

Dymen of Hudson's River

Paternal Lineage Study

Surname spelling Dymen is found in the earliest records. It is used in place of surnames Diamond, Dymond, and Dimond, all of which are used in the patrilineage.



Draft 2.07.2011

Ancient Ancestry II

Dymen within haplogroup Q

There are several ways to compare our Dymen lineage with other Q. One of these is Frequency Distribution. Another is utilizing Phylogenetic Drawing software.

Frequency Distribution within Haplogroup Q

When evaluating matches with other people, it helps to know our markers frequency relative to others in our haplogroup population, in our case the Q population. In the chart that follows the most important column is % in Q. This column tells the percent of people in haplogroup Q which have matches that share the same measurement at a marker to our Dymen lineage.

Frequency Distribution within Haplogroup Q										
Marker	Dymen Allele Values	% in Q		Marker	Dymen Allele Values	% in Q		Marker	Dymen Allele Values	% in Q
393	14	5		460	10	15		436	12	92
390	23	77		Gata H4	11	77		490	12	100
19	13	92		YCA II a	19	98		534	16	11
391	10	93		YCA II b	23	78		450	8	100
385a	15	14		576	18	37		444	12	42
385b	18	9		570	20	40		481	25	79
426	12	98		CDY a	37	3		520	21	47
388	12	97		CDY b	38	8		446	13	39
439	13	4		442	13	6		617	12	92
389-1	14	54		438	11	92		568	11	97
392	14	81		531	11	97		487	13	50
389-2	31	15		578	8	100		572	11	45
458	14	38		395S1a	16	11		640	11	100
459a	9	98		395S1b	16	49		492	12	100
459b	9	99		590	8	100		565	12	97
455	11	99		537	11	95				
454	10	38		641	10	97				
447	26	43		472	8	100				
437	14	96		406S1	12	97				
448	21	42		511	10	89				
449	31	15		425	12	100				
464a	12	2		413a	23	8				
464b	19	5		413b	23	82				
464c	19	12		557	18	3				
464d	20	5		594	11	97				

Allele values indicated in **bold red** are found in < 5% of the Q population. These are very rare.
 Allele values indicated in **bold black** are found in < 25% of Q population

Using marker 578 as an example we see that in the Q haplogroup, 100% of Q haplogroup members will have a measurement of 8. Therefore this is not a useful marker to determine how closely we match with another Q since we match everyone.

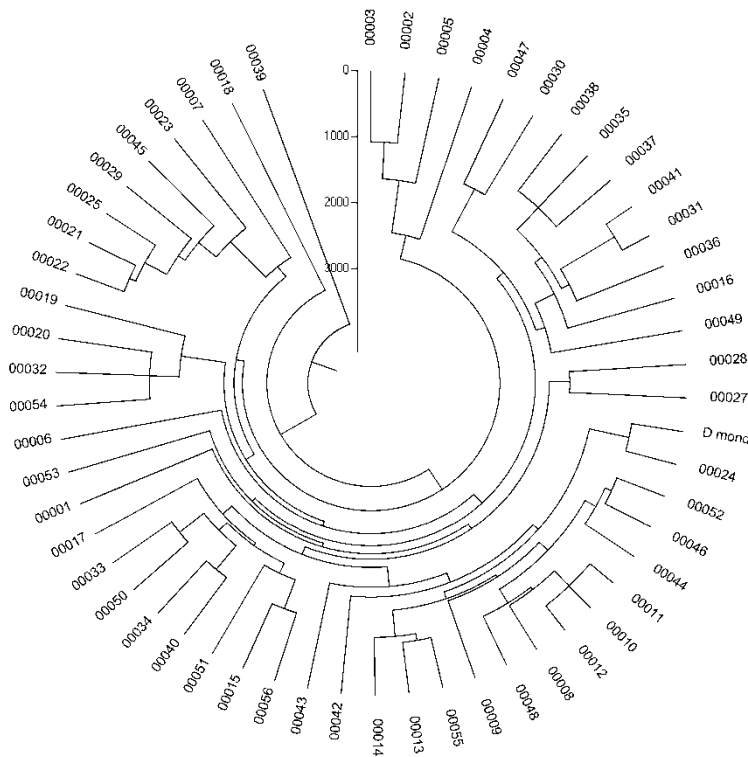
Looking at marker 393 we see that only 5% of the Q population will have a value of 14. We can consider this measurement of 14 repeats on marker 393 *rare* in haplogroup Q. So when trying to determine how closely we actually match another Q individual at this location, the odds are very good that the match is something more than circumstantial convergence.

By monitoring potential matches at these markers, we are able to ferret out matches by convergence and focus on matches that are meaningful and useful.

On a larger scale, frequency comparison can be useful in looking at tribal patterns and determining relative degree of relationship.

This is best illustrated using **Phylogenetic** drawing software.

Dymen within Q-M3 Population



Our haplogroup tells us very clearly of our ancient paternal ancestry. It is not as cut and dried in men of European ancestry. We stem from a relatively recent population that was isolated and bottlenecked in Beringia before spreading throughout the America's.

With Phylogenetic drawing software we can create a tree model of our specific population cluster. To do this a list of men found in public databases who have been tested positive for the SNP mutation M3 was created. Currently there are approaching 200 some M3s in these databases. Many of them are 12 marker haplotypes. 12 markers get us to around 3000 years ago. This would make for very low resolution trees. At the 67 marker level there are very few complete haplotypes available so I opted to use 37 marker haplotypes and discarded the very fast mutating markers CDYa and CDYb. The 35 marker haplotypes will give us a resolution of 300 years +/- 100 years.

American Indians adopted surnames in areas that became the US until the late 1600s and early 1700s at the earliest and in many cases not until the 1800s, making this an interesting exercise and one that cannot be achieved by other means.

There are fifty-six 35 marker haplotypes used in this model. Haplotype data was extracted from yDNA Geographic and Haplogroup projects at *FTDNA* and the public research database *Y Search*.

The data is limited but illustrates what is possible and does give us a sense of where the Dymen lineage fits into the overall Q-M3 population.

Model Construction

Infinite allele mutational model

35 markers

95% probability

Mutation rate of 0.044

30 years per generation

Software: Phylip v3.65 using the Kitch program and the Fitch-Margoliash method

Random seed used: 9

Number of jumbles: 99

Model Drawing

Software: Mega v.3.1 Tree drawing

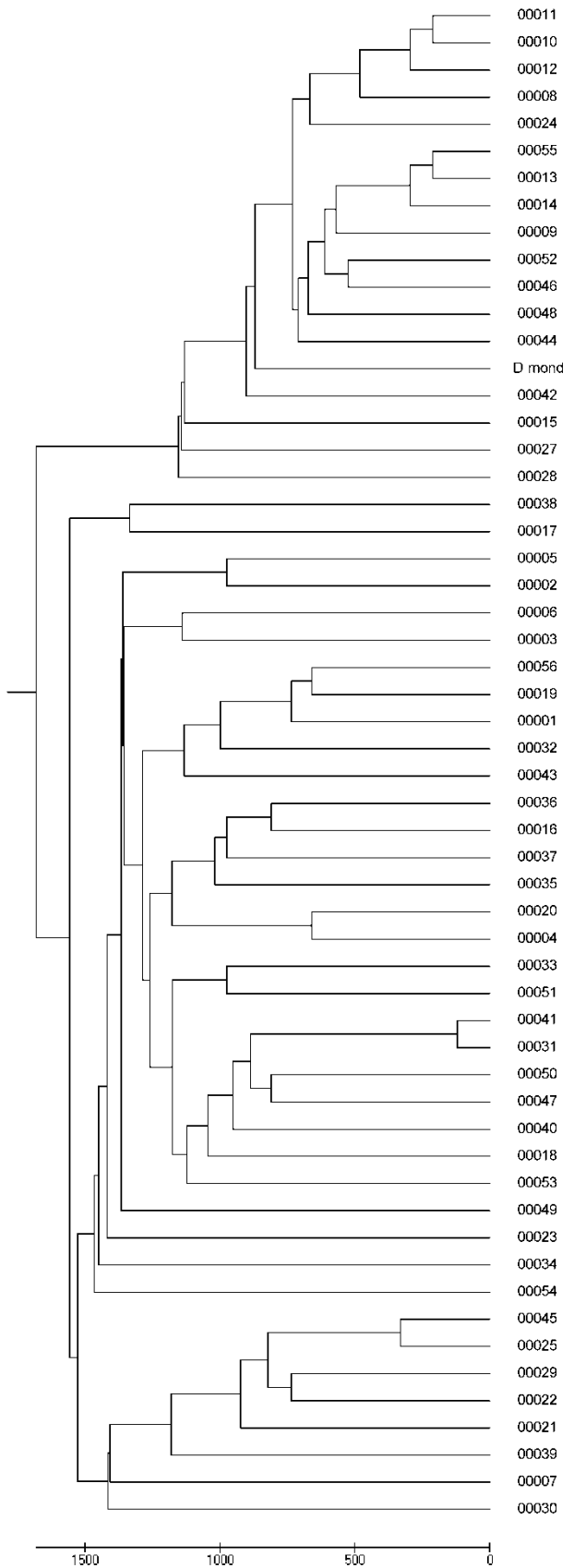
DATA

1	N58430	Mississippi	Page	29	31277	Texas	Hernandez
2	70521	Mexico	Lovato	30	94178	not listed	Castruita
3	N2073		Van Gilder	31	82894	Mexico	Cindad
4	26203	Mexico	Burquez	32	140999	not listed	Fox
5	N14781	Guatemala	Janssens	33	114720	Mexico/SW US	Senna
6	63844	North Carolina	Helton	34	109512	Mexico	Cervantes
7	62146	Mexico	Gonzalez Vido	35	120237	Mexico	Franco
8	N7284	Virginia	Tapp (Taptico)	36	158012	New Mexico	Manzanares
9	57553	Alabama	Scott	37	15295	Mexico	Moreno
10	18904	Virginia	Doggett	38	52300	Mexico/SW US	Diaz
11	23764	South Carolina	Stricklin	39	133836	Mexico/SW US	Carerros
12	40122	South Carolina	Logan	40	143412	Mexico/SW US	Suarez
13	27302	North Carolina	Freeman	41	63BDR	Mexico	Perez
14	30719	Florida	Dennis	42	67YGW	North Carolina	Tucker
15	81981	New Mexico	Yturrietta	43	8EN7Y	Mexico	Rodriguez
16	N69517	Montana	Medicine Crow	44	9Y7Y7	unknown	Lolly
17	N48159	New Mexico	Garcia	45	AWEBZ	Mexico	Zavala
18	57797	North Carolina	Woodall	46	BRRRK	Canada	Snively
19	N77270	unknown	Pembroke	47	CEFKS	unknown	Olson
20	72564	not listed	Zamora	48	DVP38	Illinois	Palmer
21	40621	New Mexico	Romero	49	FU8T8	unknown	Hill
22	34511	Mexico	Ramirez Forcier	50	KY7Z4	Mexico	Rivera
23	113223	Argentina	Peluzzi	51	M52MY	Jamaica	Chambers
24	60641	Kentucky	Gilmore	52	QEDGE	North Carolina	Hersey
25	102201	Mexico	Corbera	53	SB8SH	unknown	Madrid
26	D_mond	New York	D_mond	54	UD9WC	unknown	Chavez
27	44050	not listed	Augustine	55	W5PNN	Tennessee	Marsh
28	N28692	Alabama	Sanderson	56	Z6J5Y	unknown	Hosselton

35 Marker Tree Drawn from Data

Time scale is years.

The chart lists either the Y Search Id or the FTDNA Id, the location as known by the contributor, and the surname.

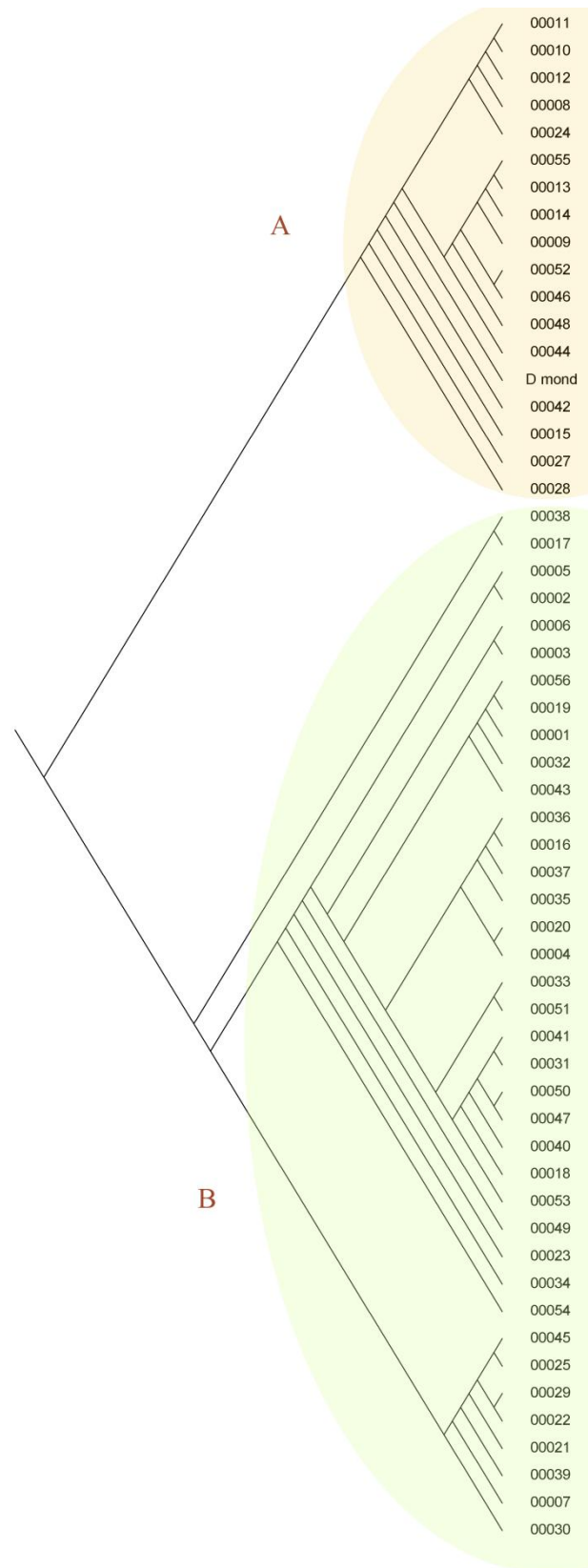


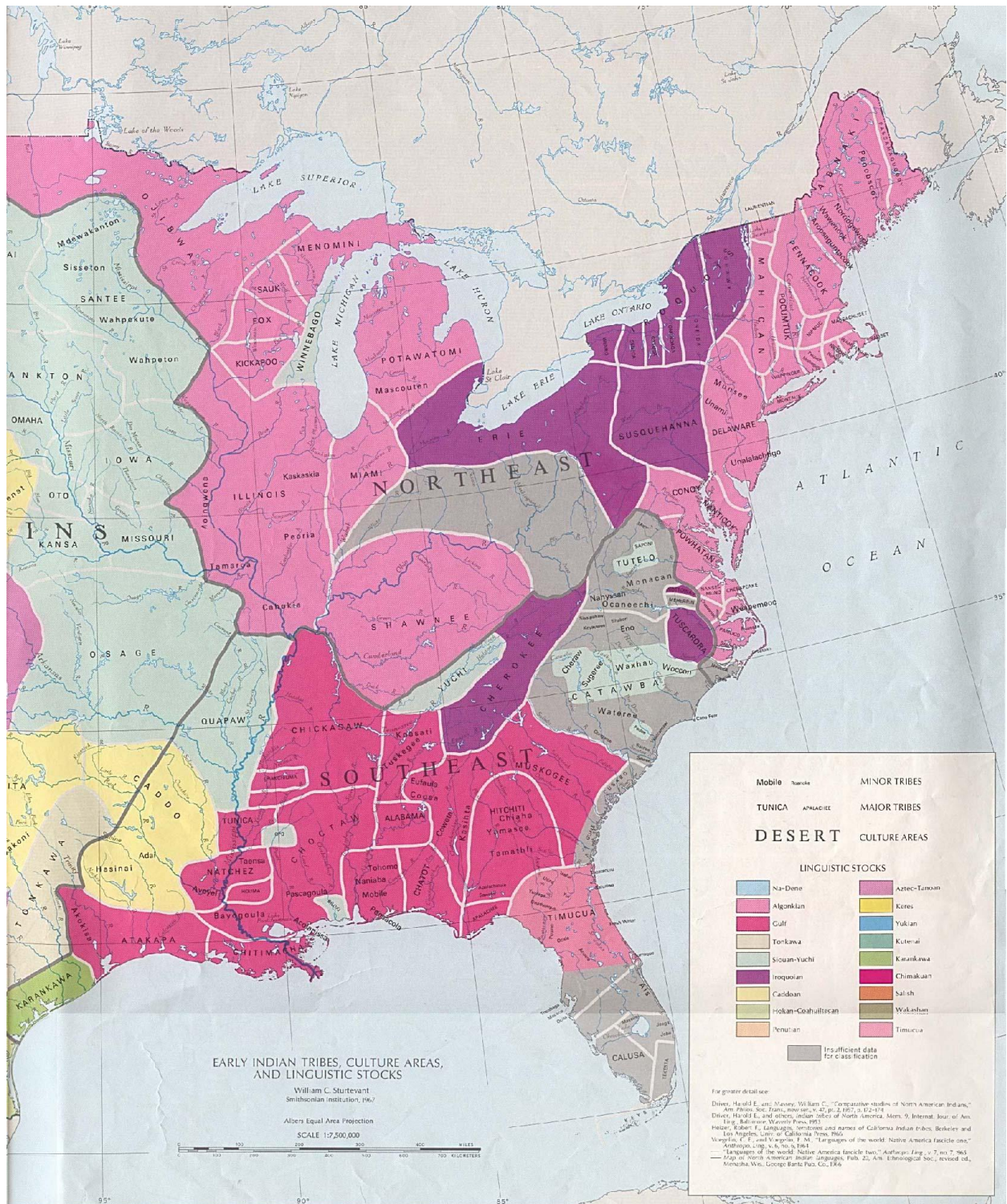
Another way to visualize the 35 marker tree

Dymen are among those in cluster 'A'. Cluster "A" is comprised of men that come from areas that correspond to the geographic spread of Algonquian speakers. That is not to say that all Algonquian speakers would be found to be members of cluster 'A'. Cluster 'A' may be in reality a set within a larger set. In the 'B' population we see three branches. All of these men come from the American southwest and southward into Mexico and beyond.

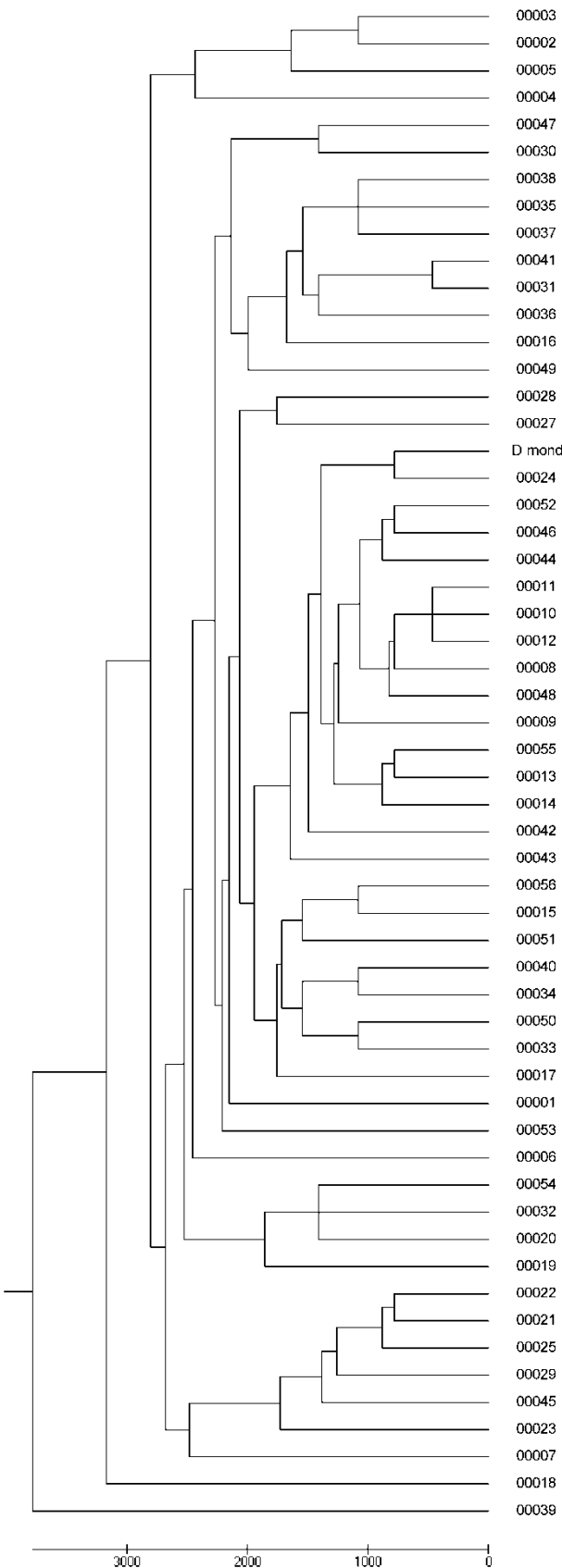
Proto-Algonquian originated with people to the west, perhaps in the Plateau region of Idaho and Oregon or the Rocky Mountain-Great Plains boundary of Montana, and then moved east, dropping off subgroups as people migrated. By this scenario, Blackfoot was the first language to branch off, which coincides well with its position as the most divergent language of Algonquian. In west-to-east order, the subsequent branching were:

- Arapaho-Gros Ventre, Cree-Montagnais, Menominee, and Cheyenne;
- then the core Great Lakes languages: (Ojibwe-Potawatomi, Shawnee, Sauk-Fox-Kickapoo, and Miami-Illinois); and
- Finally, Proto-Eastern Algonquian.





Early Culture Areas and Linguistic Stocks



This model is using only **12 marker haplotypes** illustrating branching from common ancestors at a deeper time scale.

1	N58430	Mississippi	Page
2	70521	Mexico	Lovato
3	N2073		Van Gilder
4	26203	Mexico	Burquez
5	N14781	Guatemala	Janssens
6	63844	North Carolina	Helton
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23	113223	Argentina	Peluzzi
24	60641	Kentucky	Gilmore
25	102201	Mexico	Corbera
26	D_mond	New York	D_mond
27	44050	not listed	Augustine
28	N28692	Alabama	Sanderson
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48	DVP38	Illinois	Palmer
49	FU8T8	unknown	Hill
50	KY7Z4	Mexico	Rivera
51	M52MY	Jamaica	Chambers
52	QEDGE	North Carolina	Hersey
53	SB8SH	unknown	Madrid
54	UD9WC	unknown	Chavez
55	W5PNN	Tennessee	Marsh
56	Z6J5Y	unknown	Hosseton

Note 00026 Dymen and 00024 Gilmore. It shows the node at which point there was split into two lineages

from a single common ancestor approximately 1000 years ago.

Where are Q-M3 Today?

There are very few surviving Q-M3 patrilineage surviving today. The highest numbers are found in Central and South America. There are small numbers found in and around reservations in the US and Canada.

Recent papers by various researchers indicate a range of between 47% and 88% of American Indian males (tribal members) are European admixed down the paternal line. This is an east-west gradient with the highest admixture in the east and the lowest in the west. This is not true down maternal lines where pre Columbian genes are still found at a very high level among First Nations people.

Databases of recreational genetics are skewed by economics, region and national boundaries.

US Native tribal members are opposed to and generally hostile to Y DNA testing. There are highly charged political issues. Traditionally, tribal memberships have been by blood quanta and genealogy. Y DNA would seem to be a natural fit. But due to the very high European admixture among present day Amerindians many tribal members would be excluded based on Y DNA. Tribal recognition and membership are now based on 'living' culture rather than DNA or Blood quanta. Each federally recognized tribe has the right to set membership requirements.



Testing economics is the primary reason for lack of data in the rest of the world.

The day is coming

Regardless of the barriers the day is coming when we will have full genome sequencing. What this will mean is that each paternal line will be defined by some 50 or so Y SNPs that will delineate an accurate tree of descent right up to the present generation.

Connections

There is always a point in time at which we cannot get past in our ancestry. For those with colonial American roots it is making the connection to the old world. For our paternal lineage the point is the transition from the American aboriginal culture to the first generation that adopted the newly dominating colonial culture. The transition was not recorded, or if it was it is buried in documents in New York that are yet to be deciphered.

There are a few cases among those in the tree diagrams where there is some knowledge.

00001	Page	Choctaw
00010	Doggett	Bushrod Doggett was the illegitimate child of Sarah Ann Doggett born about 1760. Stories passed down in the family say the father was William Tapp, grandson of Taptico King of the Wicocomico Indians. Note the tree relationship to the Tapp lineage (8)
00012	Logan	Logan 1725–1780 was of the Cayuga nation by birth. Logan's father Shikellamy, who was of the Oneida nation, worked closely with Pennsylvania official James Logan in order to maintain the Covenant Chain relationship with the colony of Pennsylvania. Following a Native American practice, the man who would become Logan the Mingo took the name "James Logan" out of admiration for his father's friend.

Iroquois who migrated to the Ohio Country were often called "Mingos." Logan was a war leader like his father. Logan maintained friendly relationships with white settlers moving from eastern Pennsylvania and Virginia into the Ohio Country, the region which is now Ohio, West Virginia, Kentucky, and western Pennsylvania.

Awhile after Logan moved into the Ohio Country, he helped start the Dunmore's War. His revenge for the killing of his family members by American frontiersmen helped spark the 1774 conflict known as Dunmore's War. The war started in 1774 and ended soon after it started in October of 1774.

- 00013 Freeman Descended from Chief Tom Freeman who was a Chowan (Chawanac) 1734 in Chowan County, North Carolina. The Chawanac were Algonquian speakers.
- 00017 Garcia Pueblo
- 00052 Hersey/Kersey Lumbee