ANOMALOUS MITOCHONDRIAL DNA LINEAGES IN THE CHEROKEE (PHASE I AND PHASE II)

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Abstract. A sample of 52 individuals who purchased mitochondrial DNA testing to determine their female lineage was assembled after the fact from the customer files of DNA Consultants. All claim matrilineal descent from a Native American woman, usually named as Cherokee. The main criterion for inclusion in the study is that test subjects must have obtained results *not* placing them in the standard Native American haplogroups A, B, C or D, hence the use of the word "anomalous." Most subjects reveal haplotypes that were unmatched anywhere else except among other participants. There proves to be a high degree of interrelatedness and common ancestral lines. Haplogroup T emerges as the largest lineage, followed by U, X, J and H. Similar proportions of these haplogroups are noted in the populations of Egypt, Israel and other parts of the East Mediterranean.

The Cherokee

The Cherokee Indians are a Southeast U.S. indigenous people traced by anthropological science to at least the sixteenth century, when Spanish conquistador Hernando de Soto invaded the region. Archeological excavations have established continuity between today's Eastern Band of Cherokee Indians in North Carolina and the Qualla Phase of occupation of the Appalachian Mountains from 1450 CE, "or earlier," i.e., the Pisgah Phase (Fogelson 2003:338). According to Cherokee elders and keepers of their traditions, notably Keetoowah priests, their age is much more ancient, and their origins and migrations before settling in the Great Smoky Mountains quite complex. Their pre-contact population may have been as high as 30,000 (Thornton 1992:17), and although their numbers dwindled in the aftermath of European contact, typhoid, smallpox and warfare, they were the most numerous of the so-called Five Civilized Tribes of Indians displaced across the Mississippi in the years before 1838. After removal, about 1,500 remained to be registered on Indian census rolls in the East (Fogelson 2003:341), while many more doubtless were in hiding or were sufficiently assimilated to go unnoticed. According to a 2007 report from the U.S. Census Bureau, the Cherokee are the largest tribal group today, with a population of 331,000 or 15% of all American Indians. This figure seems to reflect mostly or exclusively those enrolled in the three federally recognized tribes of the Cherokee Nation of Oklahoma, United Keetoowah Band in Arkansas and Oklahoma and Eastern Band of Cherokee Indians in North Carolina, not Cherokees or their descendants who have never been placed on a U.S. government roll. No Cherokees live on reservations. The most numerous community, in fact, resides in the Greater Los Angeles area.

Despite their numbers, the Cherokee have had few DNA studies conducted on them. There

are only three known reports on Cherokee mitochondrial DNA. A total of 60 subjects are involved, all from Oklahoma. Possibly the reason the Cherokee are not recruited for more studies stems from their being perceived as admixed in comparison with other Indians. Accordingly, they are deemed less worthy of study. Yet only 9.5 percent of Native American samples are judged "unmixed" in the first place. One study that maintains the "Atlantic seaboard and several regions of the Southeastern US have the highest admixture rates, which approximate 50%," also admits that firmly established genealogies for the Navajo, believed to be one of the most unmixed tribes, show that even they have "not inconsequential numbers of genes of European origin" (Crawford 1998:134-35). No matter how you look at it admixture is a problem in the study of American Indians. When geneticists use the word it designates lineages that do not belong to one of the five generally accepted American Indian mitochondrial DNA haplogroups A, B, C, D and X. This is true of the two examples of H and one of J reported in Cherokee descendants by Schurr (2000:253). Schurr takes these exceptions to prove the rule and regards them as instances of European admixture.

DNA Studies That Include Southeastern Indians

mtDNA Haplogroup	n=	A	B	C	D
Cherokee					
Oklahoma Stillwell (Malhi 2001)*	37	10.8	45.9	43.3	0.0
Oklahoma Red Cross (Mahli 2001)*	19	21.1	21.1	52.5	5.3
Smith et al. 1999 (and Schurr 2000)	4	0.0	0.0	25.0	0.0
Total	60	13.3	35.0	45.0	1.7
Choctaw					
Weis 2001 (and Bolnick & Smith 2003)	27	74.1	18.5	3.7	0.0
Chickasaw					
Bolnick & Smith	8	12.5	75.0	12.5	0.0
Creek					
Weis; Lorenz & Smith; Bolnick & Smith	39	35.9	15.4	20.5	28.2
Merriwether & Ferrell; Bolnick & Smith	71	36.6	15.5	9.9	38.0
Total	110	36.4	15.5	13.6	34.5
Seminole					
Huoponen (1997), incl. Bolnick & Smith	40	62.5	25.0	7.5	5.0
Grand Total	**257**	**36.6**	**23.7**	**19.1**	**16.0**

*Includes Lorenz & Smith (1996); repeated in Bolnick & Smith (2001).

The logic governing American Indian sample selection seems to go as follows: Lineage A, B, C, D and X are American Indian.

Therefore, all American Indians are lineage A, B, C, D and X.

If any haplogroups are discovered that are *not* A, B, C, D or X, they are rejected from the study (as evidently in Bolnick and Smith 2003). The reasoning of many anthropologists and geneticists can be summarized as: "All men are two-legged creatures; therefore since the skeleton we dug up has two legs, it is human." It might be a kangaroo.

Description of This Study

The present study concentrates on the "kangaroos"—the documented or self-identifying Cherokee descendants whose haplotypes do not fit the current orthodoxy in American Indian population genetics. Cases come from the customer files of DNA Consultants, a testing service founded in 2003. The method used is the standard one adopted for differentiating mitochondrial DNA lineages by characteristic mutations on a control sequence known as the D loop, which contains two segments called Hypervariable Region (or Section) I and Hypervariable Region (or Section) II (Richards and Macaulay 2000). Included are 52 individuals who ordered a Native American mitochondrial DNA test, and whose matrilineal ancestry, as it was determined in testing, happens to fall outside the haplogroups A, B, C and D. (Additionally, seven instances are adduced of X , which can be Native American or Eurasian.) Comparisons were made to the databases known as Richards, Cambridge Concordance and Mitosearch. Raw data appears at the end of this book. All test subjects have given permission for their names and results to be published in this article. All have submitted detailed genealogies naming, insofar as was known to them, a Cherokee female ancestor. A list of haplotypes and earliest known female ancestors follows.

List of Phase I Participants by Ancestry

Hg		Genealogy
1	H	New England Indian, Norse?
2	X2	Annie L. Garrett, b. 1846, Miss.
3	J*	Native American
4	H	Native American
5	X2	Native American
6	H	Cherokee
7	X2	Agnes Weldy b. ~1707
8	H	Canadian?
9	J*	Cherokee, Emily Glover 1837-1903, Tenn.
10	X2	Seyinus from Qualla Boundary, N.C., b. 1862
11	U2e*	Cherokee wife of Jewish trader Enoch Jordan, b. 1790 Ga.
12	U2e*	Susanna Owens, Cherokee, b. 1760, Granville Co., N.C.
13	U2e*	Rosannah Alexander, b. 1749, Mecklenburg Co., N.C.
14	U2e*	Susannah Wallen or Waldon
15	U5b*	Wife of George Culver, b. 1775, d. 1830, Hancock Co., Ga.
16	U2e*	Cherokee, N.C.

17		U5a1a	Ann Dreaweah, Cherokee
18		U5*	Adopted, Okla.
19	*	U5a1a	Jane Rose of the Eastern Band of Cherokee Indians
20	*	U5a1a	Clarissa Green, wife of John Hodge, b. 1846, Wolf Clan
21		U4*	Lillie C. Wilson-Field, 1857-1937, b. Catawba, N.C.
22		U5b2	Wilma Nell Atchison, wife of Gilbert, Blackfoot (?), b. Kansas
23		K2	Sarah Ann Rose, b. Rock Creek, N.C.
24		T1*	Ann Houston, b. Va., mother of Susannah Walker
25		T1*	Native American (surrogate mother?)
26		T1*	Melungeon and Cherokee
27		X2	Mother of Ollie McCorkle, b. 1906, I.T.
28		T*	Melungeon
29		T2*	Native American
30		K	Mother of Linna Mitchell, born 1779, Choctaw Nation
31		T2*	Cherokee
32		T*	Sully Firebush, daughter of a Cherokee chief
33		Unk.	Unknown Bermuda
34		T5	Choctaw-Cherokee
35		T*	Zella Hand Rogers, adopted 1901, Red Lake Band of Chippewa
36		Unk.	
37		Unk.	Hurley Choctaw or Pitchlynn on Armstrong Rolls (?)
38		L1b1	
39		T4	Choctaw-Cherokee
40		Unk.	
41		T*	Cherokee
42		L1c2	Subject identifies as Native American
43		L3	Juanita Pratts, b. Mexico 1885; Comanche or Mexican
44		J*	Betsy Walker, Cherokee, adopted by Sen. Felix Walker
45		J*	Myra Jarvis, Melungeon, b. 1815, Ga.
46		J*	Betsy Walker, Cherokee, adopted by Sen. Felix Walker
47		X2	Polly, wife of Col. Will Thomas
48		X2	Cherokee woman married to Longhunter Wallen (Walden)
49		U2e*	Jane Campbell, b. 1828, Choctaw Co., Miss.
50		T*	Native American
51		T*	Cherokee Gentry sisters
52		T*	Cherokee Gentry sisters

Haplogroup H

Let us examine these anomalous haplotypes starting with haplogroup H, the most characteristically European. H is termed Helena in the scheme of Seven Daughters of Eve (Sykes 2001). Its highest frequency occurs in Spain and France, where Europeans wintered the last Ice Age (Achilli et al. 2004; Loogväli et al. 2004; Pereira et al. 2005). It was probably the predominant maternal lineage that gave rise to the hunter-gatherer Magdalenian culture of cave art made famous by the paintings at Lascaux and elsewhere in southern France and northern Spain and Portugal. When agriculture spread to Europe from the Middle East some 7,000 to 9,000 years ago, H was either among the recipients or bearers. It is the most common female lineage throughout Europe, accounting for approximately half the population. It is the haplogroup, in fact, of the British man whose DNA was selected as the Cambridge Reference Sequence, the norm against which mutations and other haplogroups are measured (Anderson 1981; Andrews 1999). The exact same sequence makes an early European appearance in a skeleton excavated from the Paglicci Cave in Apulia in the heel of the Italian Peninsula, dated to 28,000 years ago (Caramelli et al. 2008). Historically, H is the maternal line of French queens and kings. Marie Antoinette, whose mitochondrial DNA has been reconstructed in two modern-day forensic cases (Jehaes 2001), descends from Frederuna of France, consort of Charles the Simple, a descendant of the emperor Charlemagne. H is also the haplogroup of Queen Victoria, Prince Philip and Russian Czarina Alexandra (Gill et al. 1994).

Although this quintessentially European haplogroup would seem to be the most likely suspect if admixture were responsible for anomalous haplogroups, it plays only a minor role in our study. There are but four cases of H. **Case 1** is a Rhode Island woman who claims descent from New England Indians. Her profile matches no other in the Cambridge Concordance, FBI database (Monson 2002) or Mitosearch, although there is a one-step mutation to an individual classified as Amerind in the Cambridge Concordance. **Case 4** is unusual for a mutation at nucleotide site 16362C. This woman lives in Georgia and claims descent from a Cherokee woman. Her mutations are matched by descendants of women born in the 1860s in Wisconsin and Arkansas but by no others. There are also close but not exact matches with Korea, Japan and Mongolia. The mutation 16362C occurs in four out of five of the classic Native American haplogroups. Because Case 4's mutations are only reported in people born in North America, it seems appropriate, particularly in conjunction with a suitable oral tradition, to regard her lineage as indigenous to North America, not as admixture arriving recently from Europe. **Case 6** is marked by a mutation at 93G not instanced anywhere else. According to the subject's daughter, Joy Shorkey, the line can be traced to Sarah Smith, born 16 August 1806 in Georgia, suspected to be Cherokee. **Case 8** falls in the same category.

Haplogroup X

Haplogroup X is a latecomer to the received set of Native American haplogroups. Sykes names it Xenia ("foreign woman"), which is a good choice given its mysterious origins and world travels. Its relative absence in Mongolia and Siberia and a recently proven center of diffusion in Lebanon and Israel (Brown et al. 1998, Malhi and Smith 2002; Smith et al. 1999; Reidla 2003; Shlush et al. 2009) pose problems for the standard account of the peopling of the Americas. Today, haplogroup X accounts for about 2% of the population of Europe, the Middle East (Near East in British usage) and North Africa. It is more characteristic of the East Mediterranean and Caucasus than other parts of Europe. Particular concentrations

appear in Georgia (8%), Orkney Islands (7%) and Israeli Druze (28%, Shlush et al. 2009). Among Native American groups, it has been reported in high frequencies among the Ojibwe and other northern tribes, where it comprises up to 25% of mtDNA lineages. Among the Micmac of the northeastern U.S. and adjacent Canadian provinces, its frequency attains 50%. It is also present in lesser percentages in the West among the Sioux (15%), the Nuu-Chah-Nulth (11%–13%), the Navajo (7%) and the Yakima (5%). Two clades have been proposed. Rare X1 is predominately North African, associated with Afro-Asiatic language speakers. X2, conventionally divided into a Native American branch (X2a) and all others (X2b-f), is much more common (van Oven and Kayser 2008).

We have seven instances of haplogroup X. They all belong to X2, but it is not possible to assign them all to subclade X2a. (If we compare our own and other known X2a haplotypes with the X2's reported in Shlush et al.'s study of the Israeli and Lebanese Druze, the same common mutations are observed. It would appear that the demarcation between Native American and Old World forms of X2 is an artificial one.) Significantly, both "branches" have the same estimated time to coalescence, 20,000 to 30,000 years before present. But usually, if an X2 is found in the New World it is automatically assigned to X2a. No two haplotypes are exactly alike, although the shared motifs 153G, 195C and 225A in HVS2 are recurrent. All genealogies reported lead to a Cherokee woman. **Case 2** derives from Annie L. Garrett, born 1846 in Mississippi; there is an oral tradition in the family of her being Cherokee. **Case 7** is the mitochondrial DNA of Michelle Baugh of Hazel Green, Alabama, traced to Agnes Weldy, born about 1707. Descendants include enrolled members of the Eastern Band of Cherokee Indians. **Case 10** goes back to Seyinus, a Cherokee woman born on or near the Qualla Boundary in North Carolina in 1862. **Case 27** is the son of Gladys Lulu Sutton, born in Indian Territory in 1906; her birth certificate specifically states that she was a Cherokee Indian. Her mother was Olivia McCorkle Walker Ginn, born in West Virginia in 1865. This line matches that of Penelope Greene Fraser, born 1779, in Walton County, Georgia (Mitosearch ID 3M6H6). **Case 47,** James Stiles Riddle, has a genealogy descending directly from the Cherokee woman called Polly, who had a daughter out of wedlock, Angelina Demarius (born 1827, married Sherrill), with Col. Will Thomas, the founder of the Eastern Band of Cherokee Indians in North Carolina. Polly was the namesake for the Qualla reservation (the sound *p* lacking in the Cherokee language and being rendered with *qu*). **Cases 44** and **46** below also have a connection to Col. Thomas through another paramour of his who was evidently of haplogroup J. Finally, **Case 48** reflects descent from a Cherokee woman who married a Walden/Wallen of the same surname as Longhunter Elisha Wallen, one of the first white explorers of Tennessee, and a member of the Melungeons, a mixed ethnic group of East Tennessee. **Case 5** has unknown antecedents, believed, however, to have been Native American.

Haplogroup J

The most common forms of J, termed Jasmine in the scheme of Oxford Ancestors, seem to have originated in present-day Lebanon approximately 10,000 years before present and to have moved north and west into Europe. Views about J are still evolving. Previously restricted to theories based on HVS1 sequences, its phylogeny continues to be articulated with the benefit of full genome sequencing (Logan 2008). All four of our J's are to be classified as J* (all J not

otherwise characterized and subdivided). The overall haplogroup is found throughout Europe with particularly high concentrations around the eastern Baltic Sea, Russia and among the Bedouins and Yemeni, where it reaches frequencies of 25% or higher. It is a major Jewish female lineage (Thomas 2002), and it is a strong contributor to Arab, Greek and Italian populations as well. It is also relatively common in India. Along with male haplogroup J, it is believed to have been instrumental in spreading agriculture from the Middle East about 7,000 years ago. Haplogroup J has been linked to longevity and a certain form of hereditary blindness.

Case 9 has a J haplotype distinguished by the unusual mutation 16162C. The subject's mutations are also associated with Native American lineages A and D (Comas 1996). Like the others in this study the specific haplotype is matched or nearly matched only with rare mitochondrial lineages reported in people born in the Americas. And like all the others, too, it goes back to a Cherokee source. Case 9 is Jerry W. Moore, the father of Michael Wayne Moore, who has traced the line to Emily Glover, born in Tennessee in 1837, reportedly a Cherokee. Both **Case 44** and **Case 46** trace their line back to Betsy Walker, a Cherokee woman born about 1720 in Soco (One-Town). Betsy was given as a child to Sen. Felix Walker to raise. While he was an apprentice for the Walkers, young Will Thomas (later chief of the Eastern Cherokees) fell in love with Catherine Hyde, her descendant. Catherine Hyde is the 6th-great-grandmother of test subject Kimberly McFadden Hill. Her sister Annie Hyde married Holloman Battle and produced the other instance of Betsy Walker's mitochondrial haplotype in modern-day descendant Sharon Crisp Bedzyk. The fourth example of J*, Judith Alef (**Case 45**), is a descendant of presumed Cherokee Myra Jarvis, a Melungeon woman born in 1815 in Georgia.

Haplogroup U

Haplogroup U is a complex mega-lineage with an estimated age of more than 50,000 years. It is the oldest European haplogroup that is Homo sapiens rather than Homo erectus or Neanderthal, representing the first colonization of Europe by its present inhabitants. Human societies with haplogroup U4, U5 and U5a may have come into contact with Neanderthals living in Europe at the time. U shows up in the archeological record in Delphi and Spain around 50,000 years ago. Today U5, the most common clade, accounts for about 10% of matrilineal types in Europeans. Other clades of U are responsible for about five and a half percent, making U the second largest haplogroup after H. It has been found in high frequencies in the Indian subcontinent and at a low frequency in the Japanese, the North African Berber population, Ethiopians and Senegalese (Torroni et al. 1996, Passarino et al. 1998, Macaulay et al. 1999). In Finland, a population with a relatively small number of founder types, it has been associated with several rare medical conditions (Finnilä et al. 2000). One important divide in subcluster U2 goes back to the earliest millennia of the migrations of humans out of Africa, with U2e splitting off and expanding north into Europe, probably traveling along the Zagros Mountains, and U2i settling in India, where it reaches frequencies of around 25% today. With the exception of a single instance of U6 in a study of Mexican Indians, where it is attributed to European admixture (Green et al. 2000), haplogroup U has never been reported in American Indians to my knowledge. In our sample it covers 13 cases or 25% of the total, second in frequency only to haplogroup T.

Let us first describe the U5's. **Case 20** is Mary M. Garrabrant-Brower. She belongs to U5a1a* but has no close matches anywhere, unless a one-step mutation on HVS2 with an Asian and two Chinese samples are to be taken into account. Her great-grandmother was Clarissa Green of the Cherokee Wolf Clan, born 1846. Clarissa Green's grandfather was remembered as a Cherokee chief. Mary's mother Mary M. Lounsbury maintained the Cherokee language and rituals. **Case 19**, Bruce Dean, another U5a1a*, matches only one other person on both sectors, Marie Eastman, born 1901 in Indian Territory (Mitosearch EDCCB). Because of the precision of the match, he and the descendant of Marie Eastman who was tested and made the entry in Mitosearch are almost certainly cousins in a genealogical, as well as genetic sense. His descent is from Jane Rose, a member of the Eastern Cherokee Band whose family is listed on the Baker Rolls, the final arbiter of enrollment established by the U.S. government. **Case 22** is Michael Gilbert, who was given little information about his mother, Wilma Nell Atchison, beyond the fact that she was Blackfoot – probably the Virginia/North Carolina tribe by this name, also called Saponi, Sissipah and Haliwah. His haplotype is U5b2. Although there are four exact matches on both sectors, two of these are in the Old World (Ireland and Denmark), one is of unknown origin but American, and one leads to Arpahia Finley, born about 1827 in Albemarle County, Va. The latter location is the traditional homeland of the Blackfoot Indians. Because of the division of the matches, one could speculate that in this instance we may be dealing with a lineage that came over from northwestern Europe and *became* American Indian, only in all likelihood long before Columbus. **Case 15** is that of my wife, Teresa Panther-Yates, whose mtDNA can be designated as U5b*. It has no matches remotely close to it in either the Concordance or Mitosearch. Teresa has traced her maternal line back to Isabel Culver, who married Levin Ellis in Hancock County, Georgia, and died about 1838. There is a tradition in her family that this line was Cherokee. **Case 17**, an example of U5a1a, does have two matches – South Carolina and Norway – but the subject claims that the line goes back to Ann Dreaweah, a Cherokee woman married to a half blood Cherokee man. It may be another bifurcated lineage with representatives on both sides of the Atlantic. **Case 18** has no close matches at all and may be placed in the category of U5*. The subject was adopted in Oklahoma and knows nothing of his mother's ancestry. **Case 21** is Gerald Potterf, a U4* who traces his mother's line to Lillie C. Wilson-Field, born in 1857, Catawba County, North Carolina. She was probably Cherokee, although her ancestors may have been Catawba, a Siouan tribe from the Carolinas who joined the Cherokee in great numbers during the eighteenth century. U4 is associated with North Africa and the Middle East.

Our survey of U's leaves the five haplotypes classified U2e*. **Case 11** is my own, for which there are no close matches. This line evidently arose from a Jewish Indian trader and a Cherokee woman. My fifth-great-grandmother was born about 1790 on the northern Georgia and southwestern North Carolina frontier and had a relationship with a trader named Enoch Jordan. The trader's male line descendants from his white family in North Carolina possess Y chromosomal J, a common Jewish type. Some Jordans, in fact, bear the Cohen Modal Haplotype that has been suggested to be the genetic signature of Old Testament priests (Thomas et al. 1998). Enoch Jordan was born about 1768 in Scotland of forbears from Russia or the Ukraine. My mother, Bessie Cooper, was a double descendant of Cherokee chief Black Fox and was born on Sand Mountain in northeastern Alabama near Black Fox's former seat at Creek Path (and who was Paint Clan). The Cooper line goes back to William Cooper, a scout

and road builder for Daniel Boone, who married Malea Labon (Hebrew first and last name), the daughter of a Choctaw woman and a French trader. The Cooper surname often appears in lists of common Melungeon names. I said there were no close matches for my mtDNA, but **Case 12**, Phyllis LaForce Starnes of Harriman, Tennessee, turned out to match perfectly with mine on HVS2. She traces her maternal line to Susanna Owens, born about 1760, probably in Granville County, North Carolina. The family is Melungeon like the Coopers, and Starnes suffers from a disease common among Melungeons and Sephardic Jews. Both Starnes' and my haplotypes share several motifs with three other cases of U2e*. **Case 13** is a near match with **Case 16**. The former's maternal line reportedly goes back to Rosannah Alexander, born about 1749 in Mecklenburg County, North Carolina, believed to be Cherokee. **Case 14** is a descendant of Mahalia Waldon (her surname coming from a famous Longhunter and Melungeon family). Mahalia was born in 1834 in Hancock County, Tennessee, in the Melungeon population center. All U2e* cases appear to have Melungeon, Cherokee and Jewish connections. The most frequent Cherokee clan mentioned in their genealogies is Paint Clan.

Haplogroup T

Maternal lineage T ("Tara") is believed to have originated in Mesopotamia approximately 10,000 to 12,000 years ago and to have moved northwards through the Caucasus and westwards from Anatolia into Europe. It shares a common source with haplogroup J in parent haplogroup JT (Finnilä et al. 2001). Ancient people with haplogroup T were likely some of the first agriculturalists and probably comprised the group which first brought agriculture to Europe with the Neolithic Revolution. T is the same haplogroup as Sykes's, who named it Tara after the ancient center and capital of Ireland. The matches with the Russian Tsar Nicholas in a famous case (Gill 1994) prove that T was the matrilineal line of much aristocracy (along with H, above). Maurice, prince of Nassau, England's Charles I and King George I of Great Britain were all apparently T. The haplogroup includes slightly fewer than 10% of modern Europeans. The closer one goes to its origin in the Fertile Crescent the more likely T is to be found in higher frequencies.

All our T's are unmatched except in some cases with each other. **Case 35**, Jonlyn L. Roberts, has a puzzling, but typical genealogy that led her to embark on a lifelong quest for answers. Her mother, Zella, was adopted by the George and Mary Hand family of Hand County, South Dakota in 1901. Little information was passed down, but piecing together clues from her childhood, Roberts believes that her mother's original family might have come from the Red Lake Ojibwe Indian Reservation or one of the North or South Dakota reservations. At any rate, her mtDNA haplotype is a unique form of T*, one similar to others in this study. **Case 32**, another T*, leads to an unknown ancestor in Oklahoma. **Case 28**, also T*, is an individual reporting Melungeon ancestry. His mtDNA matched four people on both sectors in Mitosearch. All these were born in the United States; one traces back to Birdie Burns, born 1889 in Arkansas, the daughter of Alice Cook, a Cherokee (ID AB3YK). **Case 41**, Gail Lynn Dean, is the wife of Case 19; both claim Cherokee (among other) ancestries. No near match has her mutation 236C. **Case 32,** Linda Burckhalter, is the great-great-granddaughter of Sully Firebush, the daughter of a Cherokee chief who married Solomon Sutton, the stowaway son of a London merchant, in what would seem to be another variation of the "Jewish trader marries

chief's daughter" pattern. Rounding out our T* haplotypes are the two matching **Cases 51 and 52**, both descended in different lines from the historically documented Gentry sisters.

Cases 24, 25 and **26** are perfectly matching T1* individuals completely unknown to one another before testing. Two of them claim Melungeon ancestry; the other's is unknown. Case 26 is a distant cousin of mine with the same surname whom I did not know before he became a customer. Case 24 is the aunt of Case 12. **Cases 29** and **31** are examples of unique T2*'s. Both were ignorant of the origins of their maternal line, suspecting only that they were Native American. **Case 29**, which is T4, is from an extended family that claims Choctaw-Cherokee ancestry (like my own). The sole instance of T5, **Case 34**, took not only the mitochondrial test but also our CODIS-marker-based population matching ancestry test, DNA Fingerprint, to validate "Cherokee or Jewish ancestry" from her mother. She has scattered matches but none on both sectors. The results of her DNA Fingerprint Test show Ashkenazi Jewish in the No. 1 position, as well as American Indian admixture.

Discussion and Conclusion

Our small survey shows a great deal of diversity both of haplogroups and haplotypes. It contains several examples of people who discovered through testing they are related and share the same Cherokee ancestry and even the identical matrilineal clan. It cannot be emphasized enough that our sample was assembled after the fact from individuals who did not know each other, and who came from all over the country. Unlike the U.S. majority population, the sample exhibits a mix of haplogroups that turns the usual pattern on its head. Haplogroup H, instead of an expected 50% dominant position, is one of the smallest, with only 7.7%. Haplogroup U, an older lineage representing the first wave of colonization of Europe before the ascendency of H, is numerous and highly diversified at 25% of the total number of participants. Haplogroup X, marked by an exiguous presence in the Old as well as New World (where it is found in large numbers only in select groups), attains a frequency more than tenfold that of Eurasia or Native America (13.5%). But the most startling statistic is the frequency of occurrence of T haplotypes. At 26.9 %, they figure as the leading haplogroup, with 14 individuals. Several of these evidently come from the same Cherokee family or clan, although they have been separated and scattered from their original home by circumstances and the events of history. The many interrelationships noted above reinforce the conclusion that this is a faithful cross-section of a population. No such mix could have resulted from post-1492 European gene flow into the Cherokee Nation. That would have required a large influx of non-European women marrying Cherokee men. The anomalous types of mitochondrial DNA (added to already documented examples of A, B, C and D haplotypes that are not part of this article) must reflect a pre-Columbian population structure.

If not from sources in Siberia, Mongolia and Asia, where do our non-European, non-Indian-appearing elements come from? The level of haplogroup T in the Cherokee (26.9%) approximates the percentage for Egypt (25%), one of the only lands where T attains a major position among the various mitochondrial lineages. In Egypt, T is three times what it is in Europe. Haplogroup U in our sample is about the same as the Middle East in general. Its frequency is similar to that of Turkey and Greece. J has a frequency not unlike Europe (a little less than 10%). Our five instances of J sometimes have matches or near matches with European Jews.

But the most telling evidence in my opinion concerns haplogroup X. This, as we have seen, ranks as the third largest haplogroup. The only other place on earth where it is found at an elevated level apart from other American Indian groups like the Ojibwe is among the Druze, an endogamous population living for thousands of years with little genetic influx in the Hills of Galilee in northern Israel and Lebanon. The work of Shlush et al. (2009) demonstrates that the homeland of the Druze, because of the diversity of X haplotypes in it as well as their high frequency, is the center of a worldwide diffusion for X. It is the hallmark of a population of which the Druze are the lasting surviving heirs. The region acted as a refugium for humans during the last Ice Age much as the Iberian Peninsula did for other lineages (chiefly H). Haplogroup X (and to a lesser extent, K) is one of the distinctive signatures of the first out-of-Africa settlers in the land of Canaan (present-day Israel and Lebanon). In other words, the peculiar Druze sect preserves the genetics of the bedrock population.

In the case of this genetic refugium, however, I propose that since there is no star-like population expansion driving haplogroup X outward into Europe and to other parts of the Middle East, the lineage can only have spread in discontinuous fashion to the Americas and to other places where it has been noted such as North Africa, England, South America and Papua New Guinea. It must have arrived by sea. There are no genetic footsteps of haplogroup X leading to the New World across Europe, nor in Siberia or along a circumpolar route, as has been variously argued. From a genetic perspective, X survives at elevated frequencies in two separate places, Canaan or Palestine and Native North America. Its presence is particularly noteworthy in the tribes situated around the Great Lakes and Saint Lawrence Seaway like the Ojibwe and Micmac—and in the Cherokee .

On the Y chromosome side of Shlush et al.'s study, male haplogroup K was found to have a relatively high frequency of 11% in the Galilee region (2008:2). K (renamed T in the revised YCC nomenclature) has long been suspected to be the genetic signature of the Phoenicians (*Who Were the Phoenicians?*). This early seafaring people originated in the interior of Lebanon after 1200 BCE (Aubet 2001:13-16) and spread later to Asia Minor, North Africa, Sicily and Spain, creating a mining and mercantile empire. Notably, they served as mariners for the Egyptians. Herodotus, moreover, has the following account of their trade activities with "a race of men who live . . . beyond the Pillars of Hercules":

> On reaching this country, they unload their goods, arrange them tidily along the beach, and then, returning to their boats, raise a smoke. Seeing the smoke, the natives come down to the beach, place on the ground a certain quantity of gold in exchange for the goods, and go off again to a distance. The Carthaginians then come ashore and take a look at the gold; and if they think it represents a fair price for their wares, they collect it and go away; if, on the other hand, it seems too little, they go back aboard and wait, and the natives come and add to the gold until they are satisfied. Their is perfect honesty on both sides; the Carthaginians never touch the gold until it equals in value what they have offered for sale, and the natives never touch the goods until the gold has been taken away (IV.196:279).

Some readers will immediately recognize in Herodotus' account a description of the Sacred Trade Circle of American Indians. No word was ever exchanged. The principal was "what you see is what you get." Barter alone was used. The exchange could be evened out to make it

acceptable to one or another of the two parties if they were hesitant to accept it, as the Phoenicians were in the passage given above. All "sales" were final, since in the nature of things they were mutually satisfactory or else the deal would not have been consummated.

The most complete written description of the custom of the trade circle I can think of appears in a book that I wrote some years ago, as follows:

> To my knowledge, no one has ever successfully explained the origin of the term Indian giver. Was it the Indians who took back or the white man? The question is important if we are to know what to do with the Indian gift today. Seer tradition unravels the mystery as follows.
>
> When the white man first appeared in his sailing ships he left strange gifts on the shore. These were treated as goods placed on a trade blanket. It was normal for no verbal communication to take place in the sacred trade circle, though it was unusual for the two parties not to be present at the same time. Our people understood the gesture and honored it with equal return gifts. Perhaps the pile they left on the shore exceeded the value of the white man's gifts. Maybe it was too little. It was hard to tell, nor did it matter. They were accepted. All gifting is final. *The Eighth Arrow: Right, Wrong and Confused Paths According to Tihanama Elder Wisdom* (e-book). Marion: Standing Bear Press, 2007:169.

Without a doubt it was the Phoenicians, whose name unto themselves was *Cana'ni* or KHNAI 'Canaanites', not *Phoenikoi* 'red paint people' (Aubet 2001:9-12; cf. *Oxford Classical Dictionary* s.v. "Phoenicians"). They are referenced by James Adair when he observes that "several old American towns are called Kanāai," and suggests that the Conoy Indians of Pennsylvania and Maryland were Canaanites and their tribal name a corruption of the word Canaan. The Conoy Indians are the same Indians William Penn around 1700 described as resembling Italians, Jews and Greeks. By about 1735 they had dwindled to a "remnant of a nation, or subdivided tribe, of Indians," according to Adair (1930:56, 67, 68). One of the oldest Cherokee clans is called Red Paint Clan (*Ani-wodi*).

The next chapter will analyze Cherokee traditions about Egypt, Greece, Cyrene, Israel and Phoenicia and present links and alignments involving language, epigraphy, culture and historical accounts in addition to the genetics reported here.

Haplogroup Distribution of Anomalous Types versus Europe and Other Populations

Hg	N	%	Europe	Mid-dle East	Egypt	Druze	Eastern Med.
H	4	7.7	53.5	36.8			
J	5	9.6	9.5	11.4	6.3	7.0	12.7
X	7	13.5	1.5	3.5	1.6	27.9	4.8
U	13	25	22.2	26.3	7.8	11.6	16.4
K	2	3.8	5.8	6.2	3	16.3	3.6
T	14	26.9	8.4	11.9	25	4.7	6.0
L	3	5.8					
Unk.	4	7.7					
Total	52	100	n=1021	n=2736	n=64	n=43	n=165

Source: Suppl. data from Richards et al. (2000); this study

MORE ANOMALOUS MITOCHONDRIAL DNA LINEAGES IN THE CHEROKEE (PHASE II)

Abstract. A sample of individuals who took a mitochondrial DNA test to determine female lineage (n=67) was created from participants in DNA Consultants' Cherokee DNA Project Phase II. Almost all beforehand claimed matrilineal descent from a Native American woman, usually believed to be Cherokee, and often named in genealogy research undertaken by the customer. The majority of subjects revealed "anomalous" haplotypes not previously classified as American Indian. Many matched others in Phase I. Several individuals overcame the barrier of a sealed adoption to find biological relationships, often to other participants. As in Phase I, a Middle Eastern type, haplogroup T, emerged as the most common lineage (19.4% in Phase II, 22.7% overall in the project), followed by H, U and J, all Eurasian types. Sub-Saharan African haplogroup L (9%) was prominent as a minor category. Old Europe haplogroups I, N, V and W occurred in small amounts and should be considered strikingly new, unreported signals of authentic Cherokee ancestry.

Background

Ever since the pioneering work of Douglas C. Wallace, Rebecca L. Cann and others on the use of human mitochondrial DNA as a marker for genetic ancestry and disease, scientists have insisted on a very limited and rigid number of ancient Asian female founders for present-day American Indian populations. In 1993, Satoshi Horai of the National Institute of Genetics in Mishima, Japan was the lead author in a study with the agenda-setting title, "Peopling of the Americas, Founded by Four Major Lineages of Mitochondrial DNA." That same year, Antonio Torroni of the University of Pavia coined the term haplogroup in a publication in the *American Journal of Human Genetics* in which he and his co-authors postulated but four lineages, A, B, C and D to account for mitochondrial ancestries in their sample. Also in 1993, Anne C. Stone (Arizona State University) and Mark Stoneking (Max Planck Institute for Evolutionary Anthropology) confirmed the four haplogroups in a 1300 CE burial ground in central Illinois, the Norris Farms site. The year 1993 was truly an *annus mirabilis* in American Indian genetics. It remained only for the minor haplogroup X to be added to the original four lineages (Brown et al. 1998, Malhi and Smith 2002; Smith et al. 1999).

In the ensuing twenty years, academic studies, textbooks, the popular media and governmental policies fell into lockstep about the "peopling of the Americas." Despite a number of voices being raised in criticism (Jones; Guthrie; Jett), the model restricting American Indian ancestry to mitochondrial lineages A, B, C, D and X has remained intact. When direct-to-the-consumer DNA testing became available in 2000, commercial companies hopped on the abecedarian bandwagon. To paraphrase Henry Ford, you could have an Indian DNA test say anything you wanted as long as it was A, B, C, D and sometimes X. But were these haplogroup rules possibly equivocal and not conclusively decidable anyway?

Etched in stone along with the five classic Native American mitochondrial haplogroups has emerged a belief that all American Indians can be traced to a single entry from Siberia roughly 10,000 years ago across the Bering Strait, supposed at that time to have formed a land bridge. This prevailing notion was summarized and defended by Kemp and Schurr (2010). According

to University of Florida doctoral dissertation writer Joseph Andrew Park Wilson, "Today it is rare to find a molecular anthropologist who favors more than two distinct migration events, and a majority of researchers are enamored with the single-origin hypothesis, which postulates just one founding group ancestral to all Native Americans." Wilson cites the following studies in support of this observation: Bonatto and Salzano 1997; Fagundes et al. 2008; Goebel et al. 2008; Kolman et al. 1996; Merriwether et al. 1995; Mulligan et al. 2004; Rubicz et al. 2002; Stone and Stoneking 1998; Tamm et al. 2007; Tarazona-Santos and Santos 2002; Zegura et al. 2004 (p. 102).

Band-aids on the Battleship

This "A-D" thesis continues to stand with minor alterations. Perego et al. (2009) proposed on the basis of phylogeographic analysis of 69 mitochondrial types a "simultaneous but independent Asian source populations for early American colonists." But this modification of the theory involving "two roads taken" still kept within the A-D canon and maintained the primacy of the Bering land bridge (aided in a minor way by a seaborne route from Asia using the "kelp road"). Eventually, the lineup consisted of nine usual suspects: A2, B2, C1, C4c, D1, D2a, D3, D4h3 and X2a (Achilli et al. 2008).

After extensive examination of the subject Wilson concludes that the five mtDNA haplogroups actually have complex, multilayered histories. Moreover, the genetic story represents only one of the pieces of the puzzle; other evidence to be harmonized into a coherent "archeogenetic narrative" are languages and material culture (pp. 141-42).

Torroni and Wallace (then at Emory and La Sapienza in Rome, respectively) were apparently the first to use the term "anomalous" of mitochondrial types. However, in their important letter to the editor of the *American Journal of Human Genetics* in May 1995, they applied it rather narrowly to "a heterogeneous set of mtDNAs due either to recent genetic admixture or to new mutations that have abolished a preexisting primary marker," in other words to non-conforming types *within* the A-D paradigm.

Utterly "foreign" anomalies only came within the sights of geneticists in 2013, when a devastating shockwave hit the archeological establishment. At the epicenter was Danish researcher Eske Willerslev, who reported on two 24,000-year-old Siberian skeletons at the "First Americans Archeology" conference in Santa Fe, New Mexico. The fullest sequencing of ancient human DNA to date suggested that the people who lived near Lake Baikal at the dawn of human civilizations, and who later developed into the Native Americans of the New World, came more proximately from a westernly direction in Europe, not from Asia. Moreover, the mitochondrial haplogroup of the so-called Mal'ta boy the Danish team sequenced was U, a "non-Indian" type (M. Raghavan et al. 2014). The term anomalous now extended to entire haplogroups that did not fit the mold.

On the face of it, no haplotyping study can distinguish between deep ancestry and more recent admixture as the cause of unusual variations in DNA. Whereas tools like "time to coalescence," bootstrapping and phylogenetic trees can be used to compare types and estimate genetic distance, no logarithm can tell the geneticist *where* any given haplotype may have arisen and become characteristic. Projections of the source, spread, mutation and survival of uni-parental haplotypes can be deceptive, especially when they telescope tens of thousands and sometimes hundreds of thousands of years.

Navajo Puzzles

To consider an apposite question from Navajo research, we might ask when did certain Asian genes in the modern-day Diné matching 4000-year-old DNA from Siberia and the Tarim Basin travel to the Americas? It could have been 20,000 years ago or it could have been in the 16th century. The "genetic signature" could have arrived by gradual "star-like" diffusion or through one or more discontinuous movements, some possibly seaborne, some repetitive, some marked by diversity of types, some non-diverse, some minor, some major, some conceivably separated from each other by centuries or millennia. Similar problems beset any modeling of tribally-specific genetic scenarios. As the Jones white paper pointed out long ago, geneticists have a tendency to take the long view and telescope genetic incidents. They often rely solely on statistical modeling applying classical evolutionary components like random mating and natural selection and do not take concerted account of histories, archeology, cultural baggage like myth and religion, and family or clan genealogies.

So far, autosomal DNA analysis has not assumed a large role in elucidating haplogroup history and the subject of admixture. The Centre for GeoGenetics at the University of Copenhagen's Natural History Museum of Denmark has led the way with a new "dual ancestry" model augmenting the A-D thesis. The current issue of *Archaeology* contains the heretical suggestion that "the earliest travelers to the New World made their way more than 20,000 years ago from what is now the west coast of France and northern Spain" (Swaminathan, p. 25), but this seems to be just another shot in the dark. A quite recent autosomal study of European DNA headed by Harvard's David Reich identified three ancestral populations on the basis of ancient DNA, one of which is Willerslev's "ancient North Eurasians related to Upper Palaeolithic Siberians," called ANE (Lazaridis et al. 2014). Belonging to haplogroup U, and sharing some alleles with 8,000-year-old Scandinavian hunter-gatherers, ANE is thus an ancient link between Europeans and Native Americans, one quite separate incidentally from Turkic Chuvash and N-dominated Saami, both of which "are more related to east Asians than can be explained by ANE admixture" (p. 412). Haplogroup U has thus been established as an ancient founding haplogroup in Native American populations, dating back 24,000 years ago to the same time period as the A-D canon.

With the blossoming of phylogenetic and phylogeographic studies utilizing complete mtDNA sequences (Torroni et al. 2006), it is to be hoped that genetics will embark on a fundamental new approach to the study of American Indian haplotypes. Promisingly for Cherokee research, Willerslev's team in Denmark has included several participants in the present ongoing project as part of a larger study. The Danish initiative has sampled the 35,000 members of the Echota Cherokee Tribe of Alabama: Dr. Joel E. Harris, Sr. maintains a communication page.

Procedure and Methodology

The purpose of the Cherokee DNA Project is to sample and investigate the genetic heritage of persons who may be of Cherokee descent and establish a reference collection of their DNA results and genealogies. Enrollment in Phase II began in October 2009 following the release of Phase I results in the blog post "Anomalous Mitochondrial DNA Lineages in the Cherokee" (August 31, 2009). Data were published in Yates (2012) pp. 161-62.

As in Phase I, a notice of the search for volunteers was publicly displayed on the company's

website. Holli Starnes has acted as administrator throughout. All candidates signed up when they purchased either a mitochondrial DNA HVS1+2 ancestry test or a mitochondrial "report only" based on previous testing. After receiving fulfillment of their personal order, they were requested to execute and mail back a standard informed consent form. Participation was at no extra cost. Open enrollment via the website lasted until August 31, 2014, at which time 67 candidates were verified and accepted into the final sample. All had learned in their personal report that they probably had direct female descent through mitochondrial DNA from a Native American woman.

The sample selected for Phase II is composed of 39 female (58%) and 28 male (42%) subjects. Two husband-wife couples enrolled. Sometimes the subject's test was ordered by a family member, but no participants knew they were closely related *a priori*. Ages varied from 30 to 90. Participants mostly lived in the United States and Canada, where they were residents of scattered locations, from New Hampshire and Florida to California, Texas and Hawaii. One joined from as far away as New Zealand. No single state (such as Oklahoma or Tennessee) stood out in the demography.

Of the 67 subjects, eleven of them (16%) tested with other companies first, including Family Tree DNA, Ancestry.com and DNA Diagnostics Center. About half (47%) got first-time test results from DNA Consultants' service lab, Genex Diagnostics of Vancouver, British Columbia, and about one-third tested with Sorenson Genomics of Salt Lake City, Utah. Two participants did not want to reveal the identity of their lab. Enrollment was fairly evenly distributed over five years. The largest number of tests (27) was taken in 2010, at the beginning of the study.

The numbers above are provided to emphasize that though the study is purposive in nature, its scope has proved random with regard to geographical location, date, age, sex and other factors. The sample size (n=67) is similar to that of Phase I (n=52). There are no known biases in the sample. No public or private funding was sought or obtained, no volunteer was paid, and no commercial interests were involved.

Motives, Customer Profiles and Report Fulfillment

Typical in respect to approach, background, motives and process was Sharon Benning of Roseburg, Oregon. "My grandmother and her family always said we were Cherokee and I know that they were afraid of looking too brown and would always stay out of the sun," wrote Benning in a customer inquiry on April 4, 2010. "They didn't want to be connected to Native Americans at all. I feel like I have missed part of my heritage and would like to know if this story is true." After purchasing a Native American DNA Test on April 5, she received and returned her sample collection kit. Sorenson Genomics of Salt Lake City, our service lab at the time, released her results to us in a "Certificate of Mitochondrial DNA Analysis," dated April 29, 2010. Staff then fulfilled her Native American DNA Report, which was signed by Donald N. Yates, Ph.D., Principal Investigator, on June 16, 2010.

In it, the customer was informed of hypervariable region sector 1 and 2 or control region mutations, matched to other instances of her haplotype and provided with an evaluation of its origin, history and distribution. Standard databases consulted were the Cambridge Mitochondrial DNA Concordance (version 2.0, 1998), Richards et al. (2000), mtDNA Population Database, incorporating "sequence data from the scientific literature and the

GenBank and European Molecular Biology Laboratory (EMBL) genetic databases (Monson et al. 2002, also known as Swygdam and FBI) and Mitosearch, a free online research tool from Family Tree DNA, Houston, Texas.

One limitation of the study is that coding region polymorphisms were not investigated. Nor were HVR3 mutations available.

The basis for all testing and comparisons was the revised Cambridge Reference Sequence of the Human Mitochondrial DNA, described in Anderson et al. (1981) and Andrews et al. (1999).

In the evaluation section of the report on page 3, this customer (whose haplogroup proved to be H, a "non-Indian type") could read:

> Haplogroup H is not one of the six classic Native American female lineages A, B, C, E, and X, although it has been identified in the Cherokee, where it is usually ascribed to admixture with Europeans (Schurr). Haplogroups T, J, K and U have also been found in Southeastern tribes (data on file, Bolnick). The subject's particular haplotype, with one exception, only matches descendants of women born in North America. It is probable, although still ambiguous, then, that it is Native American or indigenous to North America. In conjunction with a family tradition that the maternal line was Native American, it should be considered Native American. The subject is encouraged to join Phase II of our Cherokee DNA Studies.

Benning volunteered for Phase II and became participant No. 43. Pending the completion of the project, she was issued a certificate that specified "Female Lineage: H, Prob. Native American."

Typical of participants who submitted previous mitochondrial results for evaluation and possible inclusion, in other words who tested with another lab, was Juanita Sims. Her niece, Elizabeth DeLand, contacted Dr. Yates in July of 2014 and succeeded in enrolling her aunt as participant No. 67—one of the last to be accepted in Phase II. "Aunt Juanita originally had the test done because her grandmother and great-grandmother spoke Cherokee and she is trying to find it in her DNA," wrote DeLand. "She is U5 haplogroup and was told it was not Native American." Sims became one of six U5's in the second phase, joining six others in Phase I. Additionally, 9 of 135 in the old Family Tree DNA Cherokee Project were U5's. Sims' form of U5 exhibited two unmatched single nucleotide polymorphisms (SNPs), 16291T and 272G, although it loosely matched four other U5's in the study.

Juanita Sims was originally tested by Family Tree DNA and thus received no certificate from DNA Consultants, as hers was a "report only." Family Tree DNA did not certify her mitochondrial line as Native American but as Eurasian. Under its rules at the time, "Native American mtDNA Haplogroups are A, B, C, D and X," *tout court.* The Federal Bureau of Indian Affairs, Cherokee Nation of Oklahoma, Eastern Band of Cherokee Indians and United Keetoowah Band adopt similar definitions for what they consider "true" American Indian DNA types. Our study made no presumptions about the ethnicity or affiliation of haplogroups.

In addition to cross-references within the project, all participants were compared to 135 mitochondrial records from the Cherokee DNA project begun in 2002 under the late Chief Joe White of the Central Band of Cherokee of Lawrenceburg, Tennessee. The project met with a

large response and remained active until 2011 under longtime administrators June Hurd, Marcy Palmer and Holli Starnes. It was closed for unknown reasons in 2011. Members' records and administrators' names were all peremptorily removed. Its replacement project at Family Tree DNA shows 51 records, has the same name and lists Roberta Estes as administrator, but is not to be confused with the original project. Fortunately, the CBC generously gave access and granted permission to DNA Consultants to make a study of this valuable collection before it was taken offline.

Summary of Phase II Results

To tabulate haplogroup assignments, 56 individuals from Phase II (83.5%) proved to have anomalous haplogroups and 11 (16.4%) "non-anomalous" A-D or X. These proportions are quite consistent with Phase I. In the project to date overall (n=119) there have been 101 anomalous types (85%) and 18 (15%) A-D or X. The CBC mitochondrial data (n=135) show 97% anomalous (H, I, J, K, L, T, U, W, no N or V) versus 3% non-anomalous (C, X, no A, B or D).

In Phase II as in Phase I, the largest haplogroup represented was T. This was the haplogroup of 13 individuals, or 19.4%, in Phase II (n=67). In Phase I (n=52), there were 14 T's (26.9%). Project-wide (n=119), the T's number 27 and account for 22.7% of participants.

Haplogroup U made the second highest appearance. Phase II had 10 individuals (14.9%). There were rather more U's (13, or 25.0%) in Phase I, bringing the total for both phases to date to 23, or 19.3%.

H was represented by 11 subjects in Phase II (16.4%) and 4 (7.7%) in Phase II. The total number of H's in the project is 15 (12.6%). In the CBC data, H is the largest haplogroup, accounting for 40.0% of individuals. The top three haplogroups (T, U and H) thus covered about half of participants across the two phases of the project.

Second tier anomalous types in Phase II were J (6, or 9.0%), L (6, or 9.0%) and K (4, or 6%). These moderately well represented haplogroups (J, K, L) accounted for about 21.8% of all participants and about 25% of anomalous types. The leading haplogroups T, U and H made up an average 45% of the anomalous samples.

At the bottom frequencies, anomalous haplogroups with 2 or fewer individuals were I (3.0%), W (3.0%), N (1.5%) and V (1.5%). These minor types accounted for 7.6% of the anomalous results in Phase I. They did not appear in Phase I. Project-wide, they represent 5% of results, and combining with CBC, which had 1 I and 2 W's, the minor anomalous types amount to 3.5% of haplogroup assignments. In addition, there have been four unknown haplogroups, all in Phase I, totaling 1.6% of the greater sample (n=254).

Haplogroup	n=	freq.
A-D, X	11	.164
H	11	.164
I	2	.030
J	6	.090
K	4	.060
L	6	.090
N	1	.015
T	13	.194

U	10	.149
V	1	.015
W	2	.030
Total	67	100%

Unique Single Nucleotide Polymorphisms

In Phase II, comparisons in all readily available worldwide databases (chiefly the Cambridge Mitochondrial DNA Concordance, Monson et al. and Mitosearch) produced 55 rare, unreported or unique SNPs on HVR1 and HVR2. A list of these mitochondrial DNA mutations of interest along with the haplogroups in which they occurred is provided in the figure opposite. A number of these yield matches within the project, or by comparison with CBC tested individuals, but there remain many individuals with such rare mutations that they do not match anyone in the world or at best only partially match others in the three samples (n = 254).

The results of our analysis seem to implicate a specific, coherent and diverse gene pool of ancient structure and origin among present-day Cherokee descendants. Such a characterization is supported by the distribution of female haplotypes; invariable pattern of matches leading to mitochondrial linkage in North America, often to persons identified as Native American, and sometimes even as Cherokee; occurrence of very old mutations; and presence of unique SNPs that match with others in the sample, if with anyone.

The role of admixture depends on what population one "privileges." From the perspective of entrenched models and theories of genetics, the finding of H or any of the other anomalous haplogroups in the Cherokee, no matter how many or in what proportions, should naturally be explained as the result of post-1492 European intermarriage or "random mating" with Native Americans. In the scheme "A-D and sometimes X," the presence of T, U, J or any other anomalous type in the Cherokee *must* be attributed to recent admixture.

Unique and Rare SNPs

np	Hg	Phase II	Phase I
16086C	C, L	20, 51	
16124C	H, L	52	
16129C	U	55	11, 12, 13, 14, 16
16147A	N	2	
16153A	T	22	34
16154C	N	2	
16163G	T, L	5, 6, 16	24, 25, 26, 32, 50
16166C	W	30	
16182C	U, T, B	23, 56, 58	2, 11, 16, 51, 52
16183C	U, T, B	23, 56, 58	2, 11, 16, 51, 52
16187T	H, K, L, T	34	31
16188G	H, L	45	
16188T	T	21, 59	
16189D	T, L	51	24, 25, 26, 32, 36, 50
16192.1T	L	51	

16193.1C	U, H, T	14, 42, 44	6, 41
16193.2C	U, H, T	14, 42, 44	6, 41
16209C	L, A, J	47, 61	
16218T	T	37	
16222T	J	8, 63	
16231C	J, K	35	17
16248T	N	2	
16257T	T, H	21, 32, 59	
16258G	T, U	40	
16261T	J	8, 63, unknown	37
16265R	L	52	
16295T	L	47	
16309A	U, L	36, 64	21
16316G	L, H	51	
16324C	T	1	50
16327T	L	50	
16343G	A, H, U	33, 36	21
16355T	N, L	2, 51	
16357C	H	43	
16391A	U, B, I	4, 46, 48, 54, 60	18
16482G	H	24	
16526A	U	65	
143A	C, L	20	
149.1C	L	50	
150T	T, U, L	22, 36, 40, 44	15, 16, 18, 34, 43
152D	J, L, Unknown	35, 52	33
185A	J, U, Unknown	3, 32, 41	4, 8, 15, 16, 36, 45
189G	H, W, L, J	12, 30, 31, 47, 63	43
194T	D, H, W	25, 30, 31, 62	
199C	N, I, L, U	2, 48, 51, 52, 54	20
207A	J, W, L	8, 30, 31, 54	
214R	H	24	
234R	J	32	
236C	I, T, L	48	41
242T	J	8	
244G	L	51	
249D	C	20, 66	
250C	I	48, 54	
290D	C	20, 66	
291D	C	20, 66	
310.1T	J, K	35, 53	

We have seen, however, that cracks and whole chasms have developed in the formerly tidy, tied-up-with-ribbons "peopling of the Americas" hypothesis. Even if anomalous population components are ascribed to admixture, though, we still want to determine what time or times in the past, and from what source or sources, did that admixture enter into the picture. The condition that mitochondrial-line admixture is female-mediated, not male-mediated or autosomal, demands that we have a source population with a great number of women. Moreover, the female genetic founders must approximate the distribution, age and diversity of haplogroups in the study population (Cherokee descendants in the strict female line).

Gene flow into Native American populations historically has been almost exclusively the result of privileged European men taking lesser status American Indian female partners. Very few European women in colonial times bore the babies of Native American men. In the conquest of North America, Indian male lines were preferentially reduced and extinguished, while Indian women often became the prizes of war or simply an inevitable choice in a world overflowing with single males. If Native American women had children with European men, their daughters and maternal granddaughters perpetuated Native American mitochondrial DNA.

It bears repeating that only women can pass down trans-generational mitochondrial markers. The corollary is also true: men cannot be responsible for mitochondrial ancestry. All present-day mitochondrial haplotypes must trace back to a woman, usually to a mother who had at least two daughters.

Can our admixture be explained as coming from other time frames and possibly non-European origins? If it is ancient and deep seated rather than recent, does it even make sense to regard it as admixture?

Of the eleven cases of classic Native American haplotypes, none knew beforehand they had an "approved" type. None belonged to a Federal tribe or lived on a reservation, although two (Michael Joseph Little Bear, Sr., participant 17, A, and Tino De la Luz Thundereagle, participant 10, D) had Native American names. The majority joined the project just like the others to confirm genealogical rumors or traditions of having an Indian ancestor somewhere in the family tree (usually a distant unknown grandmother). Their primary motive for testing, in other words, was to find the truth, not to qualify for tribal enrollment or benefits. Many came from Latino or Hispanic backgrounds. Among American Hispanic people, at least, Indian ancestry or identifying as *indio* has historically not been seen as a socially desirable family trait, though a nationwide trend in recent years has witnessed Hispanics using "American Indian" to identify themselves on census forms (Roth 2012; Decker 2011).

The results of the test, according to Jesse Montes, a third generation American (20, C), were both surprising and galvanizing. "I always had a gut feeling that I was Native American, and it was such a relief to find out I have a strong line of it from my mother. I am usually a very quiet person, but I am so excited about this that I want to be recognized. This is me!" His mitochondrial type had five unique SNPs and fully matched four Puerto Rican matrilines, and no other type in the world. His mother's maternal grandmother was born in the southern part of Puerto Rico near Ponce. Family traditions mentioned Taino in both his mother's and father's lines. "I am hoping to now be able to connect with some of my ancestors online on my mom's side to discover even more from the Native American DNA test," said Montes. "It has given me a golden key." (See interview by Teresa Panther-Yates, September 23, 2014, on DNA

Consultants Blog, "Jesse Montes: Where Do I Come From.")

Leroy James (25, D) had a rare mitochondrial type that matched the descent of just three people worldwide (HVR1 only), Kitty Prince of Bear River Athabaskans (Mattole), an anonymous Caucasian American (Twygdam 69) and an unknown line in Mitosearch (7MP7K). Katherine Frances-Prince was the wife of James Prince of the Mattole and a member of the Bear River Band of Rohnerville Rancheria located south of Eureka, in Loleta, California.

Kitty Prince in 1921. Native American Indian - Old Photos Facebook Page (public domain photos). Kitty Prince's DNA (haplotype D) matched that of participant 25.

Nancy Ward Statue. See Yates (2012) 107. Nancy Ward's DNA matched that of Patricia Gurule of Denver, Colorado. © D. Ray Smith. Used with permission.

Patricia Gurule (66) was a walk-in client at Denver DNA Center, an affiliate of DNA Consultants. She knew "absolutely nothing" about her heritage before taking an autosomal ancestry test from us and then joining the Cherokee DNA project. Her type of C matched, among several New Mexican, Sonora, Zacateca and Chihuahua lines, the DNA of Nancy Ward, the Cherokee Beloved Woman and Tribal Mother (ca. 1738–1822 or 1824; Mitosearch record 8U6AP and CBC 115669, Allene Gay Kearney; see Yates [2012], Chapter 8, pp. 106-117 on Ward). It also matched Gayl A. Gibson Wilson, an enrolled member of the Cherokee Nation of Oklahoma and participant in our pilot project, Southern U.S. Native American DNA. Wilson, who is Wolf Clan, has traced her descent to Sarah Consene, a daughter of Dragging Canoe, born about 1800 in the Cherokee Nation East (see Yates [2012] 48-49, 158). This is evidently an ancient and widespread haplotype in Mexico and the United States, linked in Cherokee genealogies with the Wolf Clan, the traditional clan of war chiefs and most prevalent affiliation of Cherokees since the nineteenth century (Panther-Yates [2013] 4-10). In "Nancy Ward DNA" we have a clear example of exact correspondence between genetic matriline and a historically documented, genealogically proven, tribally specific clan.

Haplogroup H: Thorn in the Side of Theory

Before our studies, haplogroup H had been reported in small frequencies in surveys of the Cherokee but routinely explained as post-Columbian European admixture (Schurr 2000). As noted in "Anomalous Mitochondrial DNA Lineages" (2009), it is the quintessential European haplogroup, responsible for about 40% of European populations today (Sykes 2001). If our sample reflected non-native women settling among the Cherokee and not the genetic trace of pre-Columbian founder types, one would expect the H to dominate the scene. Instead, we found H in only 16% of the samples in Phase II and 8% in Phase I. In the CBC data, on the other hand, it occupied the top position with 40%—exactly as we would expect from a cross-section of European Americans.

There were 11 subjects with H in Phase II. These were about equally divided between haplotypes that were unmatched or rare, judged to be possibly ancient Native American on the strength of the matches (5), and haplotypes of very probable recent European origin, several of them in fact corresponding to the CRS (6). All of the latter failed to submit convincing genealogies linking their form of H with descent from a Native American woman. The former (9, 11, 12, 27, 33), on the other hand, invariably had unique, unmatched SNPs combined with compelling genealogies. For instance, Joel Kenneth Harris, Sr. (11) had several unique mutations, including the rare 16319A, also occurring in haplogroups D, A and J*. Add these 5 to 3 similar cases of H from Phase I and the true percentage of likely Native American H matrilines project-wide appears to be 6.7%.

James Eric Walker (9) was one of the strong cases. He started family research only in 2010. Born in North Carolina, the 57-year-old, 6-foot-five-inch-tall Walker lives in Mobile, Alabama. "There was a lot of so-called dark stories, as in my Jewish-Cherokee Walker and James lines," he said. "So my inner drive sent me into the world of paper trail ancestry . . . I found so much sadness with my mother's side, but the stories were true . . . DNA did in fact put my mother's line to bed." In autosomal testing he matched a Native American forensic population labeled Brazilian Belem Amazonians (n=325). His documented and published family tree verifies direct descent from Nancy Beacham, born about 1845 in Virginia, the wife of an emigrant born 1837 in Russia (both died in Mobile).

Mary England (12) had the reference series on sector 1 but a rare mutation in sector 2 that caused her to match only four users in Mitosearch, all of whom reported unknown origins for the type. She traces her maternal line securely to Sally Bingham, born 1833 in Knox County, Kentucky (and tentatively beyond). An intertwined line in her family tree goes back to Hatchet Grey Letty Durham, a reported full blood Cherokee, born in Wilkes County, Georgia, who died September 1, 1843 in Floyd County, Kentucky. Another Cherokee line she has assiduously traced zigzags back to Aaron Brock (Chief Red Bird, born 1727, died February 10, 1787, Clay County, Kentucky.

Great-grandmother Beulah David Cane (married name deFleron) was born March 16, 1876, the daughter of Nancy Beacham, born about 1845 in Virginia.

Grandmother Beulah Alexandra deFleron (married name Soderquist) was born November 7, 1905 in Mobile, Alabama.

Participant 9, James Eric Walker, has H ancestry that may be Native American. His grandmother and great-grandmother were known as Seminole-Cherokee.

A third H is Sharon Rebecca Chatterton (nee Toms). Her unique configuration of mutations brings up no one in the Cambridge Mitochondrial Concordance and produces only a very few exact matches in Mitosearch, all from North America (4U6K5, GECV7, Y9UQC). One of her maternal ancestors was a Frazier.

Sharon Chatterton's grandmother Peramelia Vaughn was born September 22, 1901, in

68-year-old Sharon R. Chatterton, participant 27, of Lady Lake, Florida, is

Coffee County, Tennessee. Her mother was Mary Eveline Frazier. After marriage she went by Amelia Vaughn Street. "She could unwind her long hair to the floor," says Chatterton. She died October 7, 1987.

an H who traces her line to 3rd-great-grandmother Lucinda Gilley, born 1801 in Franklin County, Ga. Lucinda's mother was named Dorcas. She married Zachariah Bush in Rutherford County, Tennessee.

The earliest female ancestor's identity in all these cases support the phenomenon I have described elsewhere of an Indian trader, typically Jewish or crypto-Jewish, marrying the daughter of a Cherokee chief or headman (Yates 2012:46ff.). The mitochondrial evidence tells us that H was part of the pre-contact Cherokee population. H did *not* enter the Native American haplogroup array with a colonial English woman marrying an Indian ("admixture"). While it is fashionable, and even politically ordained, to dismiss the Cherokee grandmother "myth," which can be traced to a single, suspect source in the literature, and which grew legs on the Internet so that it now seems unassailable, the uncomfortable truth seems to be that a goodly number of families who do not deserve to be called "Indian wannabes" have a bona-fide Cherokee matriarch corresponding approximately to that description in their family tree (Martin 1996).

T Haplotype Diversity and Sephardic Motifs

Our initial report remarked on the high incidence of haplotype T and compared its frequency to that of Egypt (23.4%). Phase II produced T's amounting to 19.4% of haplogroups in the sample, bringing its overall presence project-wide (n=117) to 23.1%, near the proportion reported in Iraqi and Iranian Jews, 24.4% (n=217, see Bedford, Table 4). Compare the high level in our study, Egypt and Iraqi and Iranian Jews to the much lower frequencies of T in Northwest Spain (6.9%), Portugal (9.2), Ashkenazi Jews (4.8), Sephardic Jews (11-14%), Great Britain and Ireland (9.1), North Central Italy (13.7), Western Saudi Arabia (12.5), Mitosearch (mostly U.S., 9.1) and National Geographic (8.7), and the T-intensive populations can be seen to surpass all the others by a factor of 2 to 5. On the basis of this comparison, we can safely call the T an aggregate among the anomalous Cherokees Middle Eastern in scale and importance.

In 2012, attention focused on T5, renamed T2e, and Felice Bedford of the University of Arizona published her article, "Sephardic Signature in Haplogroup T Mitochondrial DNA" (2012). "It was found that the rare motif [in subhaplotype T2e] belonged only to Sephardic descendents (Turkey, Bulgaria), to inhabitants of North American regions known for secret Spanish–Jewish colonization, or were consistent with Sephardic ancestry [sic]," Bedford wrote of the new Sephardic signature, T2e5. She dated the founder of the signature back to "one woman from Iberia who lived between 500 and likely 2000 years ago." So were there any instances of the new Sephardic signature, defined by mutations 16114T and 16192T, in our anomalous Cherokees? No, unsurprisingly, since Bedford found only 12 in an exhaustive search of world databases, but there were two cases of the parent sub-subhaplotype T2e, defined by

mutations 16153A and 150T. They are Cheryl Green (Phase I participant 34) and Evie Nagy (Phase II participant 22). And as Bedford reminds us, "Suspicion of a signature in a minority ethnic group can be initiated with as little as a haplotype match in two unrelated individuals from that group."

The sheer diversity of T types in Cherokee descendants, just like their high ratio, would seem to point to a source in the Middle East, not Europe. Although the phylogeny of T subclades and nomenclature is still somewhat unsettled (Pike et al. 2010), the prevalence and absence of subhaplogroups across different studies show strong similarities between the Cherokee sample and Iraqi and Irani Jews. Thus, T2b, which occurs at an almost non-existent level in Iraq, and reaches a high of 4.2% in Great Britain, is completely lacking in the Cherokee sample. T2e (6.9%) has a relatively high presence, as in the Ottoman Sephardim, Western Saudi Arabia and Italy. T1 (5.8%) is about the same as in Iraqi and Irani Jews (5.1%). Finally, there is a large amount, one-third of T subclades, categorized as T*. Their prevalence could be read as a sign of the antiquity of the Cherokee sample, with many T types which are common in the source population, but which have died out, not survived or have escaped being studied in standard contemporary genetic surveys. This inference is strengthened by the numerous unmatched T mutations, although a caveat should be added that the branches and sub-branches of T, as already noted, have not been completely dissected. Some of the T* haplotypes may be falsely assigned or need re-assigning.

Let it be noted here additionally that many of the T's in Phase II volunteered information they were Jewish by faith and/or descent.

Tara in the New World

Kathleen Rogalla of Panama City, Fla. (49) joined the project in July 2010, after learning family secrets from her 92-year-old mother) and receiving "disappointing" results from other companies. Of one, she wrote, " My test results came in a few days ago and I was shocked and dismayed by the results. They have me as 100% European with no chance of being Native at all. That also means that there is little chance of being matched with others who have Native blood." Subsequent testing revealed "a trace" of Asian ancestry. Her maternal line traces to Elizabeth Hensley of Stafford County, Va. But her genealogy on file with the project also identifies Deborah Cook(e), wife of William Chisholm (born 1720 in Amelia County, Va.) as her remote ancestor in an unbroken female line. Amy or Annie, no last name, was Deborah's mother. Both Deborah and her husband were associated with the Cherokee in historical documents. Rogalla descends from their daughter Sarah, who married Thomas Tinsley. Another daughter, Margaret, married her first cousin John Chisholm, and their daughter, Annie, married John Walling of the well-known long hunter family in Tennessee. A son of William and Deborah Chisholm, John D., was a friend and advisor to Doublehead.

According to Rogalla's research, "A descendant's wife, Mary Ann Roberts filed an application to the Dawes Commission on behalf of her children. They were rejected. She said 'My children have Indian blood that comes from their father Eli Roberts who gets his Indian blood from his mother Joanna Tinsley (daughter of Thomas Tinsley and Sarah Chisholm) and her from her mother(Sarah Chisholm). Her mother was the sister of Absolom and William Chisholm whose names should appear on the Old Settler's Rolls west of the Mississippi River.'"

Another excellent witness for Cherokee enrollment, B.W. Alberty, testified: "I am a resident of Tahlequah, Cherokee Nation. I met Dave and William Chisholm near Belview Texas and they lived there on the [illegible] and I was introduced to them as living Cherokee's by George Harnage and also by William Harnage that is I know about them said they were kin of old Tom Chisholm of the Cherokee Nation (Thomas Chisholm was the interim 3rd Chief of the Western Cherokee Nation in Arkansas). Hornage told me they were relatives of old Tom Chisholm. That was the year of 1852 or 53. I would judge Dave Chisholm to be about 45 years old and William I think was the younger of the two."

John Ratling Gourd testified: "I am a resident of Tahlequah District, Cherokee Nation and am about 65 years old. I was acquainted with Absolom and William Chisholm when they lived low down in Georgia. This was about the time the Cherokee came to this country. They were among the first who left country and came west. They were Cherokees by blood in at least what was looked upon as such. I first saw Absolom and William Chisholm at a council on the fork called by John Ross in regard to the division of some money. These parties voted to not divide the money. They looked like Cherokee's and appeared to be half or three-fourths. I saw William Tinsley several times. I understand he married into the Chisholm family."

These historical accounts are given here in detail to document the early Cherokee affiliation of the line. More could be added. Suffice it to say that the Chisholms and all their marriage partners were well known to Cherokee leaders from the 1760s on, first in the East and later, continuously in the West. The famous Chisholm Trail was named for the family. All the names are well documented in Cherokee and Melungeon genealogies, as well as U.S. Indian treaties, chiefs-lists and agency records. If we estimate the earliest named Cherokee's birthdate to be around 1700, we are in a period when the first intermarriages between English settlers and Indian women took place. It is unlikely that Amy or Annie was the daughter of an English woman, and the line she founded was "admixture." There is every reason on genealogical grounds to regard her T* haplotype as Cherokee, not Eurasian.

Amy-Annie apparently produced many direct descendants in the United States and Canada and had distant genetic cousins in Europe. Her prolific form of T* (16126C 16294T 16296T 16519C 73G 263G 315.1C) exactly matched individuals with origins in England, Cornwall, Quebec, France, Mississippi, California, North Carolina, Russia, Texas and Florida. Many of the haplotype assignments and origins were "unknown." As it turned out, they also matched Timothy Joseph Benjamin (18), an adoptee residing in Alva, Florida, who subsequently was able to have the Catholic charity unseal his adoption records, and who learned that he was born in Burlington, Vermont, his given name at birth Joseph David Ward.

The verdict in Rogalla's report stated:

> Although not one of the classic Native American lineages (A, B, C, D, and X - Schurr), T has been discovered in the Cherokee, Choctaw and other East Coast Indians (data on file; see DNA Consultants Blog, "Anomalous Mitochondrial DNA Lineages in the Cherokee"). Most investigators attribute this to recent European admixture. But T haplotypes without exact Old World matches (we exclude T2 matches from consideration) could just as well be considered Native American if as prevalent as the subject's is in North America. The majority of the T* matches in Mitosearch are possibly Native American in our estimation. In the presence of a genealogical tradition of the female line being Native

American the haplotype should therefore be pronounced Native American. The matches in Mitosearch to Tennessee, North Carolina and surrounding states point to the Cherokees, although matches in Canada suggest a Canadian indigenous woman (where T has also been identified). The T* matches that are truly European (such as V2DER, Russia) may represent a remnant of the original Middle Eastern lineage that survived in Europe, but the largest expansion of the lineage was clearly in North America.

Mother of Kathleen Rogalla (T), Ethel Estell Caywood Christian, about 1930.*

Karen Worstell's grandmother Odessa Shields Cox (shown with her husband William M. Cox and Karen's mother Ethel as a baby about 1922) was born about 1904 in Indian Territory. She was known as Dessie. "My mother cut off all connection with her own mother sometime before I was born," says Worstell. "My grandmother has strikingly Indian features and I do wonder if perhaps she was an adopted Indian child."

Karen Worstell (56) tested as having a rather widely distributed T2c that matched Cherokees on official rolls, even though T is universally considered a non-Indian type. "There was tremendous secrecy about anything related to my Indian background," says Worstell. My grandfather used to call me 'squaw,' which would infuriate my mother."

Ward is a common Cherokee surname. A T2 who also happened to have the birth name of Timothy Benjamin (18) was Deann Ward of Vincennes, Indiana (19). Ward traced her unbroken female descent to a 3rd-great-grandmother, Olive Thompson, born about 1800, died 1850 in Lincoln County, Tenn. Her parents are unknown. Olive Thompson married Garrett Merrill of Rowan County, North Carolina, a locale bordering on the Cherokee. Ward's great-grandmother, Emily Roper (a surname common on Cherokee rolls), was born in Tennessee, February 19, 1848, the daughter of Joseph Roper.

Karen Freeman Worstell (57) is a risk management professional in Gig Harbor, Washington, who wrote on April 24, 2010, "I just learned of the potential link between Cherokee and Eastern European Jews this morning. I was told I am Cherokee by my mother, and Scottish/Irish on my father's side. I am also deeply involved in the Messianic Jewish movement." Her rather widely distributed T2c haplotype exactly matched two participants in Phase I of the DNA Cherokee Project. Patrick Pynes, a professor of indigenous studies in Arizona, was a descendant on Mitosearch, traced the line to Mildred Gentry (1792-1852) and Nancy Gentry Little (b. 1801). "According to oral tradition, Nancy Gentry was of Cherokee descent," he wrote for the record. "She moved with her family from Tennessee to Clark County, Arkansas, in 1817. During the 1830s she lived with her husband James Little and children in Washington County, Arkansas. Several of her neighbors were of documented Cherokee descent or had family connections with documented Cherokees. Nancy's mother's name was possibly 'Delilah Clark.' Her father was likely Tyre Gentry of South Carolina."

Worstell says her mother passed away after a lengthy illness at the age of 90 and kept her family origins a secret. "Once when I asked her why, she said, 'I want you to have friends to play with.'" Worstell never met her maternal grandparents but always heard stories of Cherokee relatives. One of her ancestors was on the Trail of Tears. She has published an elaborate family tree on Ancestry.com but continues, like Patrick Pynes, to find the earliest link. Her maternal line research comes to an end with direct maternal ancestor Catherine Reed, born in 1776 in Loudoun County, Va. She married John Carlin on November 13, 1799, in

Harrison County, (West) Virginia and died in Barbour County. Several of the figures she has identified in her research were labeled as mulatto in local records. Her mother's paternal grandmother was Choctaw. Says Worstell, " I don't know if I am chasing a myth or not."

Haplogroups U, U2, U5 and K

Haplogroup U is very old and deep seated in Eurasian populations. Its top-level subclades can all be seen as haplogroups in their own right. Those uncovered in this phase of our study consist of U, U2, U3, U5 and K (formerly U8). There were no examples of U4, characteristic especially of Balto-Slavic countries and Finland; U6, associated with Berbers; U7 primarily from the East Mediterranean to India; or U9, spread from Ethiopia and the Arabian Peninsula to Pakistan.

The complex mega-haplogroup was born on the edge of Northeast Africa and Arabia some 60,000 or more years ago, when the first Homo Sapiens exited the African continent. Complex human societies began with U. In Europe, where U types today (11%) are the second most common after H (40+%), U was the first lineage to encounter and interbreed with the declining Neanderthals. U was identified as a minor haplotype in surveys of Cherokee and other Southeastern Indians (Schurr, Bolnick), although its presence was attributed to "admixture." It has also reported in Mexican Indians (Green). U2 was the mitochondrial signature of a link between archaic Europeans and modern-day Native Americans discovered in the 24,000 year-old Ma'lta skeleton whose DNA was recently sequenced from near Lake Baikal (Raghavan et al. 2014).

Vivian A. Santos-Montanez (14), a Hebrew School teacher in DeLand, Fla., took a combination of Jewish and Native American DNA tests for herself and several family members. Her mitochondrial mutation set produced only one exact match in the world: Mercedes Rivera-Rivera, born about 1915 in Utuado, Puerto Rico. Based on family traditions, Santos believes her maternal line could have come from Cherokees sold into slavery during the Spanish colonial period who joined Taino Indians living in the remote mountainous region of her native Puerto Rico.

U5, U5a and U5b samples include 5 participants from Phase II and 6 from Phase I, totaling 11 for the project, the bulk of all U's. U5 is of interest because of its important role in the peopling of Europe (Malyarchuk et al 2010). It is the oldest mtDNA lineage in Europe which is human, with an estimated age estimated at 50,000 years ago, greatly predating the expansion of agriculture. In the new three-fold scheme of European ancestry, U5 is the largest contributor to the component known as WHG or Western European Hunter Gatherers (Lazaridis et al. 2014). U5 is also found in significant levels, however, in the Middle East, Northern Africa and Central Asia.

Elizabeth DeLand (67), who tested her mother Juanita L. Sims, a U5a1, had an unreported set of mutations in the Cambridge Concordance, but matched five persons in Mitosearch, all three different haplogroup assignments, U5 (Ireland), U5a1* (Alabama, Ireland) and Unknown (Ireland). DeLand reported that her grandmother and great-grandmother spoke Cherokee. The mother of Pamela Bowman, Juanita Wilson (65), was another U5a1, with no exact matches on both sectors. Her rare/unique 16526A was reported in a single case by Van Oven and has been discussed sporadically on Internet boards. Bowman is a member of the CBC. She shares her rare SNP with William Zachary Dylan Sizemore (179989), who traces his line

to Lucinda Lusk, born January 31, 1823. The SNP also appears in the U5a1a* mutations of Dr. Bruce Dean (Phase I, no. 19), whose genealogy goes back to Jane Rose, a member of the Eastern Band of Cherokee Indians, and who matched Marie Eastman, born 1901, Indian Territory.

Turning now to U2, we have an interesting U2e haplotype in Carol Myers Rymes, a genealogist, Melungeon descendant (her uncle is a Sizemore) and CBC member who has pursued her mitochondrial line for several years. In Mitosearch, her single match was a descendant claiming descent from Bridget Garrity, born about 1816 in Ireland. Rymes also matched her own record in CBC data, plus Brian Voncannon, a Williams descendant. Rymes has been active in restoring the Occoquan Burying Ground in Prince William County, Va., and wrote a book on the descendants of Samuel Rymes. There were six U2e's in Phase I.

With Charlotte Walker (36), U3, we have an exotic haplotype that seems to match only Native American lines. U3 is a minor haplogroup centered around the Black Sea, with a strong presence today in the northeastern part (Colchis, Scythia, Transcaucasus, the Steppes). It could be related to ancient Indo-Europeans. There were two exact matches in Mitosearch, one from Alvina (or Elwina), born about 1820 in South Carolina and thought to be Native American, and another from Sarah Elizabeth Snyder, born 1828, origin unknown. The information from all three congeners is incomplete and uncertain. And as textual transmission experts say, "One witness, no witness." Participant 36 is the only instance of U3 to date. There are two examples in CBC data.

K (formerly H8) is an important Jewish haplogroup, and it has a small, but significant presence across all datasets. There were 2 (3.0%) in Phase I and 4 (nos. 13, 29, 34, 53, 7.7%) in Phase II. The CBC data shows 11 K's (8.1%). Haplogroup K is represented by 17 samples in a grand total of 252 participants (6.7%), a lower incidence compared both to European populations (10%) and Ashkenazi Jews (32-50%).

Three of our K's (Ashley Nielsen 29, Earl Dulaney 34, Ann Pyle 53) had such rare haplotypes, all with unique, partly overlapping mutations, that no exact matches could be found in the databases. It was felt that this specificity spoke for types that died out and were no longer reported in the rest of the world but survived in an exotic North American population, where they had been implanted in the remote past. By comparison, the chances of a large number of unmatched modern types dating to European admixture in the Colonial window of history were estimated to be slim.

Major Jewish Haplogroup J

Haplogroup J, termed Jasmine in the scheme of Oxford Ancestors, is believed to have originated in the Old Near East and to have moved north and west into Europe, especially after the spread of agriculture beginning 5000-3000 BCE. It is found throughout Europe with particularly high concentrations around the eastern Baltic Sea and Russia, as well as in Bedouins and Yemeni, where it reaches frequencies of 25% or higher. J is a major Jewish female lineage (Thomas 2002), being a strong maternal contributor to Jewish, Arab, Greek and Italian populations. J is also the apparent carrier of congenital longevity and a host of "Jewish" diseases that are just beginning to be understood by medical science.

There were 6 J's in Phase II (nos. 3, 8, 32, 35, 41 and 63, composing 9%), 4 in Phase I and 17 in the CBC data, making for an aggregate of 10.7%, somewhat less than the level for the Middle

East and Europe (12%).

There were multiple matches between participants. An example is James Richard Stritzel (8), whose form of J1b1 matched No. 63 on HVS1 with several mismatches on HVS2. Stritzel's grandmother, Eunice Mable, was adopted out of the Mohawk tribe and given the last name Ahern abt. 1900. His rare haplotype is similar to five J's reported in Phase I. Of these, Nadine Rosebush's type is not matched anywhere in the world. In other words, these J types seem to be specific to the micro-population in which they are found today and are not widespread. One might make an argument of inferred ancestry as follows, although other interpretations are also possible. The germ line and enclosing population may have originated in classical antiquity. Instances survived to the present in North America only because they were part of the discrete and continuous existence of a "people." This "people" had spread intact by discontinuous, long-distance migration from its point of origin, where in the course of centuries its presence became extinct.

Rarest of the Rare: I, N, V and W

Turning now to the four haplogroups that first cropped up in Phase II, we have one or two individuals each with I (54 Swinney, 48 Francisco), N (2 Kellam), V (39 Ponder) and W (30 Carpenter, 31 Sponenburgh). Percentages, phylogeny and phylogeographic patterns are probably not meaningful. Let us note, however, that one of the I's (54) had no matches anywhere, while the other (48) matched Dicie Gray, born 1828 in North Carolina. The sole example, Norma Kellam, N1A, traces her mitochondrial line to Roanoke, Virginia. She had several unique SNPs and matched only a handful of other people. In medieval times, N gave birth to one of the four major Ashkenazi Jewish founder lineages, probably in the Rhine Basin.

James Stritzel (8) was told by the first labs he went to that in "no way" could his DNA be Native American. His mother's line, however, was confirmed as Cherokee (or Mohawk) despite being an unusual type. Here the Manchester, Wash. resident carves a Deer Pipe after spending part of last summer training under a sixth-generation Lakota Nation Pipe Maker.

Norma Kellam (2) of Westminster, Calif. has maternal line ancestry in Virginia and matched only five Mitosearch users, two of whom also traced to Virginia. The other three pointed to Tennessee, Mississippi and unknown origins. Her maternal grandmother was Daisy Brooks (b. 1894, m. Cronk) and great-grandmother, Nancy Ann Tingery (m. John Sellars Brooks).

African L Haplotypes

Surprisingly, there were 6 L haplotypes in Phase II (9.0%). In Phase I, there were 3 (5.8%), and the CBC data include 7 (5.2%), bringing the total across all datasets to 16, or 6.3%. The most common haplogroup was L3, the oldest African lineage, associated with and most common today in East Africa. If the African DNA were the simple effect of gene flow into the Cherokee from historical-era slaves and freemen, one would expect West African centered L2 to dominate the results, as this is far and away the most prevalent type carried by African Americans (as much as 50%). L3, on the other hand, is characterized by a relatively greater presence in circum-Mediterranean and European populations. According to one authority, "L3 is more related to Eurasian haplogroups than to the most divergent African clusters L1 and L2" (Maca-Meyer et al. 2001). Sub-Saharan African L lineages account for 10% of the population in Saudi Arabia, and L3 occupies a prominent position (72% of them; Abu-Amero et al. 2008). It has also been observed in Slavic or East European populations, especially among Ukrainian Jews, possibly vestigial admixture from ancient slaves in the Roman Empire and Islam. L3 accounts for only one-third of L lineages within Africa.

We will highlight three L3's. Shelia Maria Wilson (52), who lives in New Mexico, has 20 mutations on mitochondrial control regions 1 and 2, the highest number we have ever studied. Generally, the more mutations, the more ancient the type. There was, however, not even a remote match in databases, making hers a unique type reported only in North America. Wilson knows her genealogy only as far back as her great grandmother, Mrs. Julia Adams. The surname came from the Georgia slave master of her father Harry Adams. Harry, who called himself "Mali blasta," was kidnapped in Mali as a pre-teen shortly before the Civil War. Shelia's mother Willie Mae Adams, born in 1927, remembered seeing the whelps on her grandfather's back where he was whipped. "I had been informed by some relatives," writes Wilson, "that my great-grandmother was at least part Native American and White." Another L3 (47, Lovancia Francisco) matched a historical Native woman, A Te Anu, Muscogee.

Willie Mae Adams was born June 2, 1904 in Butler County, Ga. She was the youngest girl of seven children. Her mother was a mix of black, Caucasian and Native American.

Shelia Maria Wilson (participant 52) carries an old and rare form of L3 that apparently left no descendants except for her and her family.

Gregory Damon Haynes (no. 16) has another unique and otherwise unreported L3 haplotype, with a SNP found in no other person (16163G). His father had a rare American Indian Q haplotype with relatives on two Indian census rolls. His maternal grandmother was Lily Marie Benjamin (Blythe), born October 15, 1922 in North Carolina. Could his maternal line have been Cherokee? The question remains open, as it is extremely difficult to investigate the lines of ex-slaves.

Haplogroup Distribution versus Europe and Other Populations, Based on Richards et al. 2000.

Hg	N=	%	Europe	Egyp	Middle East	Eastern Med.
T	27	23.1	8.4	23.4	11.9	6.0
U	23	19.7	22.2	7.8	26.3	16.4
H	15	12.0	53.5	14.0	36.8	47.9
J	11	9.4	9.5	6.3	11.4	12.7
L	9	7.7		15.6		
K	6	5.1	5.8	3.1	6.2	3.6
I	2	1.5		4.7		
N	1	0.8		6.3		
Tot.	n=1 17	~80 %	n=102 1	n=6 .	n=2736	n=165

Conclusions

If we are to accept our sample as valid, several salient parameters of the study population labeled "Anomalous Cherokees" seem to leap out from the table of haplogroup frequency comparisons.

1) The first striking feature is the high amount of T lineages evident in Cherokee descendants. T is the leading haplogroup (23.1%), with a frequency on a par with modern-day Egyptians (23.4%) and Arabs (24.4%). That is more by a factor of 4 than the East Mediterranean, three times that of Europe and the United States and twice that of the Middle East. T is thus a defining mark of Cherokee ancestry. Where did it come from? We can safely rule out recent European admixture. As we have discussed again and again, there was no available source for a huge, sudden influx of female-mediated Middle Eastern DNA on the American frontier. Even Sephardic Jews (11-14%), many of whom were also Indian traders, could hardly have accounted for such admixture. Moreover, had it occurred in the colonial period or more recently the diversity, age and unique characteristics of the T haplotypes would not have yielded the patterns noticed in this paper. Most T's would have matched people in the Old World and we would simply be looking at an effect of migration. Instead, we have a North American branch of T with peculiar SNPs which is evidently a cross-section of a very old population originating in the Old World. The thesis of Donald Yates' study of Cherokee history is that an expedition of Ptolemaic Egyptians and others in the 3rd century BCE served as the nucleus of settlers that became the Eshelokee (Cherokee). If this historical model is applicable, there was a severe bottleneck of DNA accompanying the establishment of the Cherokee, with many founder effects—something suggested by the frequent cross-matches, high degree of interrelatedness and clustering of types in our data.

2) The second glaring statistic is the relatively low amount of H (12%), which is the leading haplogroup in Europeans (~50%). If the admixture were attributable to European women in the colonial period we would expect it to be much higher. Again, the level is about the same as Egypt.

3) The third observation we can make is the similarity of haplogroups strongly associated with Jews (J, K at 14.5%) to European levels (15.3%). At whatever time period admixture occurred, whether in ancient or modern times, Jewish women likely formed part of it. Men cannot pass mitochondrial DNA. Like other contributions to the gene pool, J and K came from a feeder population or sub-population that had families on board. In other words, they could not have been the result of shipwrecked Portuguese sailors, Arab or Jewish merchants, soldiers or any of the other suspects often trotted forth. Judging also from the uniqueness of JK types and their diversity, we are looking at a Jewish signal deeply embedded in the structure of Cherokee populations.

4) L haplogroup frequency (7.7%) is about half that of Egypt (15.6%). East African-centered L3 predominates, not West and Central African-oriented L1 and L2 haplogroups, which are twice as abundant, and which define the majority of slaves and their descendants in the New World. We are unsure how to read this. It may be that in the nature of things, African American lines were under-sampled. Federal regulations and the controversy embroiling the Cherokee Nation of Oklahoma in their on-again-off-again rejection of freedmen as citizens might have served as a disincentive to blacks' testing their DNA. Blacks are also hampered in tracing genealogies, unlike whites or Hispanics.

Certainly, however, our data suggests there has always been a constant African component in Cherokee DNA, one that resembles North and East African populations rather than West and Central Africans. Beginning around the start of the Common Era, the Bantu expansion swamped all Africa with L1 and L2 genes. A high proportion of L3 could mean that admixture with the Cherokee predates that event. We have records of Phoenician colonization efforts as massive as the "30,000 desert-dwelling Moors from the hinterland of Carthage" in about 500 BCE (Yates 2012, p. 32). Mining operations then and now used a large number of women slaves, who were prized for their agility in negotiating small openings as well as their becoming inured to cruel conditions (this is still the norm in Egypt, India and Bolivia, though the workers are no longer legally considered slaves; see Del Mar 1902). The clan that specifically included black-skinned people among the Cherokee was called the Blue Paint or Panther (Ani-Sahoni; see Panther-Yates 2013, pp. 30-31). It was related to the original (Red) Paint Clan, named for the Paint People, or Phoenicians (Ani-Wodi).

5) Finally, we might remark on the minor (I, N, V, W), unknown (I 33, 36, 37, 40; II 33) and missing haplogroups (G, HV, pre-HV, M and other Asian types). I, N, V and W are minimally adduced in Egyptian, Palestinian, Arab and Turkish populations. They round out our picture of the original genetic inputs to the Cherokee, showing that the source of "admixture" was deep seated and diverse. The Cherokee population structure seems to be rather an effect of long-distance travel and conquest than of gradually developing encroachment, migration or genetic drift.

Admixture, just like the word "anomalous," is a relative term. Its use depends on one's perspective. Geneticists, as we have seen, tend to privilege a rather narrow body of recent U.S. and European scientific literature. It is time to de-colonize the human past and open our eyes to the diversity of American Indian peoples. The personal genealogies of over one hundred Cherokee descendants contradict popular and professional received wisdom about Indian nations.

Addendum: Begging the Question

For science to be separated from pseudoscience, its findings must obey the rule of falsifiability. This term has often been misunderstood, but what it means according to philosophers of science is that empirical statements such as "All swans are white" must be "such that to verify them and to falsify them must both be logically possible" (Popper 2005). Otherwise, as Wolfgang Pauli famously remarked, an argument "is not only not right, it is not even wrong."

In plain language, we could say that so far from barking up the wrong tree, that dog don't hunt.

"All swans are white" is a falsifiable statement. It can be tested by observation and shown to be generally true (though false in cases of black swans). But such statements as "All American Indians descend from haplogroups A-D and sometimes X" is not falsifiable. Neither this generalization nor its converse is testable in any experiential way. No amount of corollaries, exceptions to the rule or qualifications will fix it.

"A woman of haplogroup A (or B, or X, or T, or W) founded a Cherokee matriline," on the other hand, is falsifiable. It is scientifically true in certain individual cases and datasets, as claimed in the present study ("experiment"), just as it is scientifically false in other instances.

Much of the surmises of science about the peopling of the Americas can be said to be on the wrong track. It can neither be proved true nor decided false that ancestors of American Indians crossed a hypothetical Bering land bridge at some time in the unknown past. Let us hope that the growing demand for truth from amateur roots-seekers and test takers will force professionals to predicate their research agendas and phrase their findings more carefully in the future. If they do not, they will be failing the public trust. There is also a need for science reporters and writers to frame their stories more responsibly. We have always said, "There are Indians and Indians."

Phase I	Hg	HVS1
1	H	16239A 16519C
4	H	16183C 16189C 16193.1C 16362C 16519C
6	H	16189C 16193.1C 16193.2C 16356C 16362C 16519C
8	H	16519C
3	J*	16069T 16126C 16311C 16519C
9	J*	16069T 16126C 16162G
44	J*	16069T 16126C 16172C
45	J*	16069T 16126C 16311C 16366T 16368C 16519C
46	J*	16069T 16126C 16172C
30	K	16093C 16224C 16245T 16311C 16519C
23	K2	16093C 16192T 16224C 16311C 16519C
38	L1b1	(16234T)
42	L1c2	(African sequences)
43	L3	16223T 16258T 16320T 16519C
28	T*	16126C 16189C 16193.1C 16278T 16294T 16296T 16519C
35	T*	16126C 16172C 16185.1T 16189D 16294T16298C 16399G 16519C
41	T*	16126C 16189C 16193.1C 16193.2C 16294T 16296T 16519C
25	T1*	16126C 16163G 16185.1T 16189D 16294T 16519C
26	T1*	16126C 16163G 16185.1T 16189D 16294T 16519C
24	T1a	16126C 16163G 16185.1T 16189D 16294T 16519C
32	T1a	16126C 16163G 16185.1T 16189D 16257T 16294T 16519C
50	T1a	16126C 16163G 16185.1T 16189D 16294T 16324C 16519C
29	T2*	16126C 16266T 16294T 16304C 16519C
31	T2*	16126C 16187T 16294T 16296T 16304C 16519C
51	T2c	16126C 16182C 16183C 16189C 16294T 16296T 16298C 16519C
52	T2c	16126C 16182C 16183C 16189C 16294T 16296T 16298C 16519C
34	T2e	16126C 16153A 16294T 16296T 16519C
39	T4	16126C 16256T 16294T 16296T 16519C
11	U2e*	16051G 16129C 16145A 16182C 16183C 16189C 16362C 16519C
12	U2e*	16051G 16075C 16092C 16129C 16183C 16189C 16362C 16519C
13	U2e*	16051G 16092C 16129C 16183C 16189C 16362C 16519C 16525G
14	U2e*	16051G 16129C 16183C 16189C 16362C 16519C 16525G
16	U2e*	16051G 16092C 16129C 16182C 16183C 16189C 16362C 16519C
49	U2e*	16051G 16075C 16092C 160129C 160183C 160189C 160362C 160519C
21	U4*	16342C 16343G 16356C 16390A 16519C
18	U5*	16193T 16270T 16296T 16391A
17	U5a1a	16231C 16256T 16270T 16399G
19	U5a1a*	16114A 16192T 16256T 16270T 16294T 16526A
20	U5a1a*	16192T 16249C 16256T 16270T 16399G

15	U5b*	16189C 16193.1C 16193.2G 16270C 16519C
22	U5b2	16114T 16224C 16270T
33	Unknown	16183C 16189C 16193.1C 16276A 16325C
36	Unknown	16069T 16164G 16234T 16519C
37	Unknown	16183C 16189C 16193.1C 16261T 16519C
40	Unknown	16039A 16188D 16193.1C 16223T 16290T 16319C 16362C 16519C
2	X2	16182C 16183C 16189C 16223T 16248T 16278T 16519C
5	X2	16183C 16189C 16193.1C 16223T 16255A 16278T 16519C
7	X2	16129A 16183C 16189C 16193.1C 16223T 16255A 16278T 16519C
10	X2	16189C 16193.1C 16223T 16278T 16519C
27	X2	16189C16223T 16271C 16278T 51619C
47	X2	16189C 16192T 16223T 16278T 16519C 16528T
48	X2	16189C 16223T 16278T 16519C

Phase

I	Hg	HVS2
1	H	263G 315.1C
4	H	73G 153G 195C 225A 263G 309.1C 309.2C 315.1C
6	H	73G 185A 188G 228A 263G 295T 309.1C 315.1C
8	H	257G 263G 309.1C 309.2C 315.1C
3	J*	73G 153G 195C 225A 227G 263G 315.1C
9	J*	93G 263G 315.1C
44	J*	73G 153G 195C 225A 226C 263G 309.1C 315.1C
45	J*	185A 263G 315.1C
46	J*	73G 228A 263G 295T 309.1C 315.1C
30	K	73G 153G 195C 225A 226C 227G 263G 309.1C 315.1C
23	K2	73G 152C 217C 263G
38	L1b1	73G 152C 217C 263G
42	L1c2	73G 152C 217C 263G 315.1C
43	L3	73G 152C 217C 263G 315.1C
28	T*	73G 150T 185A 163G 309.1C 315.1C
35	T*	73G 150T 185A 163G 309.1C 315.1C
41	T*	73G 152C 263G 315.1C
25	T1*	73G 150T 263G 315.1C
26	T1*	73G 263G 315.1C
24	T1a	73G 199C 263G 315.1C
32	T1a	73G 150T 263G 309.1C 315.1C
50	T1a	73G 150T 263G 279C 315.1C
29	T2*	73G 194C 263G
31	T2*	73G 152C 195C 263G 309.1C 315.1C
51	T2c	73G 152C 195C 263G 309.1C 315.1C
52	T2c	73G 152C 195C 263G 309.1C 315.1C

34	T2e	73G (or 73.1G) 153G 195C 225A 226C 227G 263G 309.1C 315.1C
39	T4	73G 263G 309.1C 315.1C
11	U2e*	73G 263G 309.1C 315.1C 385G
12	U2e*	73G 263G 309.1C 309.2C 315.1C
13	U2e*	73G 151D 152.1C 263G 309.1C 315.1C
14	U2e*	73G 152C 183G 195C 263G 309.1C 315.1C
16	U2e*	73G 149.1T 152D 263G 315.1C
49	U2e*	73G 150T 263G 309.1C 315.1C
21	U4*	73G 146C 263G 309.1C 315.1C
18	U5*	73G 185A 188G 228A 263G 295T 309.1C 315.1C
17	U5a1a	263G 309.1C 309.2C 315.1C
19	U5a1a*	(357G)
20	U5a1a*	73G 263G 309.1C 315.1C
15	U5b*	73G 152C 235G 263G 309.1C 315.1C
22	U5b2	73G 151D 152.1C 236C 263G 315.1C
33	Unknown	
36	Unknown	73G 150T 189G 195C 263G 309.1C 315.1C
37	Unknown	
40	Unknown	93G 185A 188G 228A 263G 295T 309.1C 315.1C 462T 489C 522D 523D
2	X2	73G 228A 263G 295T 315.1C 426T 482C 489C
5	X2	
7	X2	
10	X2	73G 152C 217C 263G
27	X2	73G 152C 183G 195C 263G 309.1C 315.1C
47	X2	73G 195C 263G 315.1C
48	X2	73G 195C 263G 315.1C

Phase II	Hg	HVS1 Mutations
17	A	16111T 16223T 16290T 16319A 16362C
46	A	16223T 16290T 16319A 16362C 16391A 16519C
61	A	16111C 16129A 16187T 16189C 16209T16230G 16278T 16290C 16311C 16319G 16362T
38	B	16183C 16189C 16193.1C 16217C 16519C
58	B	16111T 16182C 16183C 16189C 16217C 16320T 16465T 16483A 16519C
20	C	16086C 16183C 16189C 16223T 16278T 16298C 16325C 16327T
66	C	16223T 16298C 16325C 16327T
10	D	16093C 16189C 16223T 16274A 16325C 16362C
25	D	16192T 16223T 16325C 16362C
9	H	16183C 16189C 16519C
11	H	16319A 16519C
12	H	16519C
15	H	16519C

24	H	16311C
26	H	16092C 16362C 16482G
27	H	16093C 16104T 16265G 16519C
43	H	16357C 16519C
45	H	16188G 16519C
62	H	none
33	Unk.	16051G 16162G 16343G 16519C
54	I	16129A 16223T 16311C 16391A 16519C
48	I4	16129A 16223T 16304C 16391A 16519C
3	J*	16069T 16126C
41	J*	16069T 16126C 16319A
35	J1a	16069T 16093C 16126C 16145A 16231C 16261T
8	J1b1	16069T 16126C 16145A 16172C 16222T 16261T
32	J1b1	16069T 16126C 16519C
63	J1b1	16069T 16126C 16145A 16172C 16222T 16261T
13	K	16224C 16311C 16320T 16519C
29	K	16183C 16189C 16224C 16311C 16519C
34	K	16187T 16224C 16311C 16519C
53	K	16145A 16224C 16311C 16325C 16519C
64	L2	16223T 16278T 16294T 16309G 16368C 16390A 16519C
16	L3	16163G 16223T 16320T 16399G 16519C
52	L3	16124C 16223T 16265R 16262C 16519C
51	L3*	16051G 16086C 16189D 16192.1T 16223T 16293T 16311C 16316G 16355T 16362C 16399G 16519C
50	L3e*	16179T 16223T 16237T 16519C
47	L3f	16129A 16209C 16223T 16292T 16295T 16311C 16519C
2	N1a	16147A 16154C 16172C 16223T 16248T 16320T 16355T 16519C
1	T*	16126C 16292T 16294T 16296T 16324C 16519C
18	T*	16126C 16294T 16296T 16519C
21	T*	16069C 16188T 16257T 16294T 16296T 16519C
49	T*	16126C 16294T 16296T 16519C
59	T*	16126C 16188T 16257T 16294T 16519C
5	T1a	16126C 16163G 16186T 16189C 16294T 16519C
6	T1a	16126C 16163G 16186T 16189C 16294T 16519C
19	T2	16294T 16304C 16519C
28	T2	16126C 16184T 16189C 16294T 16304C 16519C
37	T2	16126C 16218T 16287T 16294T 16296T 16304C 16519C
57	T2	16126C 16294T 16296T 16304C 16519C
56	T2c	16126C 16182C 16183C 16189C 16294T 16296T 16298C 16519C
22	T2e	16126C 16153A 16294T 16519C
14	U	16172C 16189C 16193.1C 16193.2C 16234T 16311C 16519C
42	U, T or H	16189C 16193.1C 16193.2C 16356C 16362C 16519C
55	U2e	16051G 16129C 16183C 16189C 16362C 16519C

36	U3	16343G 16390A 16519C
7	U5	16256T 16270T 16399G
65	U5a1	16192T 16256T 16270T 16278T 16362C 16526A
60	U5a1*	16192T 16256T 16270T 16391A
67	U5a1*	16256T 16270T 16291T 16399G 16519C
44	U5b	16093C 16189C 16193.1C 16193.2C 16270T
40	U5b2	16258G 16270T 16292T 16362C
39	V	16126C 16298C
30	W	16166C 16189C 16192T 16223T 16292T 16325C 16519C
31	W	16223T 16292T 16362C 16519C
23	X	16104T 16145A 16182C 16183C 16189C 16223T 16519C

Phase II	Hg	HVS2 Mutations
17	A	64T 73G 146C 153G 235G 263G 315.1C
46	A	64T 73G 146C 153G 235G 263G 309.1C 315.1C
61	A	
38	B	73G 263G 309.1C 309.2C 315.1C
58	B	73G 263G 309.1C 315.1C
20	C	73G 143A 249D 263G 290D 291D 315.1C
66	C	73G 215G 249D 263G 290D 291D 315.1C
10	D	73G 211G 263G 315.1C
25	D	73G 194T 263G 315.1C
9	H	263G 309.1C 315.1C
11	H	72G 146C 195C 263G 315.1C
12	H	189G 263G 309C 315.1C
15	H	146C 263G 315.1C
24	H	195C 214R 263G 315.1C
26	H	239C 263G 309.1C 315.1C
27	H	263G 309.1C 315.1C
43	H	263G 315.1C
45	H	263G 315.1C
62	H	73G 194T 263G 315.1C
33	H, H1a, A or U3	73G 263G 315.1C
54	I	73G 199C 204C 204C 207A 250C 263G 315.1C
48	I4	73G 199C 204C 236C 250C 263G 315.1C
3	J*	73G 185A 228A 263G 295T 315.1C
41	J*	73G 185A 228A 263G 295T 315.1C
35	J1a	73G 149.1T 152D 195C 215G 263G 295T 310.1T 315.1C 319C
8	J1b1	73G 146C 207A 242T 263G 295T 315.1C
32	J1b1	73G 185A 188G 228A 234R 263G 295T 315.1C
63	J1b1	73G 189G 263G 315.1C

13	K	73G 146C 152C 263G 315.1C
29	K	73G 146C 195C 200G 263G 315.1C
34	K	73G 195C 263G 315.1C
53	K	73G 149.1T 152D 195C 203A 204C 263G 310.1T 315.1C
64	L2	73G 146C 152C 195C 263G 315.1C
16	L3	
52	L3	73G 152C 195C 199C 263G 315.1C
51	L3*	73G 146C 152C 195C 244G 263G 315.1C 340T
50	L3e*	73G 149.1C 152C 195C 203A 204C 263G 309.1C 315.1C
47	L3f	73G 189G 200G 263G 309.1C 315.1C
2	N1a	73G 152C 199C 204C 263G 315.1C
1	T*	73G 263G 309.1C 315.1C
18	T*	73G 263G 309.1C 315.1C
21	T*	73G 263G 309.1C 315.1C
49	T*	73G 263G 315.1C
59	T*	73G 263G 309.1C 315.1C
5	T1a	73G 152C 195C 263G 309.1C 315.1C
6	T1a	
19	T2	73G 152C 263G 309.1C 315.1C
28	T2	73G 152C 263G 315.1C
37	T2	73G 146C 263G 309.1C 315.1C
57	T2	73G 263G 309.1C 315.1C
56	T2c	73G 195C 263G 315.1C
22	T2e	73G 150T 263G 309.1C 315.1C
14	U	73G 195C 263G 315.1C
42	U, T or H	140T 263G 315.1C
55	U2e	73G, 152C, 217C, 263G, 309.1C, 315.1C, 340T
36	U3	73G 150T 263G 309.1C 315.1C
7	U5	73G 263G 309.1C 315.1C
65	U5a1	73G 263G 315.1C
60	U5a1*	73G 263G 315.1C
67	U5a1*	73G 263G 272G 315.1C
44	U5b	73G 150T 263G 315.1C
40	U5b2	73G 150T 263G 309.1C 315.1C
39	V	72C 263G 315.1C
30	W	73G 189G 194T 195C 204C 207A 263G 315.1C
31	W	73G 189G 194T 195C 204C 207A 263G 309.1C 315.1C
23	X	73G 146C 153G 309.1C 315.1C

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