Applying Genetic Genealogy: The Genetic Genealogy of the Brockman Surname in the UK and the USA

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What is Y-DNA and Genetic Genealogy?

Do you remember the Y chromosome (Y-DNA) from your high school biology class? It's the short strand that makes men male. Women are XX and men are XY. All eggs carry the X chromosome. Contrary to the belief of Henry VIII the sperm conveys either the X or Y that determine gender. The Y chromosome is different than every other chromosome. Every other chromosome is mixed 50% with each generation, and as a result we have little genetic relationship with our ancestors of 10 generations ago.

The Y chromosome is different. Like a biological surname it passes ***unchanged*** from father-to-son except for random mutation events that happen at a certain rate from generation to generation. That means we have a biological, male-to-male marker that should follow the traditional surname lineage of European nations. It only has a few important functions so its sequence cannot easily be used by insurance companies to unscrupulously scam higher rates – so it is relatively safe to share Y-DNA information. Y-DNA information does enjoy use in forensics, and there are those who can dream up misuses for the information. But the primary role of Y-DNA is to trigger the fetus to develop as male, and it has relatively few other roles. Furthermore it can be collected with a painless cheek swab using a q-tip. The test generally costs about $200 US. This makes the Y chromosome one of two ideal genealogical markers.

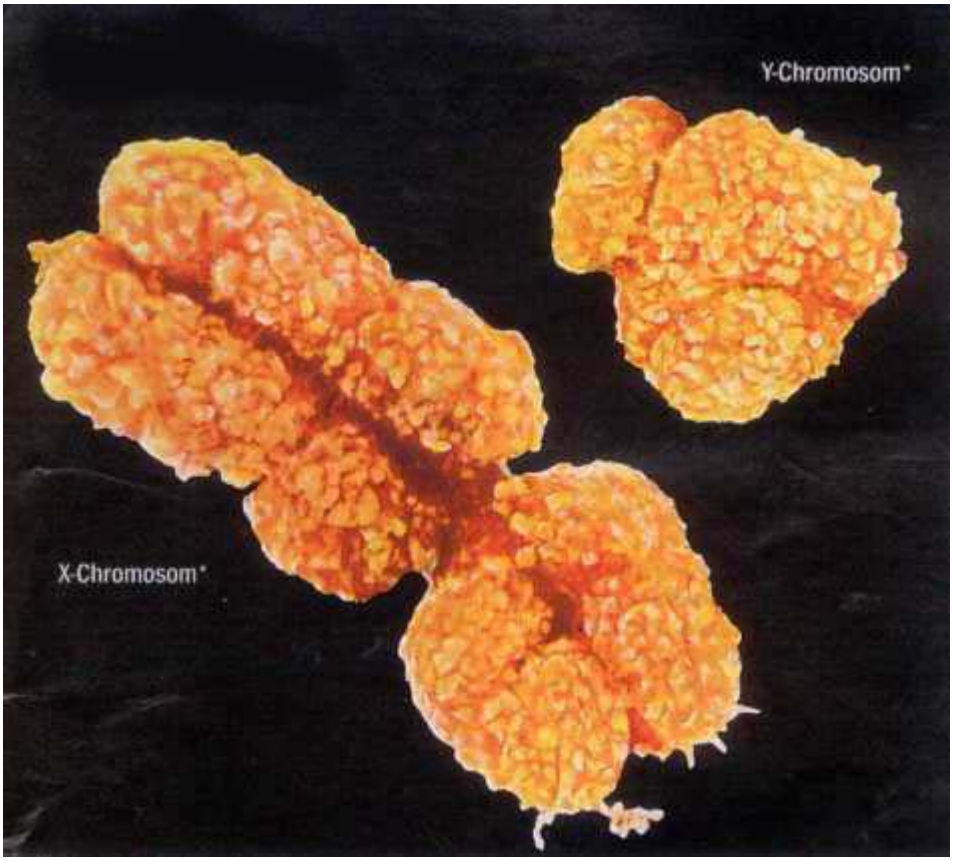


Figure 1: The X and Y Chromosome

Mitochondrial DNA can be thought of as the opposite of Y-Chromosomal DNA (Y-DNA) from a genealogical perspective. While The Y chromosome is passed down, intact, from father-to-son with no maternal contribution, Mitochondrial DNA (mt-DNA) provides a matrilineal marker. This mtDNA is passed from mother-to-child with no contribution from the father, except in extremely rare events. Only daughters can further transmit mtDNA except for extremely rare events. The mtDNA is also very rugged, and unlike Y-DNA, does not quickly degenerate upon death. Therefore mtDNA is much more useful for archaeology. This discussion will only concern Y-DNA. Furthermore, this discussion is only important to a single strand in the genetic tapestry – the patrilineal Brockman strand.

Types of Y-DNA Tests:

There are two types of Y-DNA tests. These are (1)Y-STR (this is a haplotype test), and (2)Y-SNP (this is a haplogroup test). STR stands for "Short Tandem

Repeat" and SNP stands for "Single Nucleotide Polymorphism". The SNP test defines one's ***haplogroup*** and the STR test defines one's ***haplotype***. The important thing to remember here is that there are two categories of information from testing – haplogroup and haplotype. The Y-SNP test is a separate test and another $200. The haplogroup can also be predicted by the haplotype and most results available on the web are predicted results. Three of the lines examined in this study were confirmed by SNP testing.

Haplo-*group* vs. Haplo-*type*

A Haplotype is an individual-specific sequence generally referred to in a Y-STR test by the number of repeats at a series of alleles. That all sounds complicated. You can think of "***Alleles***" as synonymous with "***Markers***". A 43 Marker test was used in this study and each individual has a series of numbers, on number for each Marker. If two individuals share the same series of numbers they are related.

The haplogroup defined by the SNP test is very broad and usually many millions of people share a haplogroup. Haplogroups are given names like R1b, R1a, and I1a.

The haplo-***type*** is very specific to an individual while a haplo-***group*** is very broad and applies to something more like what we think of as an ethnic group (in ancient terms – these groups have mixed with many others over the millennia. Only closely related people have the same haplotype, but it requires many markers to be specific. Both haplogroup and haplotype are important in genetic genealogy. If cartography/map-making were to be used to draw an analogy, haplogroup might be like the nation/country and haplotype could be thought of like a specific town. The reason both are important is that there are at least two towns named Boston in the world – one in the UK and one in the USA. A haplotype can look a lot like a specific ethnic group at low resolution, because it is only a few markers not the whole gene. The haplogroup, as revealed by the Y-SNP test helps too by giving the whole Y chromosome look, or at least more of a look, short of a full sequence. The haplogroup gives one a rough idea very quickly regarding where one's ancestors spent the last ice age.

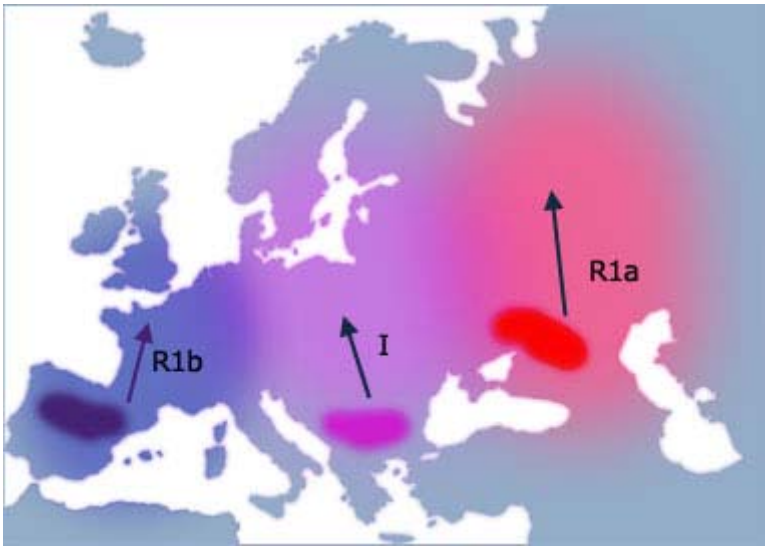


Figure 2: The spread of three European Haplogroups out of ice age shelters

The bright oval shapes shown above show locations where the haplogroups R1b, I1a, and R1a spent the last ice age, and how they spread northward as the glaciers retreated.

Mutation Rates

The Y Chromosome does not mix during reproduction. Therefore it only changes by ***mutation***, the random process of slow change when the chromosome is transferred from father-to-son. Some markers are thought to be more conserved than others, ie. they only mutate very slowly. Some are thought to be "faster" or "less conserved" and others are thought to be "highly conserved" but these are early days in the testing, so some of his is conjecture. There are many easy analogies for this. Humans are born with two eyes and this is a highly conserved trait, there aren't a lot of Cyclops around. The color of our eyes can change more easily. Some genetic traits are more plastic, more changeable than others, and are more easily subject to mutation.

As a general rule, Y-DNA markers are thought to have a 0.5% chance of mutating each generation. Therefore, there would be a 100% probability of a mutation in 200 generations on a single allele. But as another general rule the marker "DYS390" is thought to be more conserved, but no one has monitored it for 200 years to confirm it stays put, the claim that it is conserved is based on population statistics. As a rough estimate, since we are testing 43 markers, each one of those has a 0.5% chance of mutating, or a 21.5% chance that 1 of

the 43 markers could change with each generation. Therefore 1/43 markers should change every 4-5 generations. That'll be important later.

That's the end of the basics of the testing. There is much more information available in encyclopedias such as: **http://en.wikipedia.org** and elsewhere on the web and in print.

Study Design & Lines Tested in this Study:

Four Lines of Brockmans were included in this study. They are referred to here as Greenway, Whitfield, Drake, and Beiste Village.

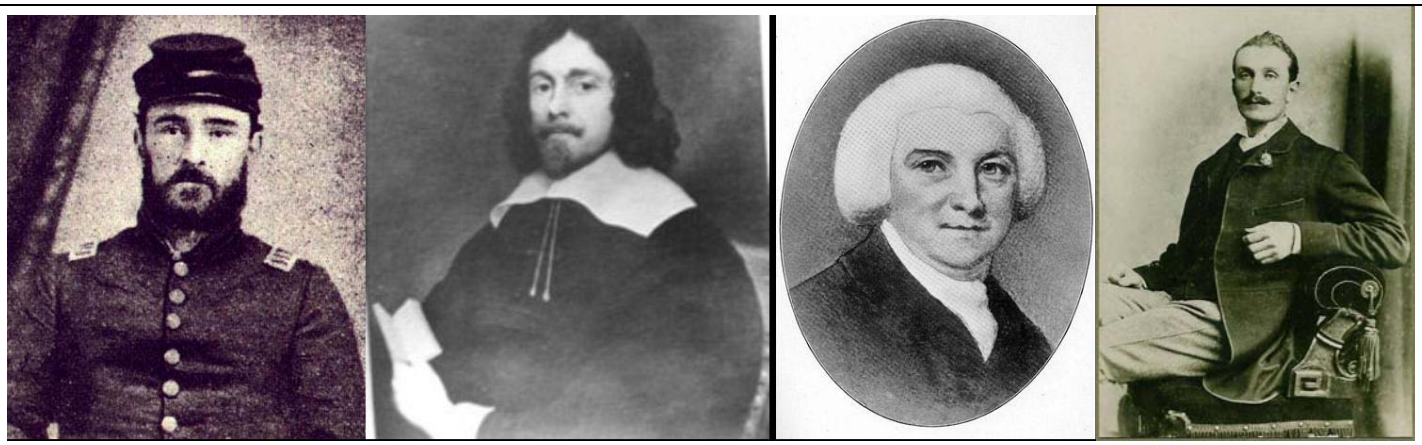


Figure 3: Pictures of Ancestors. These are some eldest known ancestors for which we have images from 4 lines. Leftmost is Benjamin T Brockman, a Greenway Brockman from the USA Civil War era (about 1865). Center-left is Sir William Brockman, a Beachborough Brockman ca 1635. The Beachborough Brockman line has no proven male descendants today but may connect in a more remote fashion to other English lines. Cener-right is Rev. Ralph Drake-Brockman bo. 1781 who was adopted as heir to the Beachborough estate and heritage, and who married Caroline Brockman. Some Greenway Brockman genealogists have hypothesized a connection between their founder Henry and the UK Brockmans, but this may be difficult to prove. Rightmost is William Albert Brockman, a Whitfield Brockman, picture taken about 1865.

Greenway Brockmans:

These Brockmans trace their earliest ancestor to a Henry Brockman born 1647 who landed in Maryland in 1667. The oral tradition of this family is that this ancestor was English in heritage. Cousins from Michigan, Kentucky, and South Carolina were tested in this line. These cousins do not share a common ancestor until Henry's son Samuel who was born around 1685. A father and son were tested from South Carolina as a positive control. The nomenclature referring to these lines is as follows: Greenway [XX-USA] where XX is replaced by the state abbreviation. Greenway is the name of a farm in Orange County Virginia where the

house owned by Samuel Brockman is located. They may eventually prove to have a common ancestor with the Beachborough/Newington Brockmans.

Whitfield Brockmans:

This is an English line of Brockmans from Whitfield, Kent. The earliest known ancestor at this time is a Christopher Brockman who died in 1615. They are not thought to be related to the patrilineal Drake line of the Drake-Brockmans. They may eventually prove to have a common ancestor with the Beachborough/Newington Brockmans.

Drake Brockmans:

This line of Brockmans inherited the name as a hyphenated name through a maternal line in the 18th century, so their Y-DNA should not match the Y-DNA collected for Brockman lines that trace their ancestry to older lines. Many Brockmans dropped the hyphenation and use only the Brockman name, so this information could be useful to help those Brockmans determine if they are Drake-Brockmans. The first and oldest ancestor in this line is Rev. Ralph Drake-Brockman, born a Drake in 1724.

Beiste Village Brockmans:

This line of Brockmans is of German origin. Their most distant ancestor is a Gerdt Brockman who was born 13 Jan 1675.

The overall strategy used in this study was simple. It was originally founded with the intention of helping the Greenway Brockmans find a definitive link to Europe and also to learn more about the ancient origins of that line. But it grew into a broader project supporting multiple families. The goal was to sequence as many Brockmans as possible and see what patterns emerge. Of course it was particularly intriguing to see if there is a link between Brockmans around the world. There are many notable Brockmans such as Sir Ronald Brockman who served with Mountbatten, Sir Edward Lewis Brockman who was secretary general of the Malay states, and many less notable-but-still-interesting cousins and non-cousins who carry the surname around the world, more of whom we learn more about every day. In fact, the 1841 census from the UK National Archive lists around 182 Brockmans in England. Like other Germanic language group nations, the Olde English speakers probably adopted the name Brockman in multiple families around the turn of the millennium, when

surnames began to be required by European governments. Brockman, probably referring to something like 'water-man,' would thus arise in multiple locations in Saxon England, just as the name did in Saxony, Frisia, and North Sea Germanic areas.

Haplotype Nomenclature

The markers each bear a name such as "DYS388". The DYS 388 allele has a certain number of repeats. So the Y-STR 'short tandem repeat" test reveals the number of repeats at each marker. The six I'll show below are commonly used on the internet to compare rough origins without revealing much of one's unique signature. A lot of what is on the web is nonsense – 6 markers reveal very little about the possible relationship between two people. Some websites claim that the 6 markers are generally chosen because they are highly conserved, and others say they were just the first six identified. Academic studies are very valuable because they recruit many test subjects and are peer reviewed by experts; but they suffer limited budgets and thus limit themselves to six alleles and hundreds rather than thousands of subjects. Such academic studies have proposed interesting correlates that are thought to be revealing with regard to ancient origins but nothing is absolute or incontestable.

One such 6 marker group is shown below. This modal 6 marker haplotype pertains to at least one of our lines and is known as the Atlantic Modal Haplotype (AMH). Those examples help show the importance of haplogroup in interpreting results. A 12 marker haplotype is then shown for the Levite Modal Haplotype to help demonstrate the importance of the number of markers.

The Atlantic Modal Haplotype (AMH):

The AMH haplotype is very interesting for a number of reasons, as noted above, but differences from the AMH can prove quite interesting. The Atlantic Modal Haplotype is shown below. The AMH is the most frequently occurring haplotype amongst human males in Atlantic Europe. It is characterized by the following motif:

• DYS388 12 • DYS390 24 • DYS391 11	• DYS392 13 • DYS393 13 • DYS19 14

Drake Brockman Haplo-*type*

AMH+1 is the AMH with 1 variation. The Drake Brockmans fall into this category. They differ from the AMH only on marker DYS393 which has 14 repeats in their case. The AMH+1 haplotype is commonly referred to as falling within the Atlantic Modal Cluster (ie. One difference or less from AMH).

• DYS388 12 • DYS390 24 • DYS391 11	• DYS392 13 • DYS393 14 • DYS19 14

Greenway Brockman Haplo-*type*

AMH+1 is the AMH with 1 variation. The Greenway Brockman motif is distinctly different on three alleles, so it is AMH+3, or perhaps, ***simply not AMH***. Here is the "Greenway Brockman Haplotype" for these six alleles:

• DYS388 12 • DYS390 23 • DYS391 11	• DYS392 12 • DYS393 13 • DYS19 14

So what does this mean? DYS390 is thought to be very highly conserved but Greenway is 23 rather than the AMH 24. It should change very slowly. DYS391 is also thought to be highly conserved, and Greenway is 11. These 2 differences on what are thought to be highly conserved alleles are sometimes referred to on the internet as "23/11". A "23/11" pattern for those two is thought to indicate a "Frisian" background… as will be explained shortly but that is very controversial. How does one prove that the Suebi tribe (another ancient Germanic tribe) did not provide this motif for example?

CAUTION: 6 markers mean little, 2 means even less and the Frisian assertion for 23/11 is not without controversy. That being said, peer reviewed literature has been conducted that provide a more sound basis for a Frisian assignment to the 6 marker haplotype, in conjunction with YHRD searches for the Greenway haplotype that provide a single hit for the 10 allele sequence.

The Greenway DYS392=12 does not seem to be very common, as published via the web, but no special interpretation of it has been found as of this writing. One assumes that the Greenway Brockmans simply had a point mutation long ago on that marker.

Whitfield Brockman Haplo-*group*

The Haplogroup of the Whitfield Brockmans is R1a. That means that the ancient ancestors of the Whitfield Brockmans spent the last ice-age somewhere near the Ukraine and moved north into eastern Europe as the ice sheet retreated. This is how DNA Heritage describes the R1a Haplogroup:

"Likely originating between the Black and Caspian Seas in the Ukraine, theories suggest that this haplgroup may have spread not long after the end of the last ice age (10-12,000 years ago) or possibly much more recent in line with the Kurgan culture (domestication of the horse). This haplogroup is seen in central and western Asia down through to the Subcontinent. Within Europe, it predominates in the East and into Scandinavia. It is associated with the Vikings although is seen in many other populations."

The Whitfield Brockmans have a very similar haplotype to that published by Helgason et al [7] in a study of Icelandic Norwegian Viking men. However, a few conserved alleles differ significantly, which may lead one to hypothesize that an R1a1 Viking settling in Eastern England could have been derived from a different group and time than an R1a1 Viking settling in Iceland. However, an extensive study would be required to make a concrete assertion about the nature of R1a1 in Eastern England or Kent.

Beiste Village Brockman Haplo*group*

The Beiste Village Brockman Haplogroup was I1a, or Indo-European. This group spent the last ice-age further east, in the general vicinity of the Caucuses, and spread northwards and west into the steppes, northern Europe and Scandinavia.

Greenway Brockman and Drake Brockman Haplo*group*

The Greenway Brockmans and the Drake Brockmans are R1b. The Greenway Brockmans have further identified their haplogroup to be "R1b3*" also known as "R1b1c" via an SNP test. Sadly, the testing companies haven't subdivided us boring Europeans too much. That's too bad, because Europeans are arguably as much in the dark regarding their ancient tribal heritage as anyone else, if not more so. R1b3* covers an absolutely enormous percentage of Europeans. The R1b haplogroup spent the last ice age on the Iberian peninsula around the vicinity of modern day Portugal.

Other Haplotype Motifs; Importance of Sufficient Markers

Another interesting haplotype is the levite haplotype shared by another priestly group of Jews known as the Levites. Here is that haplotype:

Levite:	Whitfield Brockman:
DYS19 = 15	DYS19 = 15
DYS388 = 12	DYS388 = 12
DYS390 = 25	DYS390 = 26
DYS391 = 10	DYS391 = 10
DYS392 = 11	DYS392 = 11
DYS393 = 13	DYS393 = 13

Looking at the six allele sequence it appears that the Whitfield Brockmans might match this sequence, save for the DYS390 allele. But this is misleading. The DYS390 allele is thought by some to be very highly conserved, so a difference on that allele is possibly a big difference, the "tip of an iceberg" so to speak. Furthermore, the 12 allele sequence is available for this motif:

Levite R1a:	Whitfield R1a:
DYS19 = 15	DYS19 = 15
DYS385a = 11	DYS385a = 11
DYS385b = 14	DYS385b = 14
DYS388 = 12	DYS388 = 12
DYS389-I = 13	DYS389-I = 14
DYS389-II = 17	DYS389-II = 17
DYS390 = 25	DYS390 = 26
DYS391 = 10	DYS391 = 10
DYS392 = 11	DYS392 = 11
DYS393 = 13	DYS393 = 13
DYS426 = 12	DYS426 = 12
DYS439 = 14	DYS439 = 10

When we add 6 more markers, we find that the Whitfield Brockman sequence differs by 6 mutations out of 12. It is ~50% different. The Levite Haplogroup is R1a, just like the Whitfield Brockmans, but the 12 allele sequence shows them to be quite different indeed. This example demonstrates the dangers of making too much out of a 6 allele sequence, even within the same haplogroup. The Levite haplotype does not present a significant challenge to the hypothesis that the Whitfield Brockmans are of Viking origin as supported by archeological evidence regarding migrations to England and the lack of any Jewish oral tradition or Jewish link by traditional genealogy. It is interesting that the Levites have this haplogroup, which is thought by some to be the result of an entire kingdom converting in mass to Judaism. This kingdom was the Khazar Empire and was located north of the Black Sea. Some further postulate that the mixed race of the Levite priests made them a slightly lower caste than the Cohanim priests in some ceremonies.

The Full Results (43 Markers)

The following table is the comparison of 43 Y-STR markers that comprise the best haplotype test available (to our knowledge) in 2006:

Brockman Line	DYS19	DYS385a	DYS385b	DYS388	DYS389i	DYS389ii	DYS390	DYS391	DYS392	DYS393	DYS426
Greenway[SC-USA(son)]	14	11	12	12	13	29	23	11	12	13	12
Greenway[SC-USA(father)]	14	11	12	12	13	29	23	11	12	13	12
Whitfield [Kent-UK]	15	11	14	12	14	31	26	10	11	13	12
Greenway [KY-USA]	14	11	12	12	13	29	23	11	12	13	12
Greenway [MI-USA]	14	11	12	12	13	29	23	11	12	13	12
Beachborough[Kent-UK]	14	11	14	12	13	29	24	11	14	13	12
Bieste Village [NDS-DE]	14	14	14	15	12	28	23	10	11	13	11

	DYS437	DYS438	DYS439	DYS441	DYS442	DYS444	DYS445	DYS446	DYS447	DYS448	DYS449
Greenway[SC-USA(son)]	15	11	12	13	12	12	12	13	25	19	30
Greenway[SC-USA(father)]	15	11	12	13	12	12	12	13	25	19	30
Whitfield [Kent-UK]	14	11	10	13	12	14	12	12	24	20	31
Greenway [KY-USA]	15	11	12	13	12	12	12	13	25	19	29
Greenway [MI-USA]	15	11	12	13	12	12	12	13	25	19	29
Beachborough[Kent-UK]	15	12	12	13	11	12	12	13	25	19	29
Bieste Village [NDS-DE]	16	10	11		12				23	20	26

	DYS452	DYS454	DYS455	DYS456	DYS458	DYS459a	DYS459b	DYS460	DYS461	DYS462	DYS463
Greenway[SC-USA(son)]	12	11	11	15	17	9	10	11	12	12	22
Greenway[SC-USA(father)]	12	11	11	15	17	9	10	11	12	12	22
Whitfield [Kent-UK]	11	11	11	15	14	9	10	11	11	11	22
Greenway [KY-USA]	12	11	11	15	17	9	10	11	12	12	22
Greenway [MI-USA]	12	11	11	15	17	9	10	11	12	12	22
Beachborough[Kent-UK]	11	11	11	15	16	9	10	11	12	11	22
Bieste Village [NDS-DE]		11	18	14	17	8	9	10			

	DYS464a	DYS464b	DYS464c	DYS464d	GATAA10	GATAC4	TAGAH4	GGAAT1B07	YCAIIa	YCAIIb	Haplo
Greenway[SC-USA(son)]	15	15	17	18	13	23	11	10	19	23	R1b
Greenway[SC-USA(father)]	15	15	17	18	13	23	11	10	19	23	R1b
Whitfield [Kent-UK]	12	15	15	15	13	23	12	9	19	22	R1a
Greenway [KY-USA]	15	15	17	18	14	23	11	10	19	23	R1b
Greenway [MI-USA]	15	15	17	18	14	23	11	10	19	23	R1b
Beachborough[Kent-UK]	15	15	17	17	12	24	12	10	19	23	R1b
Bieste Village [NDS-DE]	12	14	15	16							I1a

The four lines do not match one another and no exciting connections were made that were not expected given traditional genealogical evidence. The Greenway results from South Carolina, Michigan, and Kentucky match quite well. The father and son positive controls from South Carolina are identical. That's as expected as a single point mutation only has about a 20% chance of occurring each generation.

Greenway Brockman Results:

The match between the Kentucky, Michigan, and South Carolina samples are exciting in that they confirm the traditional genealogy for that line. There is no common male ancestor uniting all four of those samples until Samuell Brockman born ~1685, the only son of Henry-the-Colonial born 1647. That's around 10 generations to a common male ancestor. At 20% probability of a mutation one would expect 2 mutations for that period of time. That is exactly the number of mutations that are observed. This confirms the paper-based genealogical record for the family tree of the Greenway Brockmans all the way back to 1685. Samuel Brockman appears to have received 300 acres of land from his father Henry Brockman and his homestead now sits on a farm called "Greenway Farm", hence the name chosen for this line.

Whitfield Brockman Results:

The Whitfield Brockmans are an R1a haplogroup and thus Baltic-Viking ancient origin. As noted earlier the six allele haplotype happens to be somewhat similar with the haplotype of the theoretical Khazar Empire Levites[6], but this is deceiving, the 12 allele sequence shows them to be 50% different. While the Whitfield Brockmans may have shared a common ancestor with the ancestors of the Khazars prior to the last ice age, it is far more likely that they are Norwegian Viking in origin given the archeological and genealogical records, and that their haplotype is a closer match to results from studies of Norwegian Vikings in Iceland[7]. In fact, in Weale's work[1], a six allele haplotype found predominantly in Norweigans is only 1 mutation different than the Whitfield haplotype. That haplotype only shows 2 hits in Weale's study, and only in Norway.

Drake Brockman Results:

The Drake Brockmans were expected to possess a unique Y-Chromosome relative to the other lines because it is known that they adopted the Brockman surname through a maternal line. While some UK Brockmans have dropped the Drake hyphenation from their name, it was also anticipated by paper based genealogy that the Whitfield Brockmans would not match the Drake Brockmans and these results are consistent with the paper genealogy in that regard.

In a very ancient sense, the Drake Brockmans share a male ancestor with the Greenway Brockmans prior to the last ice age as they are both R1b haplogroup. There are about 15 mutations of difference between the two sequences of the 43 markers tested. One could estimate that is about 60 generations to a common ancestor, but that is a very rough estimate indeed and some of the mutated alleles are thought to be highly conserved, such as DYS390. Because the Drake Brockmans are AMH+1, they actually share an ancient origin with much of Britain and Atlantic Europe since the last ice age.

Bieste Village Brockman, and Other International Results are Desired:

The Beiste Village Brockman is also unique with an I1a Haplogroup. This indicates a Caucuses/Indo-European ancient origin. Jewish Brockmans, Swedish Brockmans, and Dutch Brockmans/Broeksma/Broekstra would also be interesting to test. A

very ancient match between the UK and the continent or a match between USA and the old world could be discovered with further testing.

The Linguistic/Archeological Record and Genetic Genealogy

Michael Weale (formerly at college of London, now at Duke University) and other researchers are also excited about genetic genealogy. They aren't so interested in near genealogy, so much as, the prospect of matching genetic results of mummies and people with the archeological and linguistic record to fill in the gaps of early and prehistoric movements of people. Two papers from Dr. Weale's former group at University College London are referenced in this article and permission was granted by Dr. Weale to utilize some of the figures from his work. Three of the lines studied here figure prominently in Weale's data. R1a, AMH R1b, and a haplotype similar to the Greenway haplotype are all studied with reasonable sample size.

From Weale's work, the following figure illustrates the average genetic difference between the Y-Chromosome results of several towns in England and Wales, as well as locations in Norway and Friesland… can you spot Friesland clustered with the English towns?

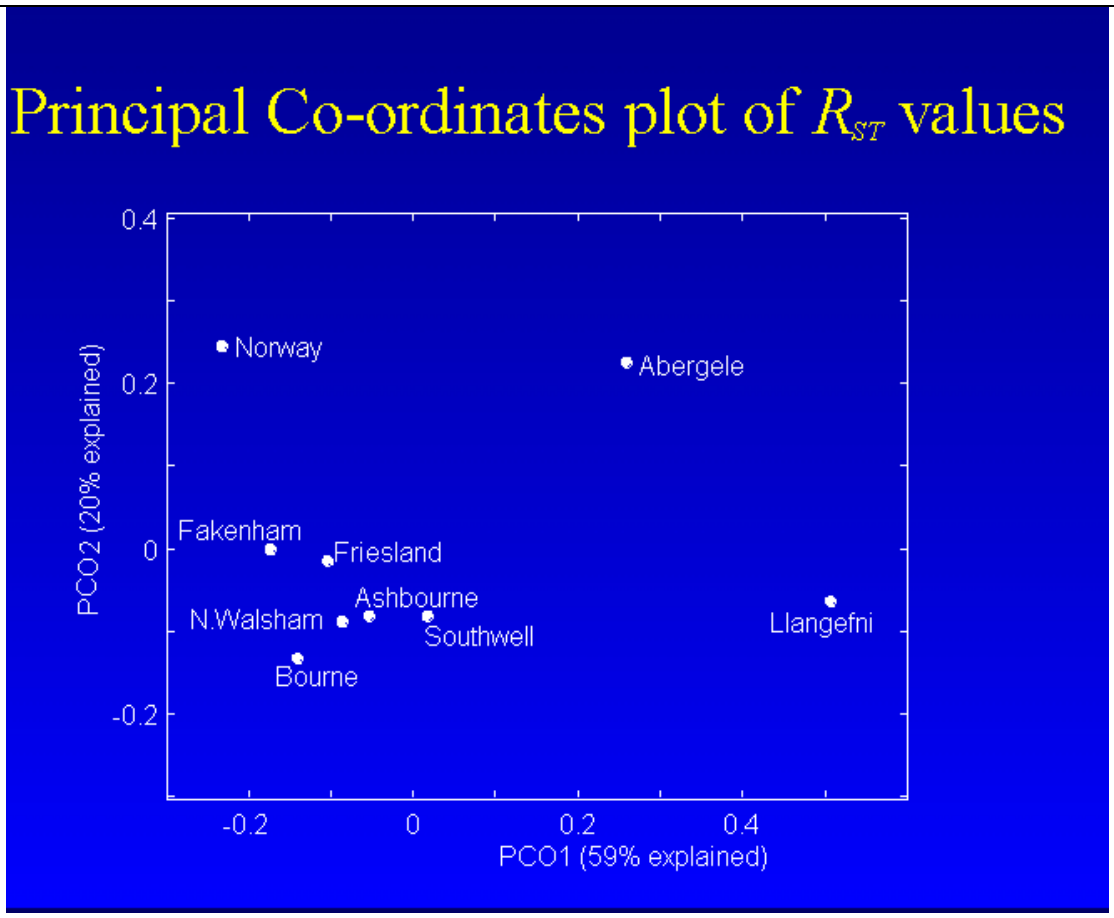


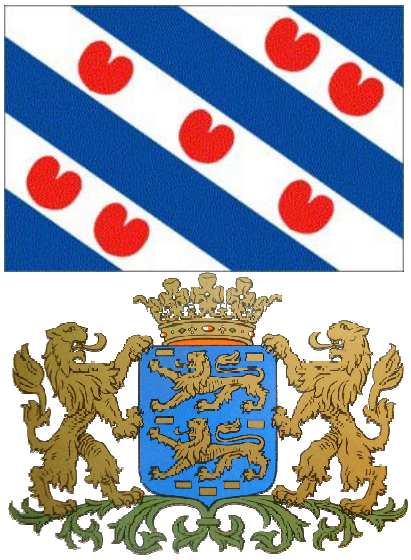
Figure 4: Genetic distance plot, from the work of Michael Weale et al. 2002, used by permission.

Friesland is tightly grouped in the figure above with 5 small English towns mentioned in the Domesday book of 1066 that are thought to have experienced very little migration in the modern era. Also note that the Welsh towns of Aberglee and Llangefni are very distinct from England, and each other. In this figure, genetic difference is translated into distance on an X-Y axis on the above plot. Dr. Weale's presentation on this topic is very good, and is available at:

http://www.ucl.ac.uk/tcga/presentations/ASdemo/AS-26-11-03b.html

I urge you to have a look while the presentation is still there! Dr. Weale has recently moved from the University College of London to Duke University, so the presentation may not be available much longer!

Basis for the Frisian Connection:



The Frisian Flag & Arms

Friesland Province, the Netherlands

As mentioned above, Weale et al.[1] published a study in the Oxford Journal Molecular Biology and Evolution in which 6 of the Y-STR alleles were tested in 313 males from seven towns located along an east-west transect from East Anglia to North Wales. Then they further sampled 177 males from Friesland and Norway. Their ability to control that the males were "indigenous" to the locations was of course very limited. They chose small market towns that have not experienced mass migration, they required that the subject and the paternal -grandfather were born in the town, and that the towns had been well recorded even back to the Domesday book of 1066. The Central English towns were genetically very similar, whereas the two North Welsh towns differed significantly both from each other and from the Central English towns. The data from the samples collected in Friesland were statistically indistinguishable from the Central English and Frisian samples. The samples from Norway were also distinct.

That data confirmed what linguistics and archeology has been telling us for a long time. It is thought, for example, that the Roman migration was primarily one of ideas rather than people, while the Anglo-Saxon migration was a migration of people - and their genes. The Ancient Britons and Romans retreated into Wales and defended it when the Anglo-Saxons and other groups began migrating into England after the fall of the Roman Empire. According to Weale, the North Sea and English Channel is less of a genetic barrier than the

Welsh English political and cultural barrier. The English/Frisian match is best explained by a mass migration event in the view of Weale and his co-authors.

Weale Haplotype #1 (Atlantic Modal Haplotype)… Similar to Drake Brockman Haplotype

• DYS388 12 • DYS390 24 • DYS391 11	• DYS392 13 • DYS393 13 • DYS19 14

Weale Haplotype #2… Similar to the Greenway Brockman Haplotype

• DYS388 12 • DYS390 23 • DYS391 11	• DYS392 13 • DYS393 13 • DYS19 14

The Drake Brockmans differ at only one marker from the first motif (DYS392=14) and Weale's results even list their specific 6 allele halotype (#34). The Greenway Brockmans differ at only one marker (DYS392=12) from the second haplotype. Both of those motifs account for a large percentage of the tested Frisians, but they also matched a large percentage of Welsh and English test subjects. Weale's haplogroup #1 (hg1) aka R1b, is essentially noise. It is such a wildly successful haplotype throughout Atlantic Europe that it is difficult to determine an ancient origin for those results.

Here are some selected 6 allele haplotypes from Weale's data showing that their percent frequency within each geographical location:

Hg	Ht#	Haplotype	Llan(80)	Aber(18)	Ash(54)	South(70)	Bourn(12)	Fak(53)	N. Wal(26)	Fries(94)	Norway(53)	Count
1	1	14-12-24-11-13-13	0.275	0.056	0.13	0.186	—	0.113	0.231	0.128	0.060	72
1	2	14-12-23-11-13-13	0.063	—	0.111	0.086	0.083	0.094	0.077	0.17	0.024	43
1	3	14-12-24-10-13-13	0.025	—	0.13	0.129	—	0.075	—	0.021	0.036	27
1	4	14-12-25-11-13-13	0.113	0.111	0.037	0.014	0.083	0.038	—	—	0.012	18
1	5	14-12-23-10-13-13	0.025	—	0.037	0.014	0.167	0.019	0.077	0.021	—	12
3	112	15-12-26-11-11-13	—	—	—	—	—	—	—	—	0.024	2
3	107	16-12-25-11-11-13	—	—	0.019	0.014	—	—	—		0.036	5
3	108	15-12-25-10-11-13	—	—	—	—	—	—	—	0.011	0.048	4
3	109	15-12-25-11-11-13	—	—	—	—	—	—	—	—	0.024	3
3	110	16-12-25-10-11-13	—	—	0.019	—	—	—	—	—	0.012	2

*Table from the work of Michael Weale et al. 2002, used by permission. Hg1 correlates to R1b and Hg3 correlates to R1a. Haplotype# (Ht#) 1 is similar to Drake and is common throughout Atlantic Europe. Ht# 2 is similar to Greenway and is slightly better represented in Friesland than in England, but common in both. The decimal number in each column can be multiplied times the parenthetical value that shows the number of subjects tested in each header. For example 0.170 Frieslanders tested positive for Ht#2, 0.170 X 94 = 16 Frieslanders had Ht#2 out of 94 tested.

Here is a table that breaks out the haplotypes that are within 1 mutation of the three Brockman lines relevant to Weale's paper and the percentage representation for each of those lines.

Ht#	Haplotype	Wales	England	Friesland	Norway
1, 34	Beachborough+AMH	24.5%	15.0%	13.0%	5.7%
2	Greenway	7.0%	9.3%	17.0%	1.8%
112,108	Whitfield	0.0%	0.0%	1.0%	7.7%

Literature Interpretation of Drake Brockman Results

In corresponding with Dr. Weale, he agreed that it is safe to think of such a successful haplotype as the AMH+1 as "noise" with respect to trying to discern ancient origin and mass migrations. It is ubiquitous. We cannot attribute any ancient origin to the Drake Brockmans other than that observed for all R1b's. On the other hand they are still unique. No matches were found for the 43 marker haplotype on any of the databases!

Literature Interpretation of Greenway Brockman Results

The Greenway haplotype are ***slightly*** less ubiquitous, and there is more of a shift towards Frisian origin, but more data would be reassuring. More data is available at the YHRD database and is shown below. There is no 10 marker match for the Greenway Brockmans on any of the databases except for YHRD, and that match is in Friesland. Also, there are 2 additional haplotypes one marker away from Greenway not shown in the data above. Using those data, the percent Frieslander is 20%, English 10.4% et cetera. The assignment of an ancient origin of Frisian to the Greenway Brockmans is thus ***more*** plausible but it should not be stated as a fact.

Literature Interpretation of Whitfield Brockman Results

The Whitfield haplotype appears non-ubiquitous, and is significantly more represented in Norway in Weale's work. Helgason's work also supports a Norwegian Viking origin for the Whitfield Brockmans.

Other Literature Result Summaries

As depicted in the picture at the beginning of this article, there were three separated pockets of human habitation in Europe during the last major glaciation (the end of the paleolithic and the Pleistocene), on the Iberian peninsula, in the Balkans and in the Caucuses. The Y chromosome haplogroups

from these populations are thought to correspond to R1b (Iberian – note the Greenway/Drake Brockman samples), I1a (Balkans – Note the Beiste Village Brockman sample) and R1a (Caucuses – note the Whitfield Brockman sample), these three haplogroups occur all over Europe, but their frequencies are not spread uniformly.[2][3]

The preponderance of the R1b haplogroup on the Y chromosomes of English men (about 70%) indicates that they are descended primarily from the earliest paleolithic peoples thought to have recolonised western Europe after the end of the last major glaciation some 10-12 thousand years ago.

Y chromosome analysis of people from Britain, Denmark, Ireland, Germany, Norway, Friesland and the Basque Country of Northern Spain and South Western France has further revealed that the Germanic (Danish/North German/Frisian) component in the male line of descent is higher in some areas of England than others.[5] It is highest in York and Norfolk, where the Germanic Y chromosome occurs in about 60% of men, while indigenous Y chromosomes comprise about 40%.[5] The research cannot distinguish between Danish (the presumed source of Danish-Viking settlers to East and Northern England), North German (Schleswig-Holstein, modern era) and Frisian (Anglo-Saxon) Y chromosomes. It concludes these data are consistent with the presence of some indigenous component in all British regions.[5] Also, this research cannot make reference to the extent of settlement by Anglo-Saxon/Danish-Viking women. Therefore even in places like York, the total genetic contribution of these peoples would be less than 60% if fewer women than men migrated, and conversely it would be greater if more women than men settled. Computer simulations have shown that it is theoretically possible for a small Anglo-Saxon population that was politically and economically dominant to support larger families, which in turn could have resulted in a faster population growth for the dominant class. These data assume that there is a 50-100% Anglo-Saxon Y chromosome occurrence throughout England, but this assumption has previously been shown to be questionable.[5] In some areas, notably Cornwall (and to a lesser extent Cumbria), some people claim a stronger ethnic connection to the ancient Britons, consequently some historians claim that Cornish people are distinct from English people.[4]

Database Searches

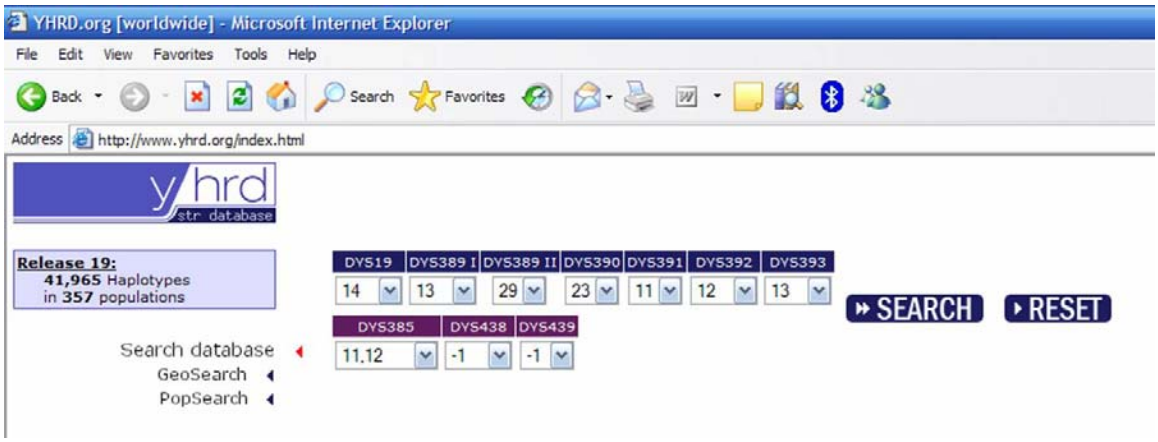
Additional databases can be searched to locate distant cousins and research origins with those who have conducted genealogical research. The Following Table is a list taken from a search of **www.ysearch.org** on the first 8 markers of the Greenway haplotype, allowing for ***1 mismatched allele*** (there are zero

hits with no mismatches). Only the DYS390=23 results are shown. This table doesn't mean that much as stated earlier, but it provides some indication of the diversity of names and English origins around the haplotype with a DYS390=23 Greenway Brockman motif. It should be noted that upon contact none of the extended sequences showed any promise of finding lost cousins.

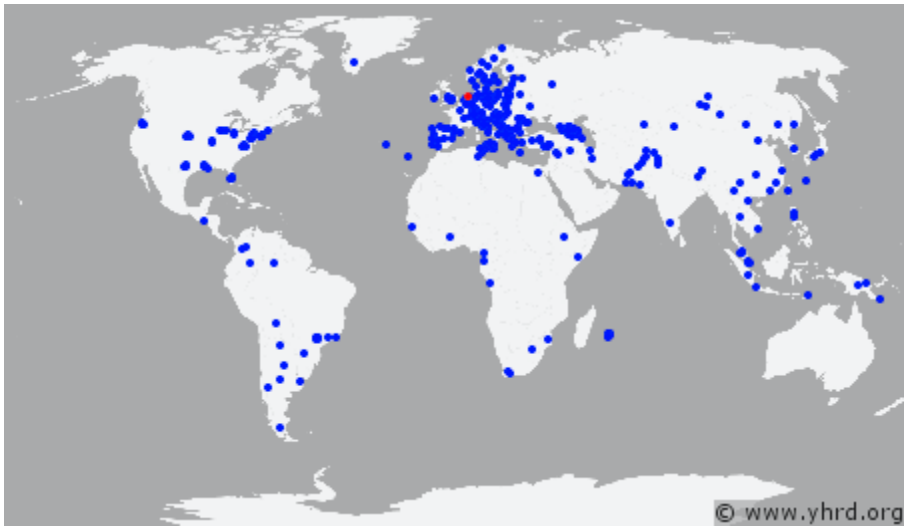
User ID	Last Name	Origin	393	390	19	391	385a	385b	426	388	439	389-1	392	389-2	458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
225UF	Penix	Maryland, USA	13	23	14	11	11	12	12	12	11	13	13	29	18	8	10	11	11	24	15	19	29	15	15	16	18
26E3E	Brewer	Marks Tey, England	13	23	14	11	11	12	12	12	12	13	13	29	17	9	10	11	11	24	15	19	30	15	16	17	17
2GCHD	Graves	England	13	23	14	11	11	12	12	12	13	14	13	30	17	9	10	11	11	24	15	19	29	15	15	17	18
2V2ZC	Harman	Unknown	13	23	14	11	11	12	10	12	13	13	13	29	17	9	10	11	11	25	15	19	30	15	15	17	17
4R5EY	Bruce	France	13	23	14	11	11	12	12	12	11	14	13	31													
5H4NU	Ross	Scotland	13	23	14	11	11	12	12	12	12	13	13	29	18	9	10	11	10	25	15	19	30	15	15	17	17
7AVKH	Philbrook	England	13	23	14	11	11	13	12	12	13	13	12	29	19	9	10	11	11	26	15	19	28	15	15	17	18
7BSHM	Bruce	Unknown	13	23	14	11	11	12	12	12	11	14	13	31	17	9	10	11	11	25	14	19	29	15	15	17	18
8KW7A	Corcoran	Clonfert, Portumna, Ireland	13	23	14	11	11	12	12	12	12	13	13	29	17	9	9	11	11	25	15	20	29	16	16	17	17
9N8R4	Shoemaker	Hamburg, Germany	13	23	14	11	11	12	12	12	12	13	13	29	17	9	9	11	11	25	15	19	29	15	16	17	18
A7H4J	Hill	USA	13	23	14	11	11	13	12	12	12	13	12	30	17	9	10	11	11	25	15	19	30	15	15	17	18
AX9WW	voss	Unknown	13	23	14	11	11	12	12	12	12	13	13	33													
BCDFF	Philbrook	Bures St. Mary, England	13	23	14	11	11	13	12	12	12	13	12	29	19	9	10	11	11	26	15	19	28	15	15	17	18
EZRKK	Pinick	Pennsylvania, USA	13	23	14	11	11	12	12	12	12	13	13	29													
H7P5X	Smashey	Unknown	13	23	14	11	11	12	12	12	11	13	13	28	17	9	9	11	11	25	15	19	28	15	15	16	18
HQD82	Philbrook	Bures St. Marys, England	13	23	14	11	11	13	12	12	12	13	12	29	19	9	10	11	11	26	15	19	28	15	15	17	18
K4RN8	Shoemaker	Germany	13	23	14	11	11	12	12	12	12	13	13	29													
MDJ42	Pratt	Baldock, Hertfordshire, England	13	23	14	11	11	12	12	12	12	13	13	29	17	9	10	11	11	25	15	19	29	14	14	16	16
PCCHA	Austin	Franklin County Virginia, Virginia, USA	13	23	14	11	11	12	12	12	11	13	13	29													
Q2KCV	Bruce	North	13	23	14	11	11	12	12	12	11	14	13	30	17	9	10	11	11	25	14	19	29	15	15	17	18

A more conservative database was also searched. Using the database **www.yhrd.org**, One is able to actually find a match for the Greenway 10 allele sequence, something that was not feasible with any of the other data bases. A single exact hit pops up for the 10 allele input, with DYS438 and DYS439 excluded (the YHRD sample did not test for those two results). The red dot shown below is in Friesland, the Netherlands. That data base is not open to public alteration without establishing the basis of the testing et cetera. It is

pretty interesting that the only exact match of the Greenway 10 marker test is in Friesland. But 10 markers does not a match make! To replicate this finding go to **www.yhrd.org** and carefully enter the Greenway Sequence as pictured:



There is one match, shown by the red dot below:



Similar searches can be conducted for free with all haplotypes and various theories can be made about the meanings of the haplotype data.

That is exactly what is done in cyberspace with the data. There is plenty of debate in discussion groups about background migration and the other less documented Germanic tribes that may have migrated as far as Sicily in ancient times. Skeptics of "Greater Frisia" feel that people are too quick to connect to one ancient tribe over all others, based solely on the "23/11 hypothesis.

Skepticism and remaining open to alternative explanations as genetic anthropology continues to develop is important. While we should remain open

to change, there is some evidence to support the notion that the Greenway ancient origin is Frisian and the Whitfield ancient origin is Baltic Viking. Both of those origins would be supported by anthropology and linguistics for eastern England. The ancient tribal lineage of the Drake line is not as clear due to the wildly successful expansion of that Atlantic Modal Cluster haplotype.

Conclusions

From this study I conclude that the paper-trail genealogical record compiled over the generations by WE Brockman and Paul Brockman, and others withstand genetic scrutiny ***within the USA***.

With regard to ancient origins, the Greenway Brockman Y-DNA motifs ***is currently thought*** to be Frisian in ancient origin, and that is supportive of an English origin via the 'saxon' migrations for the Greenway Brockman patrilineal lines. The Whitfield line appears to be Norway/Baltic Viking in ancient origin, again, with the caveat of current thinking and sampling to-date.

With regard to the genetic diversity of the surname there appears to be at least two haplogroups sharing English heritage and the surname barring non-paternal events. This diversity includes R1b and R1a haplogroups. Including Germany, the I1a haplogroup is included.

Acknowledgements:

Paul Brockman, eminent family historian continues to provide information and correct my flawed memory on the Brockman story, I eagerly await his book. Wikipedia provided plenty of information on genetic genealogy. DNA Heritage, of the UK, provided the testing services, and 7 Brockmans kindly provided samples so far along with permission for me to share the information.

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Michael Weale Presenting his work with sound and animations:

http://www.ucl.ac.uk/tcga/presentations/ASdemo/AS-26-11-03b.html