A Report On The Findings Of The Gibbs Surname DNA Project
by David Lee Gibbs, Administrator for The Gibbs Surname DNA Project

This is a report of my personal analysis of the findings that have come out of the Gibbs Surname DNA Project from its inception in 2003 to the present (March 2010). It is my attempt to make accessible to others what is sometimes very technical and very confusing information from what is still emerging out of a very early stage in the development of genealogy by genetics. I do this from my layman's view point and have tried to make it understandable to laymen. In the realm of genetic science I am exactly that – a simple layman – and I make no claim to be more than that. But as an avid amateur genealogist, I try to be as well read on the application of genetics to genealogical pursuits as I can be. From this I feel well prepared to share what follows, and encourage readers to make themselves knowledgeable on the subject. Anyone better prepared than I am is welcome to contact me to offer advice on how this work might be amended, expanded or otherwise improved.

In an effort to keep the subject matter oriented to the findings of the Project I have included what I feel is most useful to the participants in the Project. To keep it simple and uncluttered, I am offering it here without citation other than the list of sources appearing at the end. Readers are encouraged to check these sources for additional information and as a check on this work. I have not vetted the sources for their correctness or the accuracy of their citations. But, where I am confident in what they present, I have drawn from them to provide as concise and clear a condensation of their more scholarly work as I can make.

GENEALOGY BY GENETICS

In the last decade new tools and methods have been developed in the genetic sciences that have the potential to revolutionized what we may learn about our ancestors and how we learn it. Great interest has arisen in the genealogical community as these tools have been made available to aid us in researching our ancestors. In particular, the testing and analysis of human male DNA (or Y-DNA) has proven very useful in researching paternal lines of descent.

This is possible because a certain part of the male 'Y' chromosomes does not break down and recombine with female 'X' chromosomes when a male offspring is conceived. Instead, this "non-recombinant" part of a father's DNA is simply passed on - intact - to his sons. Because it does not break down or recombine, it remains virtually unchanged, generation after generation, for many thousands of years. Thus, all living human males carry in their Y-DNA the unmistakable signature of their ancient forefathers. Testing is also done for mitochondria DNA (or mtDNA) which is found in males and females, but is only passed to offspring from the female parent. While mtDNA testing can also be revealing in genealogical research, it is not useful in determining a specific lineage the way Y-DNA testing is, and it is not considered in this discussion, as it lies beyond the scope of surname-based DNA projects.

TESTING Y-DNA FOR STRs AND SNPs

Geneticists have discovered two types of DNA mutations which are useful in genealogical research. These are STRs (single tandem repeats), and SNPs (single-nucleotide polymorphisms). Both can be found in the non-recombinant portion of a man's Y-DNA. All DNA is made up of just four different kinds of nucleotide molecules (referred to as A, C, G and T) that are assembled in pairs (which may be any possible combination of two of the four nucleotides; A+A, A+C, G+T, A+T, etc.). A pair of nucleotide molecules is called a single tandem.

These single tandem pairs are repeated in sequences (called Single Tandem Repeats, or STRs) along the DNA chain. The number of times a single tandem pair is repeated at a given location in the DNA chain is called an "allele value" or just an "allele". Alleles are variable, and that is what makes them useful for genealogical purposes. By counting the number of times a single tandem repeats at certain selected points (or loci) in the DNA chain, we can establish the numeric value for sets of alleles that have been found to be useful as points of comparison between different Y-DNA samples. These loci are identified by DYS (DNA Y-chromosome Segment) numbers. Selected sets of DYS loci (also called "markers") are referred to as "panels", and testing for varying numbers of panels is available commercially from DNA testing companies. Determining the numeric values of the alleles in a panel (or panels) of markers from a given Y-DNA sample establishes the genetic signature, or haplotype of the sample's donor. Typically, the more markers that are tested, the tighter the definition of the haplotype becomes.

Geneticists also test for single-nucleotide polymorphisms (SNPs), which are variations in the Y-DNA sequence that are observed in different individuals. These SNPs (pronounced "snips") are very rare and happen when one type of nucleotide is substituted for a different type at a single point in the DNA chain when genetic information is mis-copied. The result is called a polymorphism, or mutation, and it is passed on to all the male descendants of the individual in whom it first appears. SNPs are useful in determining how the human phylogenic tree has branched into the many different ethnic groups we find today.

SNPs define haplo*groups* which make up the structure of the human phylogenic tree. Thus SNP testing can reveal the ancient origins of individual males, but cannot show how they relate to others in a lineage. STRs define haplo*types* which are the distinctive DNA signatures of individual males that speak to us of our recent origins and do help us identify probable familial connections. STRs are extremely helpful when combined with conventional, documentary genealogical evidence.

Y-DNA HAPLOGROUPS AND HAPLOTYPES

The branches of the human family tree that are defined by SNP mutations are called haplo*groups*, and each of them contains myriad haplo*types*. When two men are

found to have perfectly or closely matched haplotypes, there is a very high probability that they share common ancestry. If these two men also share the same surname, then the probability exists that their most recent common ancestor lived within the historical period since the use of surnames became common. If they have conventional genealogical data to compare, knowing of a genetic connection to a common ancestor can confirm what might not be possible to otherwise document.

The Gibbs Surname DNA Project was started in March 2003 with the goal of adding the science of genetics to the genealogical research already well advanced among Gibbs researchers. The project is ongoing, and open to all males who share the Gibbs surname or a variant of it, and to females of Gibbs lineage who can participate through use of a Y-DNA sample from a male Gibbs blood relative. To date the project includes 63 participants who have submitted Y-DNA samples for analysis. Of these, 14 match perfectly or closely to at least one other participant, giving us 49 unique Y-DNA haplotypes that we may think of as the Y-DNA signatures of 49 Gibbs lineages. Close matches among 28 of these Y-DNA signatures have defined seven distinct groups (or "clades") proven to be descended from seven different founders (or common ancestors). We also have 21 unmatched participants who are known from conventional research and documentation to be descended from Gibbs lineages, but have yet to be confirmed with Y-DNA matches. Thus we potentially have identified 28 different Gibbs lineages which do not descend from the same common ancestor.

A long-held theory, shared by many researchers, was that all Gibbs lines were branches of the same family, with a single founder. However, the discovery of so much diversity among the project participants was a significant breakthrough that has completely disproven that theory. As the project has grown, and more and more matched clades (or groups) have been discovered, we have been able to use the small mutations in the STRs to define branchings within the clades. This has greatly helped to advance the conventional research of those who have discovered their shared lineages. By knowing who we match, and who we don't match, we can focus our conventional research efforts in areas that can yield the best results. This has been a major benefit of the project.

Some of the participants have gone a step further and have had their Y-DNA samples tested for SNPs to confirm their deep ethnic origins. The testing company we have used, FamilyTreeDNA.com (FTDNA), provides each participant with a prediction of their haplogroup based on patterns observed in their STR alleles. However, only SNP testing can confirm these predictions, and because it involves additional expense, most participants have been content to accept their predicted haplogroup as sufficient. Those who have been tested for SNPs have been able to improve on the predictions and have learned what sub-clade they belong to within the major haplogroups. Their participation at this level has contributed a great deal beyond the scope of our surname project, as the SNPs are compared to the entire database of FTDNA customers from all over the world, and help define the sub-groups more tightly.

The predicted and confirmed haplogroups found among the participants in the Gibbs Surname DNA Project include the following:

TABLE I. GIBBS SURNAME DNA PROJECT HAPLOGROUPS

HAPLOGROUP	PREDICTED	CONFIRMED	% OF TOTAL PROJECT
J2/J2a4b*	–	1/1*	3.22%
I1	4	—	6.45%
I2a	—	1	1.62%
G2a3b	—	1	1.62%
E1b1a	1	1	3.22%
E1b1b1c1/E1b1b1c1a*	12	1/1*	22.58%
R1a1	1	—	1.62%
R1b1	—	2	3.22%
R1b1b2	32	2	54.83%
R1b1b2a1	1	—	1.62%

*Earlier SNP tests did not always identify as many mutations as later tests. As new SNPs are discovered, additional testing is needed to confirm that individuals do, or do not, also belong in a sub-clade of their previously confirmed haplogroups. But when the STR alleles are tightly matched among confirmed individuals, we can predict that they all belong to the same haplogroup and sub-clades as the highest tested individual to whom they are tightly matched. This is not the case among individuals whose confirmed haplogroups are the same, or close to the same, but whose STR alleles indicate that a high degree of genetic distance separates them.

GEOGRAPHIC ORIGINS OF GIBBS HAPLOGROUPS

The study of population genetics, informed by work from the fields of physical anthropology, archaeology and linguistics, is beginning to give us a reasonably good understanding of the geographic origins and prehistoric migrational history of the known Y-DNA haplogroups, including those represented among the participants in the Gibbs Surname DNA Project. It is important to remember that these disciplines, which look at diverse evidence of the human past, do not always agree on how the evidence should be interpreted. Debate is ongoing within these disciplines, and between them, and a great deal of uncertainty exists even where a general consensus may have been reached. Thus, we must take the statements about the relationships between human populations and their geographic origins with appropriate reservations.

With that said, the following represents the current assessment of what genetic evidence tells us are the likely origins of our modern Gibbs haplogroups. We can expect these to change over time, as new evidence comes to light. The assessments are drawn from a number of sources that are not cited in the text, but which can all be found in the bibliography at the end of this report.

Haplogroup J2 (M172); Subclade J2a4b (M410 with M67)

Within the Gibbs Surname DNA Project we have two members who can trace their ancestry to a Gibbs lineage first found in Hyde County, NC in the 1700s. Both have confirmed their haplogroup by SNP testing, with one testing into the J2a4b subclade. Because these participants are separated by a genetic distance of "1" (one) through the 25-marker level, we can reasonably assume that both would test into the same subclade and therefore, both belong to haplogroup J2a4b.

Some studies have found that the J2a4b subclade includes approximately 15% of contemporary Jewish Kohanim, who are believed to be descended from Aaron, the brother Moses as found in the Jewish Torah. Yet there is no tradition of Jewish heritage in the known history of our two Gibbs participants. We might expect that if they do descend from the priestly class of ancient Israel there would be some immediate family history reflecting this. Can a person who is J2a4b be something other than Jewish? The answer is yes. The haplogroup existed long before Aaron's time, and many who are J2a4b come from Arab or other Semitic lineages. It seems reasonable to say that these two Gibbs lines may have originated from the segment of J2a4b that is Jewish, but also that the lack of Jewish culture in these lines tilts the odds toward a lineage that is outside the Jewish segment of J2a4b.

Bennet Greenspan, the founder of FamilyTreeDNA, wrote an important article in 2008, titled "Can DNA Testing Confirm Jewish Ancestry?" which helps us to better understand the chances of our J2a4b participants having Jewish ancestry. He makes the point that DNA testing cannot reveal if a person is Jewish, but can (under the right circumstances) reveal if he has Jewish ancestry. He states that two elements must exist to demonstrate Jewish ancestry. One is a well-defined database of known Jewish haplotypes, complete enough to represent all members of the Jewish population world-wide. The other is a testee whose DNA matches a lineage that is all, or nearly all Jewish. When that testee is compared to the database, one of four situations is possible:

1.) The testee may match only individuals who are known to be Jewish, in which case the testee has Jewish ancestry.

2.) The testee matches both Jews and non-Jews, in which case the results are inconclusive.

3.) The testee matches no individuals who are known to be Jewish, in which case the testee likely does not have Jewish ancestry. (This is especially true when the database used for comparison is the FTDNA database, which is believed to include virtually all the known Jewish lineages world-wide.)

4.) The testee doesn't match anyone in the database, in which case the testee's haplotype is a previously unknown, therefore unique, lineage. This occurs very rarely, and unless the testee knows from his own family history that he is Jewish,

there is no way to determine from his DNA if he is, or is not descended from a Jewish lineage.

In the case of our two J2a4b participants the second situation applies. However, in comparing their test results to the entire FTDNA database, it can be noted that both participants have a single-step mutation from individuals who are Ashkenazi or Sephardim (the two major Jewish cultural groups). These matches are ranked as percentages of the total number of individuals from each country in the database, with any percentage above 2% considered a significant indicator of a participant's family origins. These participant's Ashkenazi matches represent 1.9% of the individuals tested from the Ukraine; 1.8% of the tested individuals from Latvia; 1.4% from Lithuania; 1.2% from Belarus; 1.0% from Northern Ireland; and 1.0% from Iran. They also have Sephardic (Iberian Jewish) matches representing 1.1% of the tested individuals from Turkey. While these percentages are below the 2.0% considered "significant" they are the highest percentages found for these participants from all of the countries of origin in the FTDNA database, so they may be seen as somewhat indicative.

If they do not have Jewish ancestry, what might their ancient ancestor's origins be?

Haplogroup J2, the ancestor of J2a4b, has its estimated time of origin set at 18,500 (+/- 3,500) years before present. It is believed to have originated in Mesopotamia and is defined by the SNP mutation M172. In Europe, the frequency of haplogroup J2 decreases significantly the further away from the Mediterranean one travels. In the Middle East it is found in highest frequencies toward the north of the region, although it has significant presence throughout the entire Middle East. Some believe this distribution indicates an association of this haplogroup with the Neolithic demic diffusion which began in Mesopotamia and spread agriculture northward through the Levant and Anatolia, through the Balkans, and into Southern Europe around the Mediterranean.

So if J2 and its subclades are rightly considered Middle Eastern, how did our Gibbs participants' ancestors reach Hyde County, North Carolina? We know that the family was there in the Colonial Era, and that this was a British Colony then. We also know that Gibbs is an English surname, so It seems reasonable to conclude that the lineage came out of the British Isles. But if that is true, how did it get to the British Isles from its Middle Eastern homeland? It may never be possible to know for certain, but three possibilities have been suggested. Keep in mind that these are highly speculative, and no certain proof exists for any of them.

First, if the lineage is Jewish, it could be a result of Spanish or Portuguese Jews (Sephardim) emigrating to England after the expulsion of the Jews from those countries after 1492. They might then have acquired the Gibbs surname as part of a process of assimilation into the British population. The original surname may have been something close to Gibbs, such as "Gabis", "Gabishon" or "Gabison", which are Sephardic Jewish surnames derived from "Gavish" which is literally "Crystal" in

Hebrew, and describes someone who is clever. Another Sephardic surname is "Gabbai", "Gabay", "Gabbay" and other variants which are all titles or offices that translate from Hebrew as "Synagogue Treasurer". Since written Hebrew has no vowels, the spelling Gabis, rendered in Roman script, would be G_b_s. It would not be hard to anglicize it by adding an "i" and perhaps an "e". Of course, without some evidence that this took place, it is pure speculation.

A second possibility is that the J2 ancestors of our Gibbs participants may have been among the mercenary legionnaires brought to Britannia by the Romans during their occupation of that island province. This would place them there centuries before the use of surnames became common outside the upper classes of Romans. If this is the case, they could have adopted the Gibbs surname at some point after it gained some notoriety or popularity in the middle ages. Like the first theory, this one is entirely based on speculation at this time.

The third possibility is that their J2 ancestors reached the British Isles in prehistoric times, perhaps in association with the migration of early agricultural groups from the Middle East. Recent discussion among Paleoanthropologists about the populating of the British Isles seems to be producing a consensus that the earliest people to reach those Islands after the glaciers of the last ice age retreated across Europe included the J2 haplogroup along with others. This might mean the ancestors of our J2 participants were in England as long as anyone else. They may have been part of the original population of Britons who were there when the Romans arrived. The point is not settled among the paleoanthropologists and is also speculation as regards our Gibbs J2s.

Haplogroup I1 (M253) and I2a (M438/P37.2)

The Gibbs Surname DNA Project currently has five participants from Haplogroup I, split into four who are predicted to be haplogroup I1 and one who is confirmed by SNP testing to be of the I2a haplogroup. Haplogroup I developed from its ancestor haplogroup IJ contemporaneously with the onset of the last glacial maximum, approximately 22,000 years ago, probably in Europe or Asia Minor. Some suggest that the initial dispersion of this haplogroup was associated with the expansion of the Gravettian culture of the Upper Paleolithic era. Haplogroup I is closely related to haplogroup J and shares many SNP mutations with it. However, the two diverged many thousands of years prior to the advent of Semitic languages and thus the I haplogroups are not found in association with the Semitic peoples of antiquity.

As the glaciers retreated, haplogroup I gave rise to its descendant haplogroups, I1 and I2. I1 moved out of the Caucasus and swept across Northern Europe and into Scandinavia, where it is typically found at its highest densities today. The Gibbs Surname DNA Project participants from this subclade possibly descend from Norse invaders who carried their genes to the British Isles.

I2 was carried southwestwardly into the areas around Bosnia, Herzegovina, Croatia, and Macedonia where it remained for a long time and developed a high degree of sub-clade diversity, including the development of I2a, which is how it is represented in the Gibbs Surname DNA Project. I2a, with many other sub-clades, is found today in high densities in the Balkan countries, and in Moldavia and Romania. At even higher subclade diversity, but lower densities, it is also found in Slovakia and the Czech Republic.

Our I2a project participant is descended from a William Gibbs who was born in Broadwindsor, Dorset, England in 1680. As is true with our J2 participants, this William's forefathers may have reached England during the Roman era, when mercenary soldiers from the easter parts of the Empire were stationed there.

Haplogroup G2a3b (L141+)

The Gibbs Surname DNA Project currently has a single participant who has been confirmed as belonging to the G2a3b haplogroup. He was adopted as a child and raised under a different surname, but learned from adoption records that his biological father's surname was recorded as "Gibbs". Since this might not have been his biological father's true surname, there is room to doubt if G2a3b is a true Gibbs haplogroup.

The SNP mutation (L141+) that identifies this haplogroup (actually a subclade of G2a) was only identified in mid-2009, so not much is known as yet about its role in the world's early populations. Initial testing seems to indicate that this is a significant G group subclade, and samples from persons with British Isles and Turkish ancestry have been identified. Early assessments of its likeliest geographic source seems to indicate that it first appeared in Turkey or the eastern Mediterranean region.

The small number of STR mutations found between G individuals from England and Turkey indicates a origin for it sometime around 1,700 to 3,000 years ago.

Haplogroup E1b1a (E-M2)

The Gibbs Surname DNA Project currently has two participants who belong to the E1b1a haplogroup (one being predicted as such and the other confirmed by SNP testing). This haplogroup is believed to have originated in sub-Saharan West Africa approximately 20,000 to 30,000 years ago, and is found there in frequencies of over 80% today. It is considered by some to be the signature Y-DNA haplogroup representing the Bantu expansion, which was a series of migrations that lasted thousands of years, during which a diffusion of the proto-Bantu language and culture gradually spread among neighboring populations. The first leg of the Bantu expansion is believed to have begun in Cameroon approximately 5,000 years ago and moved south into the Congo/Niger region and west into eastern Africa. This was

followed over time with back-migrations from eastern Africa to the Congo/Niger region and from eastern Africa and Congo/Niger southward, finally reaching the Kalahari desert and some areas of South Africa as recently as 1,000 AD. Some pioneering groups eventually reached modern KwaZulu-Natal in South Africa by 300 A.D.

As significant numbers of men from West and Middle Africa were carried to the New World as slaves beginning in the 16th century, the E1b1a haplogroup was introduced into the British West Indies, including the mainland colonies of British America. The first to reach British North America arrived in 1619 as indentured servants who settled in Jamestown, Virginia, where they worked as laborers in conditions and legal positions similar to those of poor English indenturees, who traded several years of labor for passage to America, and after which term they were free to live as colonists in their own right. As indentured servants, Africans could legally raise crops and cattle to purchase their freedom. They could and did intermarry with Native Americans or English women as well as African woman, raised families, and by the 1640s and 1650s several African families owned farms around Jamestown and some were considered wealthy by colonial standards. Even after the practice of African enslavement in the British American colonies became more restrictive and institutionalized, slaves were freed by their owners, sometimes as acts of kindness or rewards for their services, sometimes out of guilt, or conscience, or for religious reasons. Sometimes these freed slaves were the children of their masters, but in the case of the male children's Y-DNA, it would be that of their father, and not of E1b1a origin.

Over time, as more and more African men attained the status of freedmen, many adopted English surnames as a way of elevating their position in the colonial and post-colonial society surrounding them. Slaves were not permitted surnames, and thus adopting a surname separated the freedman from his former condition in a very public way. In some cases, if freedmen wanted to continue an association with their former masters, they might adopt the master's surname as their own. Therefore, it does not surprise us to find the E1b1a haplogroup represented among the participants of the Gibbs Surname DNA Project.

Haplogroup E1b1b1 (E-M215, E-M35) with Subclades E1b1b1c1 (E-M123, E-M34) and E1b1b1c1a (E-M84)

The haplogroup with the second highest representation in the Gibbs Surname DNA Project currently has 14 participants who are either predicted to be E1b1b1 or are confirmed via SNP testing as E1b1b1c1 or E1b1b1c1a. Each of the two subclades are represented by a single participant each, but as we can see from their very tight relationships (evidenced by their STR alleles) this entire group descends from a common ancestor who probably lived in the British Isles in the mid-to-late 1600s. It is thus proper for us to regard this entire group of participants as all belonging to the E1b1b1c1a haplogroup.

E1b1b (E-M215) and its dominant subclade E1b1b1(E-M35) are believed to have originated in East Africa about 22,400 years ago. All major sub-branches of E-M35 are thought to have originated in the same general area as their parent clade: North Africa, East Africa, or nearby areas of the Near east. From this area, E-M35 was dispersed northwestward into Egypt and across North Africa around the Mediterranean basin, and also up into the Levant and Anatolia, and later toward the south into Ethiopia and as far as South Africa.

As for E-M35 lineages outside of Africa, certain sub-clades appear to have been present in Europe and Asia for thousands of years, so it is incorrect to describe E-M35 as strictly an African haplogroup. Instead, its distribution seems to be similar to that of J2 lineages from Anatolia and has been associated by some with the Neolithic expansion from the Middle East through the Levant and Anatolia, into the Balkans and Southern Europe around the Mediterranean basin.

E1b1b1c (E-M123), for example, is a sub-clade of E-M35 which probably originated in the southern Levant, just to the northeast of Egypt. Many branches of E-M78, from nearby northern Egypt are also present in the Semitic speaking populations of this region. That the Levant is not dominated by E-M35 is not surprising because the Semitic languages (and the people who used them) may have remained isolated in the Levant until not long after the written record starts in Mesopotamia.

E-M123 accounts for over 10% of all the male lines of Ashkenazi and sephardic Jews, making it the second largest founder lineage for both of these Jewish groups. However, because it is also present in low percentages among non-Jewish Balkan and southern European populations, the placement of its origin among Jewish groups is uncertain. However, the fact that it has such high representation among Ashkenazi and Sephardic populations supports an Israelite/Middle Eastern origin.

As to the question of our E-M123 participants having Jewish ancestry or not, the same analysis applied in the discussion of J2a4b above also fits E-M123. There is no known history of Jewish ancestry among our Gibbs participants in more than 200 years. But here again, if they do not have Jewish ancestry, then what other possibilities exist?

E1b1b1c1 (E-M34) is the dominant sub-clade of E-M123, and it has found in several places in Iberia, with a frequency of 10% in Galicia. This is probably the largest concentration of this haplogroup outside of Ethiopia today. This seems to be highly significant, and may perhaps indicate the presence in Galicia of a colony of Phoenician trader/agriculturists in antiquity. It does appear that E-M34 was spread throughout the Mediterranean, perhaps in association with Phoenician or Greek traders, as its presence is found among the populations of islands and mainland locations known to have been colonized by these two seafaring cultures in antiquity. It appears to have a small but significant and ancient Mediterranean dispersal. For example in addition to Northwestern Iberia, it is found in some areas of Sicily as well

as in the Albanian speaking community of Cosenza Province in Calabria. The highest M34 levels in Iberia might be on the islands of Minorca and Ibiza. These last two islands in the Balearic archipelago are well known to history as colonies of Phoenicia, Carthage, and Greece.

It has also been suggested that the presence of E-M34, along with relatively high percentages of other Middle Eastern and North African Y-haplogroups in Portugal and northwestern Spain may represent an even earlier seaborne migration of Middle Eastern and North African haplogroups in the Neolithic Era. In particular, archaeological evidence points to the Cardial culture of Northern Portugal as an early Neolithic "enclave" in Western Iberia, that defies any simple model of "demic diffusion" from East to West. Dr. João Zilhão, PhD., professor of Paleolithic Archaeology at the University of Bristol, wrote in 2000 of evidence supporting "leapfrogging colonization by small seafaring groups of agriculturalists". His theory coincides nicely with what genetic studies of Iberia have show about the presence of Middle Eastern DNA in western and northwestern Iberia. It also explains its presence in relatively isolated locations away from any other obviously related European enclave of Cardial technology. It suggest a very early migration of coast-hopping agriculturalist who reached as far as the Atlantic, and took on an African (Berber) component in their population before passing the Straits of Gibraltar.

E1b1b1c1a, the E-M34 subclade that is of most interest to our Gibbs surname project, is defined by the SNP mutation E-M84. This SNP was first discovered in October of 2008, so not too much is known as yet about its origin or distribution history. However, It appears to be the dominant subclade of its immediate ancestor, E1b1b1c1 (or E-M34).

It is my personal theory, at this time, that our E-M84 Gibbs clade, arriving as it appears in British America in the early Colonial Era, was most likely introduced into the new world by at least two immigrant ancestors who shared a common lineage that had been established in the British Isles long enough to have acquired the Gibbs surname before crossing the Atlantic. Mutations in the STRs found in our participants from this haplogroup reveal that there are two distinct branches to the family, with several sub-branches that probably occurred after the family settled in the Southern colonies in British North America. Both branches, because of the earliest locations that we have found them in are referred to in our project as The Carolina Gibbs E-M84 Clade.

How our E-M84 ancestor arrived in the British Isles probably follows the same logic as seen regarding our J2a4b project participants.

Haplogroup R1a1 (M448, M459, and M516)

R1a1 is a family of lineages dominated by the very large and well-defined R1a1a branch, which is identified by the presence of the M17 and M198 SNPs. The

paragroup R1a1* (the asterisk indicates that it is undifferentiated by any downstream SNPs) lacks both the M17 and M198 markers. Within our Gibbs Surname DNA Project we have one participant who is predicted to be R1a1, but there is a strong probability that if he were tested for SNPs he would fall into one of the sub-clades of R1b1 – most likely the R1a1a branch.

R1a1* is less rare than R1* but still unusual. R1a1a, however, is found at much higher frequencies over its entire geographic range. Most discussions of R1a origins are actually about the origins of the R1a1a sub-clade. It has been found in high frequency around two widely separated geographic regions; one around North India, and the other around Poland and the Ukraine. Population geneticists and genetic genealogists have yet to reach any consensus about the possible path or paths of dispersal of R1a1a. Studies conducted in 2009 concluded that while the R1a1a presence in these two regions are of similar age, the South Asian R1a1a appears to be older than Eastern European R1a1a, suggesting that South Asia is slightly more likely to be the region of origin.

In Europe, R1a1a is found in increasingly lower frequencies from Eastern Europe into Northern and Western Europe. It seems to have moved in these directions following the Last Glacial Maximum, as the ice retreated across Europe, perhaps as early as 11,000 years ago. This initial migration was followed by more recent gene-flow out of Eastern Europe during the Bronze Age, and in association with the spread of Slavic languages. In Norway its presence may be associated with the spread of Corded Ware and Battle-Axe cultures from Eastern Europe.

In the British Isles, R1a1a is found in very low frequencies, mainly in Scotland and Northern Ireland, with its highest frequency in the region roughly contiguous with Caithness, parts of which were occupied beginning in the 10th century by bands of Norse settlers, who probably brought the R1a1a haplotype with them.

Haplogroup R1b1 (M173, M343, with P25)

R1b1 within the Gibbs Surname DNA Project is confirmed by SNP testing for just two individuals, both of whom ordered their SNP tests in the early days of the project, before many of the downstream sub-clades of R1b1 were known to exist. Testing is currently available to upgrade their test results, but so far no tests have been ordered for the 30 additional SNP markers that could refine their haplogroup assignments. Since true R1b1* is now known to be rare, it is a safe assumption to expect them to actually belong to a sub-clade of R1b1, but without further testing we can only speculate on which sub-clade that might be.

One of our R1b1* (R-P25) Gibbs participants is closely matched by STR analysis to several other participants who have been predicted by FTDNA to belong to the R1b1b2 sub-clade, so in this case we can reasonably assume that the STR-matched R-P25 participant would also fall into R1b1b2 with further SNP testing. The other R-P25 participant has not found a close match yet within our project, but the general

pattern of his STR markers does look very similar to those of other project participants who have been predicted to be R1b1b2. Here again, we may safely assume that further testing would confirm his assignment to this sub-clade as well.

Haplogroup R1b1b2 (M269)

The R1b1b2 haplogroup has the highest frequency of any haplogroup within the Gibbs Surname DNA Project. It has been confirmed or predicted for 54.83% of our project participants, and if we include the two R-P25 participants and the single R1b1b2a1 (R-L51*) participant the actual percentage grows to 59.67%. This last participant (who is predicted, but not confirmed to have the R-L51 SNP mutation) has been closely matched to a group of four other project participants who all trace their lineage to New England in the 1630s to 1760s, with several who can prove descent from Giles Gibbs and Kathryn Carwithe of Crewkerne, Co. Dorset, England. All five are predicted to belong to the R1b1b2 haplogroup, so it is safe to assume that their sub-clade would also be R-L51. For the sake of this discussion, we will treat all of our participants who are R1b1, R1b1b2, or R1b1b2a1 as a single haplogroup. With that said, what is known about the origins of R1b1b2?

R1b1b2 is defined by the presence of the SNP mutation M269. This mutation has been found at generally low frequencies throughout central Eurasia, creating a consensus of opinion among population geneticists that this is its region of origin, with the Perm region (along the banks of the Kama River in European Russia, very near the Ural Mountains) as its center. It is found there at a high frequency (84.0%) among Bashkirs of Bashkortostan. Population geneticists estimate that R1b1b2 arose in this region about 5,000 to 8,000 years ago. From there it spread into Western Europe.

In Europe today, the dominant R1b1b2 sub-clade is R1b1b2a1a1 (or R-U106) which makes up an estimated 25% of the R1b in all of Europe. None of our Gibbs participants have been confirmed for the R-U106 mutation at present, but there are indications that it does exist among us. Before I explain, we should note that in Europe R-U106 is found everywhere, but it is distributed from the north west to the east with frequencies of 21.4% in England and Scandinavia (declining to 17.1% in Denmark), and is at its maximum frequency in the Netherlands where it is 37.2% of the males tested. The frequency declines to the east through Germany where it is 20.5% and the Alps (where it is at 13.3% in Switzerland and 22.7% in Austria); it is 13.9% in the Czech Republic and 9.4% in the Ukraine. It is found at a lower frequencies in Poland (8.2%) and Russia (7.2%). It is found at only 5.9% in Ireland, 7.1% in France and drops to even lower frequencies along the northern Mediterranean costal region. It is found at 3.5% in Italy and 0.4% in Turkey.

Studies are increasingly revealing that Western European R1b is dominated by the R-P310 sub-clade (also known as R-L11). R-L11 is, in turn, dominated by the R-U106 mutation. Within this R-U106 branch is found the most common STR Y-DNA

signature for all Western European males, which is also known as the Atlantic Modal Haplotype (AMH) or "Haplotype 15". Haplotype 15 is contrasted with "Haplotype 35", which has long been noted as a distinct type of R1b1b2, more common towards the southeast of Europe. Haplotype 35 is characterized in part by the STR value of 12 at DYS 393 and has often been referred to as the Armenian Modal Haplotype. All of the R1b1b2 Gibbs participants in our project have a value of 13 or 14 at DYS 393, which excludes them from Haplogroup 35, so by default we can see that none of the Gibbs R1b1b2 participants belong to Haplotype 35. As for Haplotype 15 (the AMH), we have only seven participants who fit the AMH perfectly out of 37 who are predicted or confirmed as R1b1b, R1b1b2, or R1b1b2a1. For these seven participants there is a high likelihood that they would test positive for the R-U106 SNP mutation.

R-U106 is believed to have originated around 3,100 to 3,900 years ago (or from 1900 BCE to 1100 BCE, which makes it post-Neolithic, and sets it firmly in the Bronze Age. This can be an important clue for our AMH positive participants as to where they can focus their research work. But what about the other 30 participants who may also be R1b1b2 but do not match the AMH perfectly? Those who are at a 1-step genetic distance from the AMH (that is, who have a different allele value of just one point at a single DYS locus out of the six that are considered in the AMH calculation) fall into what is known as the Atlantic Modal Cluster (or AMC), which is usually included in the frequency percentages given for the AMH in genetic-based population studies. Looking at our 30 non-AMH participants, we see that they all are at least two steps removed from the AMH, which places them outside the AMC as well as the AMH, and this means that their R1b1b2 heritage is probably not within the R-U106 sub-clade.

Of interest to the seven participants who do match the AMH is the following information. The Atlantic Modal Haplotype is said to reach its highest frequencies in the Iberian Peninsula and the British Isles. In Iberia it reaches 70% in Portugal as a whole (and more than 90% in north west Portugal). In Spain it reaches 90% in Galicia and has its highest frequency among Spanish Basques. One very detailed study found the distribution of the AMH/AMC combined to be 89% in Ireland (where it is 45% AMH with 44% AMC); 89% in Wales (where it is 19% AMH with 70% AMC); 90% among Basques (34% AMH with 56% AMC); and at 56% in Friesland (18% AMH with 38% AMC).

Enter Niall Noígíallach

One Gibbs Surname DNA Project participant who is R1b1b2 (predicted) has been perfectly matched to a different (non-AMH) haplotype with an interesting history. He falls within the "Niall Of The Nine Hostages" haplotype. This haplotype was first identified in a recent study conducted at Trinity College in Dublin, Ireland which showed that a remarkable number of men in Ireland (and a significant number in Scotland) share the same Y chromosome. This suggests that about one in twelve Irishmen are descended from the same ancestor, who may have been a man known to history as Niall Noígíallach (translated as "Niall Of The Nine Hostages". Niall established a dynasty of powerful chieftains that dominated Ireland for six centuries.

In the study, it was found that in one area in northwest Ireland 21.5% of the males carry Niall's genetic signature. This same area has been found in other studies to have an R1b frequency of 98% which contrasts with 90% in Southeast Ireland. Archaeologist have found that this area was the main power base of the Ui Neill kindred group, (Ui Neill translates literally as "descendants of Niall"). It should be noted that we don't have a DNA sample from Niall's remains on which to base this finding, and it could easily have been a blood relative of his (or any number of them) who is responsible for the widespread distribution of his alleged Y-DNA signature, but it is reasonable to assume that in ancient times high-status, powerful males had greater reproductive access to a wide number of females, especially when success in warfare brought captive women under their control. Niall, aided perhaps by a group of closely related kinsmen over several generations, certainly could have had such a remarkable impact on the population genetics of the areas they controlled.

Niall of the Nine Hostages is so named in Irish folklore from his taking of hostages as a strategy for controlling opposing chieftains. He was said to have been a raider of the British and French coasts and was supposed to have been killed in battle. Some sources say he was killed in the English Channel, others while he was invading Brittany, and some later sources say he was killed in Scotland. His descendants are said to have been the most powerful rulers of Ireland until the 11th century.

Although Niall lived before surnames came into common use, according to FTDNA certain modern surnames have come from this haplotype, which include (O')Neill, (O') Gallagher, (O')Boyle, (O')Doherty, O'Donnell, Connor, Cannon, Bradley, O'Reilly, Flynn, (Mc)Kee, Campbell, Devlin, Donnelly, Egan, Gormley, Hynes, McCaul, McGovern, McLoughlin, McManus, McMenamin, Molloy, O'Kane, O'Rourke and Quinn. Although not in this list we can show that at least one modern Gibbs may claim Niall as his ancestor.

CONCLUSIONS

The Gibbs Surname DNA Project has proven that those who come from long-established Gibbs lineages do not all share a common Gibbs ancestor, nor any common ancestor for tens of thousands of years. This is a surprise to many of us, who thought the opposite was true for many years. The tools of genetic genealogy have allowed us to look beyond the limits of conventional genealogical evidence to find the truth about our origins. This has allowed us to focus our research efforts more tightly on the areas that hold the highest potential to get us results that can overcome the lack of documentation and connect our lines to those we are related to. While the success of the project has been significant, it rests on what is still a very small sample of all the Gibbs males that exist in the world. Thus it is not yet time to say we have learned all we can about the genetic history of our surname. The more we test, the more we learn.

So we have learned that we share a common surname, but not a common past. Does that mean we are not all authentic Gibbses? I would not say so. All surnames were

adopted at some point by our ancestors, including our Gibbs ancestors, and the ancestors were not all members of the same family, kindred group, or ethnicity. We don't know why they took the Gibbs surname to themselves, or when, but that really doesn't make us any the less true Gibbses.

Some may ask if one Gibbs lineage is more entitled to the surname than others. Again, I wouldn't say so. Some may have a longer history of its use than others, but that doesn't make the rests of us any less entitled to it. The only illegitimate use of the surname is to try to create a false identity with an improper motive, by attaching oneself to a line from which you do not come. That is very different than when we make an honest, albeit erroneous, connection after diligent and honest research. The best way to correct an honest mistake is to find a way to disprove it. It is even better to avoid mistakes completely, and DNA testing gives us the means to do both.

The greatest contribution of any surname-based DNA testing project is to help sort the participants out by their proper lineages. Determining your Y-DNA signature gives you the empirical evidence that trumps all other evidence. Records can be wrong, and Momma may have lied to us about who our father is, but DNA always tells the truth.

Still, DNA evidence by itself is not enough, and it can never replace the documented history of one's family. DNA is our genetic inheritance, but family history is our heritage.

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