	12	10	15	15	11	13	12	13	12	31	16	8	9	11	11	26	15	20	31	11	15	15	15									

Haplogroup Frequency

- R – 55% + (R1a + R1b)
- I – 18% (higher in Nordic countries)
- J – 10%
- T – 2%
- G – 1-2%
- E, N, O, H

Updated Results

- **2006 Mega Reunion**

- 6 distinct Dillman families
- Hans Georg family – 10 part. with 37 markers + 2
- Anthony family – 7 part. with 37 markers
- Little change for remaining families
- ancestors from Germany & France

- **August 2008**

- 10 probable Dillman families
- Hans Georg family – no change
- Anthony/Elias family – 9 part. with 37 markers
- Michael family - 3 part. with 37 markers (1 German part.)
- Group 4 - 2 part. with 37 markers (Canada)
- Ancestors from Germany, France, Sweden, Russia, Switzerland

2 Approaches to Analysis

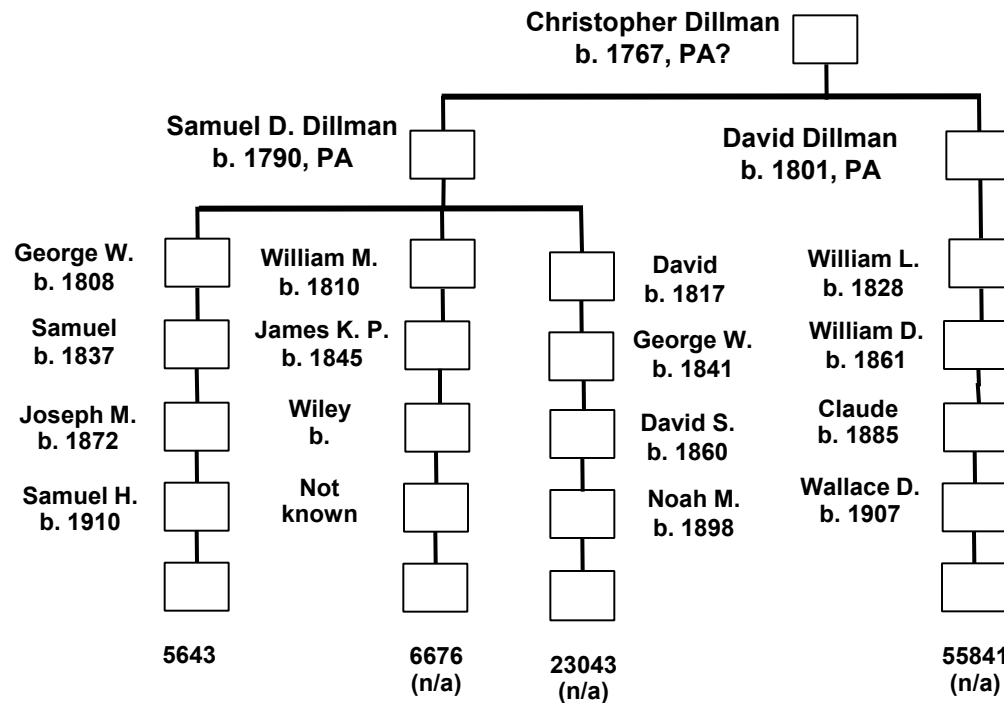
- **Analysis of mutations**

- Arriving at possible common ancestor
- Detailed look at individual generations

- **Expected number of mutations**

- Determine likelihood of proposed common ancestor
- Simple statistical analysis
- Based on average mutation rate, number of father-son relationships and number of markers used

Christopher Dillman family –2006



?? – 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

Michael Dhyllman family –2008

HAP:
I2b

Michael Dhyllmann
b. aft. 1500 Olbronn,
Germany
Michel Dillmann
b. bef. 1540 Germany
Georg Dillmann/Duellman
b. 1584 Wurmberg, Germany

Georg
b. 1621

Hans Jakob
b. 1651

Hans Jakob
b. 1680

Johann Georg
b. 1711

Christian Friedrich
b. 1743

Andreas
b. 1791

Michael
b. 1822

Matthaus
b. 1851

Friedrich
b. 1877

Erich Friedrich
b. 1915 Pforzheim, Germany
d. 2008



?? – 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

Jakob Dillmann
b. 1657, Germany

Johann Jakob Dillmann
b. 1685, Germany

George Friederich Dillmann
b. 1735, Germany

Christopher Dillman
b. 1767, PA



Samuel D. Dillman
b. 1790, PA

David Dillman
b. 1801, PA



George W.
b. 1808

Samue
I
b. 1837

Joseph M.
b. 1872

Samuel H.
b. 1910



William M.
b. 1810

James K. P.
b. 1845

Wiley
b. 1884-98

Not known



David
b. abt. 1820

George W.
b. 1841

David S.
b. 1860

Noah M.
b. 1898



William L.
b. 1828

William D.
b. 1861

Claude
b. 1885

Wallace D.
b. 1907



MUTATIONS

449 – 30 –

576 – 17 –

E1904

5643

6676
(n/a)

23043

55841
(n/a)

Michael Dhyllman Group – Hypothesis 1

Hypothesis – Michael Dhyllman is the common ancestor of the individuals tested.

$$\begin{array}{ccccccc} \text{Expected} & & \left(\begin{array}{c} \text{Number of} \\ \text{Transmission} \\ \text{Events} \end{array} \right) & \times & \left(\begin{array}{c} \text{Number of} \\ \text{Markers} \\ \text{Tested} \end{array} \right) & \times & \left(\begin{array}{c} \text{Average} \\ \text{Marker} \\ \text{Mutation Rate} \end{array} \right) \\ \text{Number of} & = & & & & & \\ \text{Mutations} & & & & & & \\ \\ 6 & & 28 & & 37 & & 0.0058 \end{array}$$

Actual - 2

Michael Dhyllman Group – Hypothesis 2

Hypothesis – Christopher Dillman is the common ancestor of 5643 and 23043.

$$\begin{array}{ccccccc} \text{Expected} & & \left(\begin{array}{c} \text{Number of} \\ \text{Transmission} \\ \text{Events} \end{array} \right) & \times & \left(\begin{array}{c} \text{Number of} \\ \text{Markers} \\ \text{Tested} \end{array} \right) & \times & \left(\begin{array}{c} \text{Average} \\ \text{Marker} \\ \text{Mutation Rate} \end{array} \right) \\ \text{Number of} & = & & & & & \\ \text{Mutations} & & & & & & \\ \\ 2.4 & & 11 & & 37 & & 0.0058 \end{array}$$

Actual - 1

Michael Dhyllman family

– Mutation Rates

#	Description	Transmission Events	Markers	Mutations	Mutation Rate ²	Statistical Uncertainty ³ (Std Deviation)	Possible Range in Values for Mutation Rate ⁴ (95% Confidence Interval in Mutation Rate)	FTDna estimated Mutation Rate
1	3 participants ⁵ markers 1-37	28	37	2	0.0019	0.0014	0.0000 - 0.0047	0.0058
2	2 participants ¹ markers 1-37	11	37	1	0.0025	0.0025	0.0000 - 0.0074	0.0058

NOTES:

1) The 3 participants are: 5643, 23043.

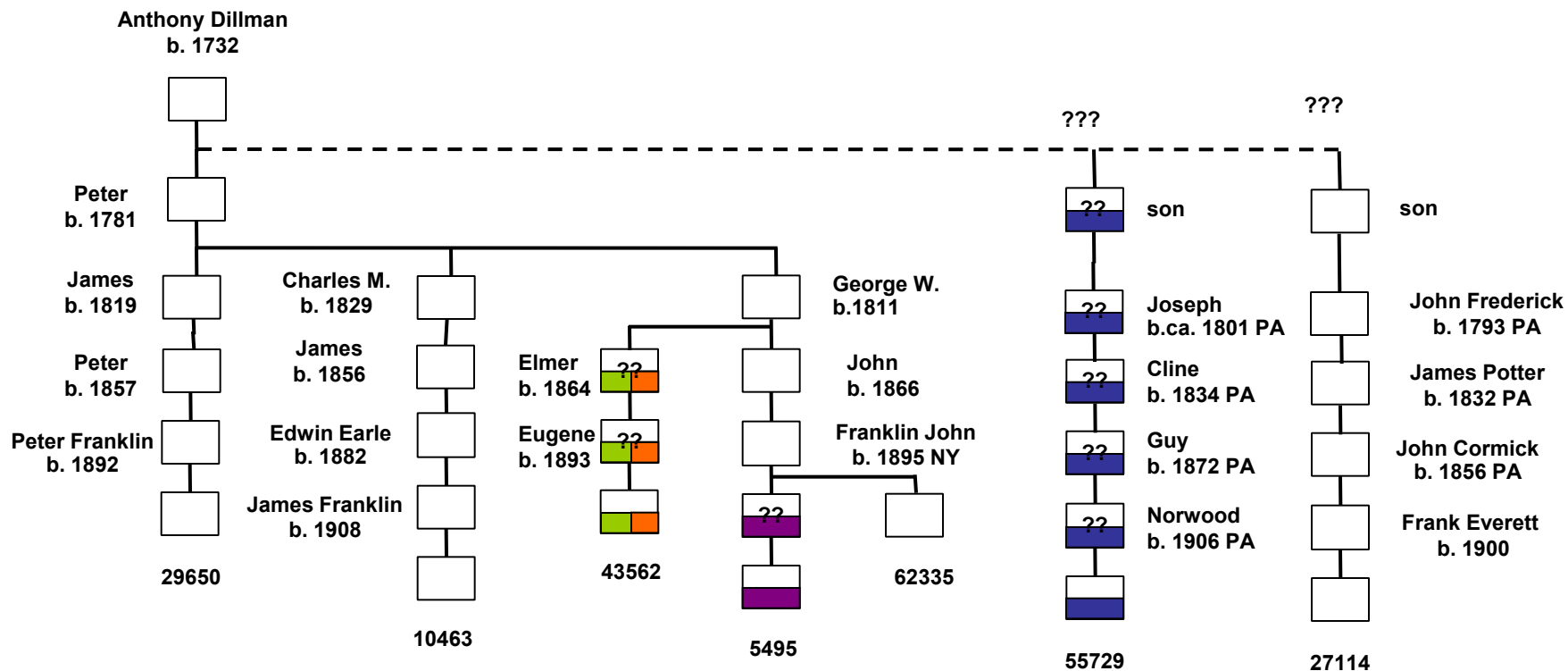
2) **Mutation Rate** is calculated as the number of **Mutations** divided by the product of **Transmission Events** and number of **Markers**.

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 3 participants are: E1904, 5643, 23043

Anthony Dillman family – 2006



MUTATIONS

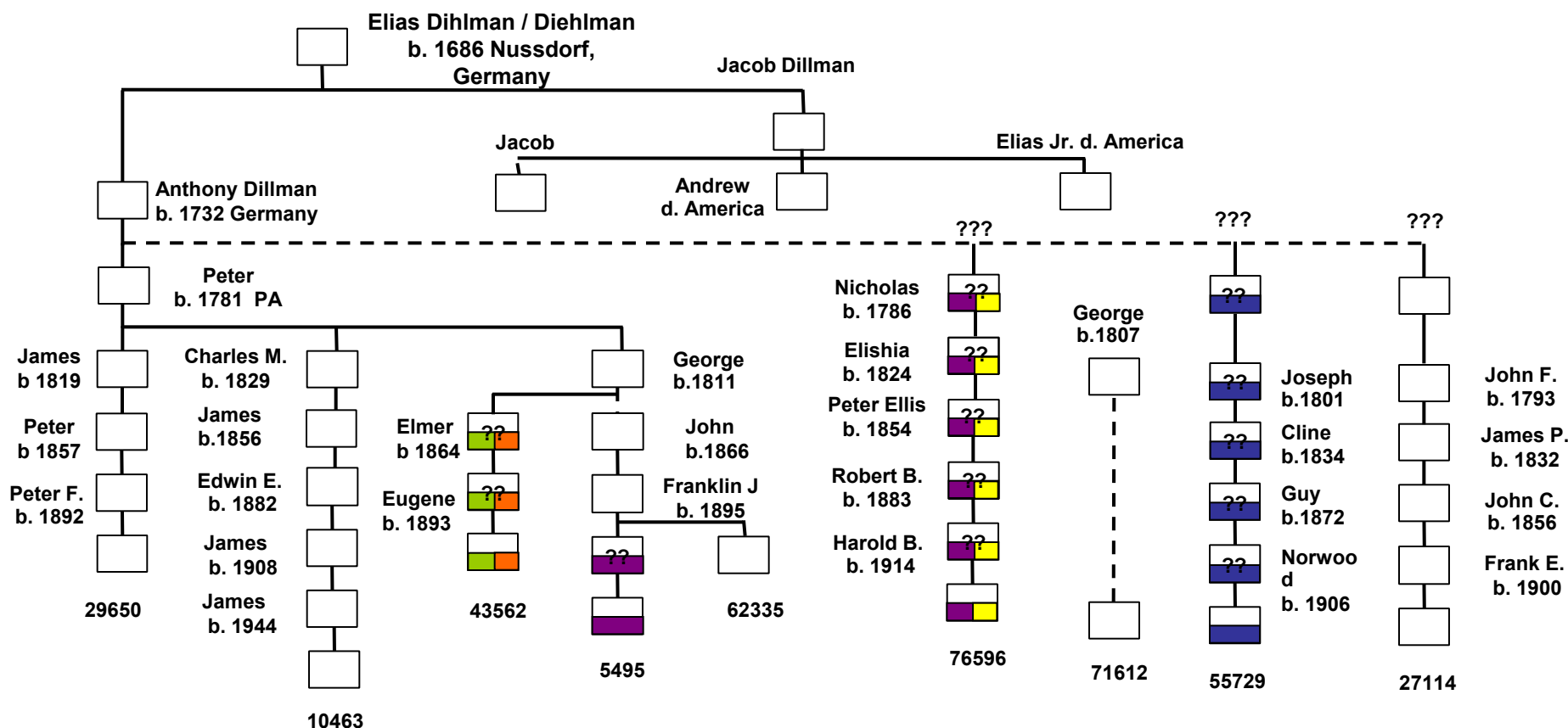
576	- 19 -	
449	- 29 -	
460	- 10 -	
442	- 11 -	

?? – 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

Elias/Anthony Dillman family – July 2008



MUTATIONS

576	- 19 -	CDY-b - 37 -
449	- 29 -	
460	- 10 -	
442	- 11 -	

?? – 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

Elias Dillman family – Mutation Rates

#	Description	Transmission Events	Markers	Mutations	Mutation Rate ²	Statistical Uncertainty ³ (Std Deviation)	Possible Range in Values for Mutation Rate ⁴ (95% Confidence Interval in Mutation Rate)	FTDna estimated Mutation Rate
1	5 participants ⁵ markers 1-37	19	37	3	0.0043	0.0025	0.0000 - 0.0092	0.0058
2	5 participants ⁵ markers 1-12	19	12	0	0.0000	0.0000	0.0000 - 0.0000	0.0040
3	5 participants ⁵ markers 13-25	19	13	1	0.0040	0.0040	0.0000 - 0.0121	0.0048
4	5 participants ⁵ markers 26-37	19	12	2	0.0088	0.0062	0.0000 - 0.0212	0.0075
5	7 participants ⁶ markers 1-37	31	37	4	0.0035	0.0017	0.0000 - 0.0070	0.0058
6	3 participants ¹ markers 1-37	12	37	3	0.0068	0.0039	0.0000 - 0.0146	0.0058

NOTES:

1) The 3 participants are: 43562, 5495, 62335.

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 5 participants are: 29650, 10463, 43562, 5495, 62335.

6) The 7 participants are: 29650, 10463, 43562, 5495, 62335, 55729, 27114.

Group 4 –2008

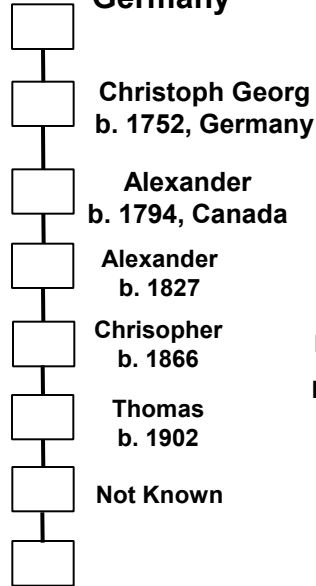
HAP:

R1b1 /

R1b1b2/

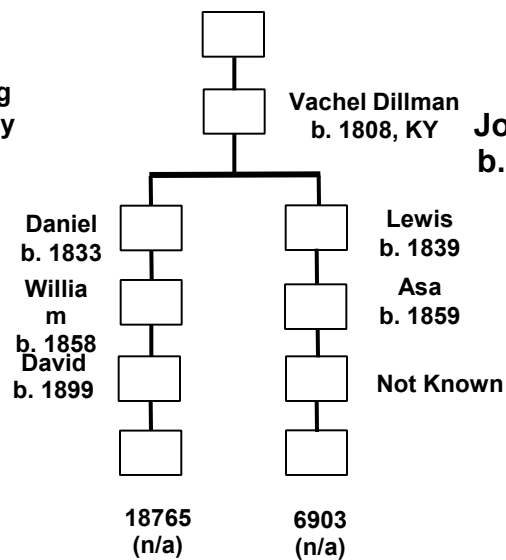
R1b1c

Johann Christof Diellman
b. 1710, Langenschwalbach,
Germany

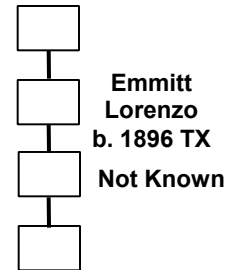


99126
(n/a)

Samuel Dillman
b. 1765

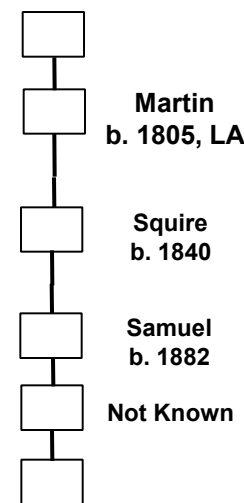


John B. Tillman
b. ca. 1855, MO



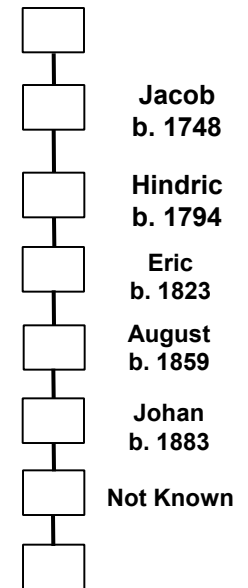
126503
(n/a)
R1b1c

John Tillman
b.ca 1782



52186

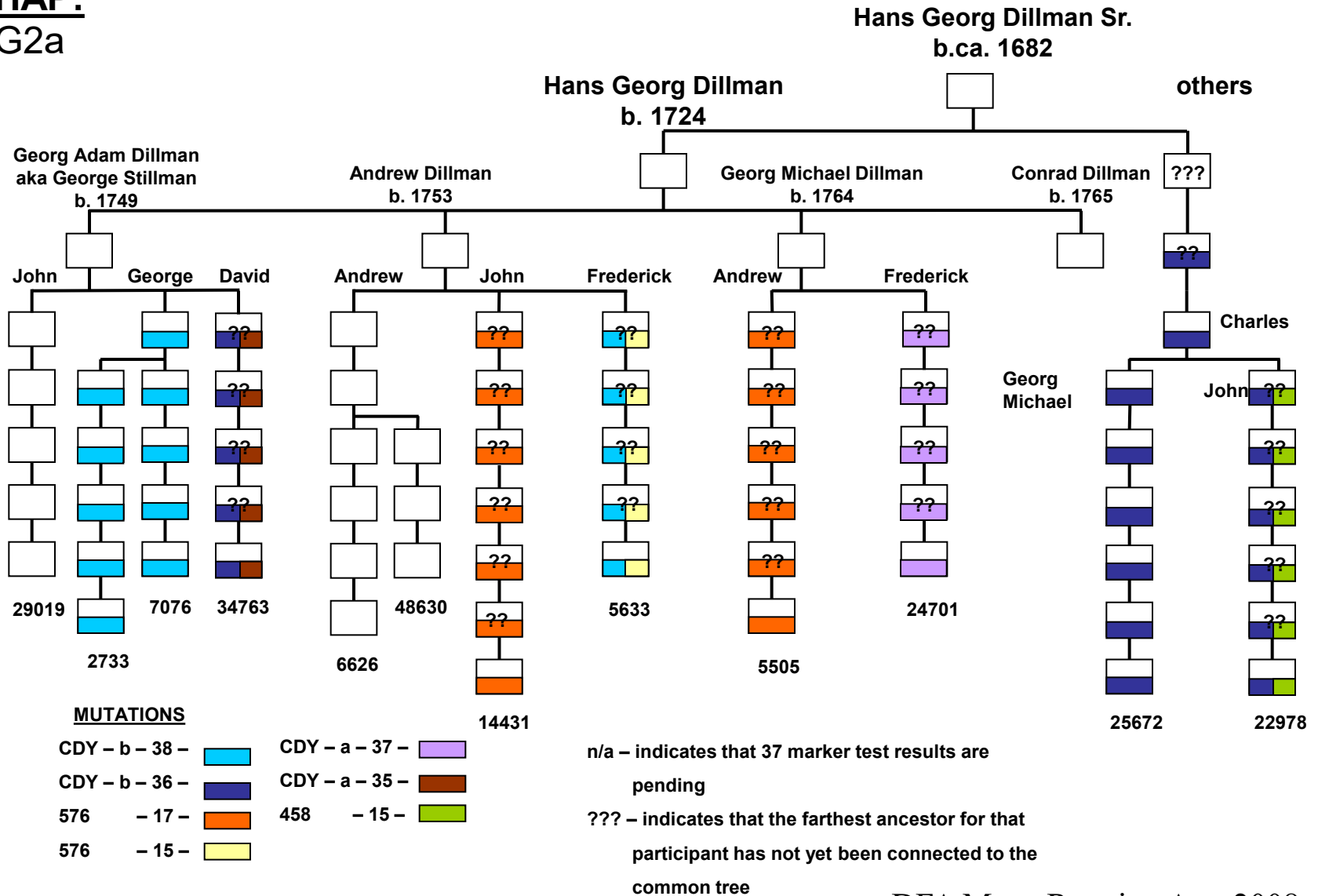
Jacob Tillman
b. 1702, Sweden



N37557
R1b1b2

Hans Georg family

HAP:
G2a



DFA Mega Reunion Aug 2008

Comparison of mutation rates for 37 marker tests

Group / Name	Participants	Rate
1 / Elias Dihlmann	5	0.0043
2 / Hans Georg Dillmann	10	0.0039
3 / Michael Dhyllmann	3	0.0019
FTDna average rate		0.0058

Recent Events in Genetic Genealogy

- **5th Annual Conference on Genetic Genealogy hosted by Ftdna in Houston November 8-9**
- **132,000 Y-dna test participants (up from 73,000 +81%)**
- **74,000 mtDNA test participants (up from 30,000 +147%)**
 - **Full genome sequencing**
- **Revised Haplogroup tree**
- **New SNPs (ie, Garvey/Ballantyne study of Gs)**
- **Acquisition of DNA-Fingerprint by FTDna**
- **SMGF allowing increased access to database via Genetree**

Recent Events in Genetic Genealogy

- GenBank
- Haplogroup G research - and mailing list
www.members.cox.net/morebanks/G2Ideas.html
- Haplogroup R1b research -
http://freepages.genealogy.rootsweb.com/~dgarvey/DNA/hg/YC_C_R1b.html
- Haplogroup I research –
http://freepages.genealogy.rootsweb.ancestry.com/~dgarvey/DNA/hg/YCC_I.html
- Haplogroup J research -
http://freepages.genealogy.rootsweb.com/~dgarvey/DNA/hg/YC_C_J.html

Haplogroup G - Origins

- Ancestor thought to have lived 30,000 years ago on eastern edge of Middle East.
- Believed to have migrated to the Caucus region over 2,000 y.a.
- Slowly migrated into Europe
- Today, North Ossetians claim to be living descendants of the Sarmatians. 50% of tested population belong to G.
- Sarmatians have been equated with the people who brought G to Europe.
- Sarmatians – nomads who spoke a language of persian origin.
- Consisted of several tribes, including the lazyges and the Alans.

Haplogroup G – Origins cont'

- Pushed westwards into Hungary ca 78 CE and Romania ca 100 CE.
- Sarmatian mercenaries sent to Britain by Emperor Hadrian to build the wall in 122 CE.
- Also employed in France, Switzerland, and southern Germany.

Haplogroup R1b - Origins

- Thought to have originated 35-40,000 years ago.
- Hunter-gatherers who populated Europe following last glacial period.
- Split into 4 main groups: Baltic-Russian, North Sea/Baltic, Alpine/South German, and Atlantic.
- Youngest and most successful group was the Atlantic, found along the Atlantic coast of Europe.

Haplogroup I - Origins

- Founder of I lived 20,000 years ago.
- Probably 2nd group to migrate into Europe.
- Several branches, including an Anglo-Saxon variety, Norse, Mediterranean.

Haplogroup J2 - Origins

- J originated in the Middle East.
- J2 spread into Europe about 7-9,000 years ago.

Haplogroup T - Origins

- T originated in Asia and moved back into Africa.
- Highest distribution of T is Somalia(10%), Oman, Egypt, and Iraq.
- Haplogroup is rare in Europe at 1.7% in very regionalized areas (southern Russia)
- Thomas Jefferson's DNA was shown to be T.

Conclusions

- **DNA testing has grown considerably (technology & acceptability) as a tool for genealogical purposes. (new tests, building databases, analyzing long term migration patterns)**
- **Testing can help to validate/refute long held family stories. (G2 – refute written history)**