

Cherokee DNA Studies II

*More Real People Who Proved the
Geneticists Wrong*

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Part 1



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Look! We have come through.

—Geoffrey Chaucer

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CHRONOLOGY

1658 BCE	First colony of Sea Peoples in Hispaniola
1646	Thera erupts, end of Minoans, rise of Mycenaeans
1155	Ramesses III defeats Sea Peoples
814	Traditional date of founding of Carthage
500	Zapotecs begin to build Monte Alban
234	Ptolemy III sends ships to circumnavigate the world
146	Romans destroy Carthage
120	Teotihuacan is laid out in Mexico (burnt CE 550)
1 CE	Algonquians, Iroquois and Cherokee cross Mississippi
117-138	Reign of Hadrian, high point of Rome
558	Toltec Empire in Mexico; Xicallans invade Mississippi, Ohio
947	Mayapan founded in Yucatan
985	Norse begin to settle in North America
1105	Inca Empire founded in Peru
1175	Aztecs first arrive in Mexico
1322	Foundation of Tenochtitlan (Mexico City)
1428	Aztec Empire (till 1520)
1453	Fall of Constantinople to Turks
1492	Columbus' first voyage
1540	Hernando de Soto's entrada in Southeast
1670	Kingdom of Apalache; British settle Charleston
1702	French enter Southeast (cede New France to England 1763)

INTRODUCTION

Genetics will make liars of historians. —Anonymous

Cherokee history is a lot like Dr. Who's spaceship. It's bigger on the inside than the outside. Like the Tardus, which outwardly resembles a conventional British red telephone box, it has surprising room in its interior. Cherokee seems to cover a multitude of sins.

We all think we know about them. From schooldays on we are familiar with the broad outlines of their story—their rapid acculturation in a remote Appalachian homeland, Sequoyah's invention of a phonetic writing system that united them into one nation, and their forced removal to Oklahoma along the Trail of Tears.

Everywhere we search, we find that even the “hard science” part is unproved. The popular storyline has never been critically examined. Long-accepted motifs usually turn out to be long-standing myths. Cherokee genealogies published online are mostly false, full of errors repeated over and over again.

Ironically, it has taken outsiders to discover the truth. These are the “real people” who joined our DNA project. Experts and officials at the big companies had failed them. Geneticists and others had told them they couldn't be who they knew they were. But they were insistent. They took genetic genealogy to its limits and opened a new frontier of knowledge.

How are we to define or describe the Cherokee? The answers have puzzled cultural anthropologists and geneticists for years. In the only known genomic study of a Cherokee tribe, based on a very small sample from the Echota Cherokees of Alabama, J. Victor Moreno-Mayer and Eske Willerslev of the Centre for GeoGenetics in Denmark found high levels of European and African admixture and a typical result of less than 1% Native American ancestry. Shocking? Even so, Echota Cherokees have more Cherokee blood

than those in the West. Some studies of “citizen enrollees” in Oklahoma cannot point to *any* Native American ancestry. According to Joel K. Harris, Sr., “The Cherokee Nation terminated the use of Degree of Indian Blood because they do not have it.”¹

Creek historian and architect Richard Thornton has built a damning case that the Cherokee did not even exist as a tribe before 1720. British Indian policy invented them out of convenience and gave them land in North Georgia taken from the Creeks. Certainly, if we look at the official websites of the Cherokee Nation, United Keetoowah Band of Cherokee Indians and Eastern Band of Cherokee Indians—the three federally recognized groups in Oklahoma and North Carolina—there is virtually *no* sound information dating to before the 1830s. And yet the adjectives “proud,” “ancient,” and “rich” are liberally sprinkled about, as they are in standard accounts such as those by John Finger, Michael Wallis and Robert Conley.² Encyclopedia articles read like puffery. Few Cherokee genealogies are credible, and they are copied and pasted ad infinitum. Not a single indigenous studies or linguistics expert is on record as stating with certainty what the tribal name, Tsalagi, means, where it came from or when it was first used.

If we turn to archeology for answers we soon learn that even the authors of the Cherokee articles in the *Handbook of North American Indians*, an admired sourcebook, couldn’t find a *single* prehistoric site or stratigraphic layer associated with the Cherokee.³ It’s as though the Cherokee did not exist until they turned up on the British colonial frontier about 1720 begging for guns and ammunition. Indeed, there are some scholars who believe they were nothing more than a band of mixed blood outlaws in French Canada until the late seventeenth century when they moved southward to take advantage of the slave trade. The Pisgah and Qualla Phases of Southern Appalachian chronology (1000-1500 CE) do not divulge the slightest evidence of Cherokee burials or their material remains. The mounds investigated in Western North Carolina by enthusiastic academic teams with government and tribal grants can’t be Cherokee: The Cherokee did not build mounds and they avoided settling on them. A Cherokee chief told the Indian agent Benjamin Hawkins that the mounds in North Georgia were created “not by the people before us but the people before them” (which seems to point to

¹ DNA Calculator for Gene Pools,” webpage accessed at http://www._Cherokeeindiansofalabama.com/DNA-CALCULATORS-GENE-POOLS.html.

² John R. Finger, *Cherokee Americans: The Eastern Band of Cherokees in the Twentieth Century* (Lincoln: U of Nebraska P, 1993). Michael Wallis, *Mankiller: A Chief and Her People* (New York: St. Martin’s Griffin, 2000). Robert Conley, *The Cherokee Nation: A History* (Albuquerque: U of New Mexico P, 2005).

³ William C. Sturtevant, gen. ed., *Handbook of North American Indians*, vol. 14: *Southeast*, ed. Raymond D. Fogelson (Washington: Smithsonian Institution, 2004).

Adena and Hopewell Era Moundbuilders). Nor did they make pottery until they gave refuge in the eighteenth century to some of the Catawba, who introduced ceramic traditions.

The Skinny on DNA Tests

Genetic markers are patterns of DNA traced to specific locations on the chromosomes and associated with particular traits, such as eye color. They are polymorphic, meaning they occur in variations. The DNA sequences of these markers in different individuals are slightly different as a result of random, sporadic mutations over time, though in general, DNA is very stable and does not change much as it is handed down. Identifying new markers is a painstaking process. Scientists analyze DNA samples from related individuals or people with the same genetic conditions to find commonalities which could be used to pinpoint particular traits. Markers are derived by looking for changes in sequences with specific mutations that help to determine when new lineages may have begun. Since changes build up over time, often over 10,000 years or more, a large number of differences between two DNA samples would indicate that the two lineages diverged long, long ago. Few differences would indicate a more recent divergence.

DNA markers that tend to be inherited together form a haplotype. A group of individuals with similar haplotypes having the same polymorphic mutations represent a haplogroup, most likely with common ancestors and a similar germline of descent.

A population's structure can be expressed as the relative frequencies of different haplotypes. For instance, today's Egyptians have T as a leading mitochondrial haplotype, while the most common haplogroup in European populations is H. A recent survey of the distribution of Bulgarian mitotypes found 38% H (of which 10% are in the subclades H1 and H3 combined), 10% J, 6.5% T, 20% U (of which 10% are in U3, 6.5% in U4, and 3.5% in U5), 13% K, 6% X2, and 6.5% other haplogroups.⁴

The difference between a haplogroup and haplotype is the same as between a branch and twig, while mutations can be compared to leaves on the tree. The mtDNA mutation rate has been recently revised and is now estimated to be on average 9.8×10^{-8} nucleotide changes a year.⁵ Such a calibration of the mitochondrial clock places the settlement of North America by proto-Indians from Siberia in a time frame of 15,000 years ago,

⁴ Mariana Yaneva, "A Genetic Analysis of the People Currently Inhabiting the Country of Bulgaria: A Biological Perspective of the Origin of the Bulgarian Ethnicity," p. 5.

⁵ P. Soares et al, "Correcting for Purifying Selection: an Improved Human Mitochondrial Molecular Clock," *American Journal of Human Genetics* 84/6 (2009), pp. 740-59.

a date that is supported by archeological finds.

Mitochondrial DNA is a circular DNA molecule present only in the mitochondria, sub-cellular organs found in almost every human cell. This DNA is inherited by both male and female children but only from the mother. Thus, males do not pass it, only females. The higher mutation rate of some parts of the mtDNA compared to the DNA in the nucleus, together with other characteristics such as a limited number of genes, small size and lack of recombination makes it possible to detect any gradually accumulated differences in its sequence during the entire maternal lineage history. This analysis allows us to establish the origin only from the maternal side.

Mitochondrial analysis is an ideal guide to female-only ancestry. Along with Y chromosome studies, it is part of uniparental inheritance. Testing is done mostly by automated sequencing of the hyper-variable segments of the D-loop region, namely HVRI and HVRII, where the stable mutations are usually accumulated. Most companies “round off” mutational matches and report a consensual result. A strict identical-by-descent reading for mtDNA haplotypes requires a complete across-the-board match, with no missing or extra mutations.⁶ Only then can two people be said to descend from the same ancient female.

Y-chromosome DNA is DNA carried only by males and is inherited only from their fathers. Y chromosomes are small and their DNA has a very low recombination activity; the non-recombining regions are the loci for the Y-DNA haplogroups. These mutations are usually single nucleotide polymorphisms or SNPs meaning only one nucleotide is changed in this DNA region. These are the genetic systems analyzed in paternity and genealogical tests. The Y-DNA haplogroups are determined by biallelic (double) polymorphisms reflected mostly by SNPs. Another test for Y-chromosomes are the so-called Short Tandem Repeats or STRs, a short DNA sequence that is repeated numerous times as a result of duplications of sequence during the DNA replication or (self-)recombination process. These hypervariable STRs have the fastest mutation rate— 2.7×10^{-5} mutations a year, or 6.9×10^{-4} every generation of 25 years.⁷ In laboratories, haplogroup analysis is performed using specific biallelic DNA markers determined directly by DNA sequencing or indirectly using polymerase chain reactions.

⁶ H. Bandelt et al, “The Case for the Continuing Use of the Revised Cambridge Reference Sequence (rCRS) and the Standardization of Notation in Human Mitochondrial DNA Studies,” *Journal of Human Genetics* 59 (2014), pp. 66–77.

⁷ L. A. Zhivotovsky et al, “The Effective Mutation Rate at Y chromosome Short Tandem Repeats, with Application to Human Population-Divergence Time,” *American Journal of Human Genetics* 74/1 (2004), pp. 50-61.

Autosomal DNA and CoDIS Markers

Autosomal DNA (atDNA) is represented by the DNA molecules of all 22 pairs of chromosomes in human cells; the 23rd of the pairs are sex chromosomes labeled XY (in males) or XX (in females). Thus, females have no Y chromosome in their DNA. Autosomal DNA is inherited from both parents in various ratios. Most frequently analyzed mutations in this DNA are at a single nucleotide level, called single nucleotide polymorphisms (SNPs). To determine genetic admixtures or relatedness between individuals or populations, significant overlaps in the determined SNPs must be present. Companies or methods that emphasize autosomal results are 23&me, GEDmatch and Family Tree DNA. These “next generation” services screen up to 800,000 nucleotides genome-wide, partially observing, partially predicting values, and report the raw data as a genomic “build.” DNA Consultants has an autosomal test, but it differs from others’ in that it is based on STR frequencies in populations, or forensic profiles of 16 key locations across your chromosomes (standard CoDIS markers).

The significant mixing of peoples over time means that a haplogroup assignment or reference population match may only provide a rough estimate of an individual’s ancestral diversity. Most people are more mixed than they realize. New methodologies are being developed to allow better preservation and extraction of DNA from archeological specimens. These usually are well preserved, minimally contaminated with modern DNA bones, teeth or hair from old skeletal remains that have been dated within a certain archeological context. Ancient DNA analysis is a multidisciplinary endeavor involving historical and biological disciplines, genetics, molecular biology, anthropology and statistics.

Cherokee Unlike Other Indians

Cherokee descendants constitute America’s largest Indian group, with between 400,000 and 4 million people claiming that ancestry. So, are Cherokees the most “diluted” Indians? Are they the most culturally deprived? Have they forgotten most of their history? We did find a strong tendency toward collective amnesia. But we also encountered widely divergent tribal memories, and a hugely diversified genetic makeup.

There are genetic oversimplifications and stereotypes about the Cherokee people as well as misunderstandings about their history. “More Real People Who Proved the Geneticists Wrong” summarizes the records of 56 volunteers in Phase III who had cogent genealogical claims that their direct female line was Cherokee (or at least American Indian) and took a mitochondrial DNA test. As in the prior two phases, most participants did *not* have any of the “standard” American Indian mitochondrial haplogroups A,B,C,D “and sometimes X.” They ended up showing a large assortment of “non-Indian” lineages, with T (Middle Eastern) and U (Old Europe) leading

the list.

Indeed, in the Cherokee study overall, expected Native American haplogroups (A-D) account for only 7.4 percent of the lineages claimed to be Cherokee.

Mutations characterizing these anomalous types match for the most part only other American Indians of the Eastern United States. Data presented in Appendix C are discussed in chapters 3 and 4 and referred to throughout the work. They appear to be deep rooted. The haplogroups that stand out usually do not seem to represent the effect of admixture in recent historical times. Only large-scale Jewish admixture seems of the sixteenth through eighteenth century and can be tracked in historical records (see Chapter 10, “The Jewish Strain”). The reasoning for an older pattern set long before colonial times goes as follows: If these lines *had* traced back to European females rather than Indian females the distribution of haplogroups would be different, with H, the haplogroup carried by almost fifty percent of Europeans, enjoying the largest showing rather than U and T.

Perhaps the low amount of American Indian admixture reported in academic studies and consumer testing is misleading? Over a hundred “real people” in our project since 2007 believe it is. It seems to be dawning on genealogists that Eastern U.S. Indians are radically different from Western U.S. Indians in origins, age, population structure and affinities. Scientists and commercial companies can’t identify Cherokee, Shawnee, Creek and certain other eastern or southeastern tribes. That is due to preconceived notions and limited knowledge about the peopling of the Americas.

Armenians, Jews and Others

Chapter 1 starts us on our time travels with a conundrum. Why do so many Cherokees get matches to Armenians? Conversely, how can true Armenians with zero New World ancestors get matches to Cherokees? The pattern is clear with the autosomal test DNA Fingerprint Plus. Our forensic database now has over 520 reference populations (effectively, every ethnic group in the world), including all the countries of Europe, diaspora groups like Israeli Jews, Romani, Melungeons and Sephardim and 62 Native American tribes/nations. The backbone of DNA Consultants’ practice since 2006, this database captures virtually every single published study of STR (short tandem repeat) frequencies worldwide. It continues to grow. The gem in the crown of our research collection is published STR frequencies for enrolled members of the Eastern Band of Cherokee Indians (U.S. – Enrolled Cherokee, n=33).⁸ In contrast, companies that use genomic algorithms

⁸ J. Ng et al, “Native American Population Data Based on the Globalfiler® Autosomal STR Loci,” *Forensic Science International: Genetics* 24 (2016), e12-e13. Online,

instead of forensics typically feature between 40 and 60 world populations. None has Cherokee data.

Downstream and Down the River

Another mystery people our Tardus pays a visit to are the whiskered white men reported by the Tomahitans down the Coosa river. Who are the Tomahitans anyway? They are the main players in a letter from Abraham Wood to John Richards, dated August 22, 1674. This critical source (transcribed in Appendix A) has been tampered with by academic historians in North Carolina to document Cherokee settlements on the Tennessee River or Holsten. We establish its true context and significance for the first time.

Autosomal analysis supplements and confirms mitochondrial and Y chromosomal haplotyping. Autosomal tests are used to explain forensic anomalies like Armenians and Croats and Jews in chapter 1 (“Mixed Results”). The next two chapters take a deep-dive into mitochondrial casework, haplogroup by haplogroup. There is still an ingrained belief among geneticists that you can’t be an American Indian without having an American Indian haplogroup. Proof positive of Cherokee lines that violate this “rule” are those of participants Dorene Soiret and Karen Garruto (H1z1), Ava Fink and Julie Burton (J2b1’s), Don Barrington and Donna Atkins (J1a’s), Peter Atkins and Linda Sponenburg (W’s) and Barbara Oliver, a citizen enrollee of the Cherokee Nation, and Robert McFarlin (H’s).

It depends on whether the rare haplotype matches only other Cherokees in the New World or has narrowly defined, numerous analogues in the Old World. In almost all instances, the mutational set either matches no one else at all or only other participants. This suggests an interbreeding population and a one-off entry across the waters, just as the one described in the Cherokee origin narrative that begins “When we lived beyond the Big Waters,” and goes on to describe the creation of the seven clans of the Eshelokee.⁹ The rare lineage in question came over with others in a deep time frame. It left descendants in a particular tribe who intermarried within the same gene pool. Afterwards, the lineage died out in the Old World (Egypt, Eastern Mediterranean, North Africa, Greece, Anatolia etc.). Only similar

see abstract and references: [https://www.fsigenetics.com/article/S1872-4973\(16\)30115-6/fulltext](https://www.fsigenetics.com/article/S1872-4973(16)30115-6/fulltext).

⁹ *The Cherokee Origin Narrative: Authentic Text of William Eubanks’ Red Man’s Origin with Notes and Illustrations*, by Donald N. Yates, Cherokee Chapbooks 1 (Longmont: Panther’s Lodge, 2017), translated with foreword by Christine Pellech, *Die Abstammung der Cherokee-Indianer: Eine Spurensuche auf der Basis traditioneller Cherokee-Überlieferungen: Neue Ausgabe des Klassikers der Cherokee* (Longmont: Panther’s Lodge, 2017), also available in Italian and Spanish versions as well as an English audiobook version narrated by Jacob Phillips (2018), German audiobook by Richard Heinrich and Italian audiobook by Christian Vivi.

(but not exactly matching) forms survived in the Old World.

All these participants have lines that track back to an ancient female founder who lived in the Old World about 2,000 to 10,000 years ago and migrated in a cohesive colony to seed the Cherokee people in America. *Old World Roots of the Cherokee* proposed that a major founding event was tied to a trans-Pacific expedition of twelve ships of Greek “Volunteer Settlers” (Etheloikioi, Eshelokee) from Ptolemaic Egypt in 230 BCE.¹⁰ Egypt seemed to be at the heart of the expedition, because of the high level of haplogroup T, but Jews and other Levantines appear to have been on board as well, to judge from old and extinct types of J and K. It was suggested that these Jews came from ancient Cyrene.

The Helen Gene and the Odin Gene

Chapter 3, 4 and 12 tackle the great diversity of U haplotypes in the Cherokee. First, however, we touch on the V haplotypes of Diana McDargh (Sami?) and Gene Ponder (Long Hair Clan?). We also discuss briefly the rarest of the rare, haplogroup R0a-60.1T of Ramona Woodrum, which, strangely, seems to have originated in a female living thousands of years ago on the tiny South Arabian island of Socotra. The U’s include Patrick Hooks (U3), Teresa Woodward and Robin Hughes Kelly (U4), Ramona George, Sally Littleton and Gary James (U5b) and Lynda Logan (U5a1). Phoenician connections and haplogroup X are discussed, along with the Tuareg in the Carthaginian interior, Minoans and other Aegean seafarer peoples.

By autosomal measures, Phoenician descent in both European and American populations is quite substantial. Migration maps such as those developed by Family Tree DNA, HomeDNA and other “big box” companies are not capable of tracking the movement of peoples across the water. The Odin Gene, a marker that emanates from “pre-Viking” Norway and “pre-Celtic” Britain and Brittany is found selectively in North and South America, particularly in the so-called Votanic Empires of Central America. Additionally, it is thought to be prominent in the background of many Canadian Metis. In one case discussed below, a man’s maternal line goes back to a seventeenth century Fille du Roi native woman, but the type is T. How could that be? Most people insist that it’s a contradiction. Like other T’s, K’s, U’s, X’s and J’s among the Acadians, such an ancestress is non-native, the effect of post-1500 admixture. One company, Family Tree DNA, even shut down an Acadian Metis project because it was finding the “wrong” type of mitochondrial DNA! But it may well be that the type has been a native lineage thriving for hundreds or thousands of years with thousands of descendants

¹⁰ Donald N. Yates, *Old World Roots of the Cherokee: How DNA, Ancient Alphabets and Religion Explain the Origins of America's Largest Indian Nation* (Jefferson: McFarland, 2012).

today. When do we speak of recent “admixture” and when do we talk of long-standing “contributions” to tribal DNA?

The Indians Came from Europe

Chapter 5, “The Ancient Indian Nations” takes as its point of departure another body of evidence scorned by twentieth century experts, the Algonquian annals in the *Walam Olum* and detailed historical works of Constantine Rafinesque (1783-1840). A timetable of American Indian history and succession of tribes is presented with narrative excerpts and paraphrases taken verbatim from Rafinesque, who believed “the ancestors of the first native nations came across the Atlantic in ships.” He called them the Cutans, from the East Mediterranean (Cherokee Ani-Kutani), and Atalans, from the Atlantic-facing West Mediterranean. We link them to the Sea Peoples of the Bronze Age and place one of the earliest colonies around the mid-second millennium in Puerto Rico and Haiti, as recorded in Taino records and by greenstone statuettes.

An important piece of the puzzle is an Iberian sun-temple discovered *beneath* three “Indian” mounds in North Georgia. Was it built by Indians or non-Indians? Do we reserve the name only for people who came from Asia? Even for *them* it seems a misnomer.

The Georgia Bronze Age sun-temple plays a similar role to the hundreds of Iron Age furnaces surveyed by Arlington Mallery. These occur stratigraphically *beneath* Adena and Hopewell “Indian” mounds throughout the Ohio Valley. The inescapable conclusion is they were built and used by people before the Indians. Are we to call them Indians or something else? The subtitle of chapter 7 is “Why Some Cherokees Have Blond Hair.” It identifies the pervasive “country rock” of the DNA landscape when the East (and large parts of the Central Plains) was dominated by European peoples we can only awkwardly name as “pre-Viking Vikings” and “pre-Celtic Celts.” All this prior to 500 BCE.

Chapter 8 assesses growing evidence for Croatian, Catalan and Italian (Venetian) settlements in North Carolina before 1500, along with survival of members of the so-called Lost Colony of Roanoke. The Lumbee Indians (as profiled in a forensic study, $n=106$) are analyzed according to their autosomal matches.¹¹ On a modal (average) basis, their top matches are Chippewa Indians, Catalans, Turkish, Melungeon, Colombian Indians and Sephardic Jewish. On a submodal (next most common) basis, they show such minor ancestries as Tunisian and Moroccan (pirates?), Armenian, Sicilian, Polish,

¹¹ Eleni N. Levelakou et al, “Allele Frequencies for 14 STR Loci of the PowerPlex™ 1.1 and 2.1 Multiplex Systems and Penta D Locus in Caucasians, Africans, Americans, Hispanics, and Other Populations of the United States of America and Brazil,” *Journal of Forensic Sciences* 46/ 3 (May 2001), pp. 736-61.

Ukrainian, Romanian and Iranian. With the exception of Croatian (and possibly Melungeon), none of these is an ethnicity or heritage recognized by ordinary researchers exploring their North Carolina family trees. They are forgotten genetic roots.

Chapter 9 guides our time machine to the Kingdom of the Apalache Indians, or Apalachites. This is where Eleanor Dare fled after the destruction of the Lost Colony according to reliable evidence. We examine that evidence and its supporters, who include Samuel Eliot Morrison and Robert Wauchope, two unimpeachable witnesses. Recall that the Apalachites were one of the oldest, most powerful of the Atalan tribes discussed in *Rafinesque*. They had by this time absorbed several waves of Caribbean, Maya, Mexican Indian and South American invasions. Their king was Christian. Huguenots and Jews lived among them. Several French-Indians and Mustees crop up with a last gasp in what may be called the “children of Moytoy.” But in less than two generations, the Apalache Indians vanish from the pages of history. They leave only a handful of words in their language and the rubble of ruined cities quarried for roadwork in North Georgia.

Appendix D gives readers a “Digression Containing a Summary of the Moral and Natural History of the Land of the Apalachites,” an English translation of select passages from Book 2, Chapter 7 and 8, of the second, expanded French edition of *Histoire Naturelle et Morale des Iles Antilles de l’Amerique*. Published by the Huguenot author Charles Rochefort in Rotterdam in 1681, it is one of the most neglected early sources for American Indian history in the Southern Highlands. The language of the Apalachites, oddly, was Ancient Greek.

Chapter 11 is “The Invention of the Cherokee People.” It has two aspects, one, the deconstruction of such myths as Sequoyah and Nancy Ward, and two, the continued piecing together of the migrations that form authentic Cherokee history, extending from the Bronze Age to the Age of European Discovery. Cherokee diversity and admixture is real. It’s ancient, and it’s distinctive, unlike any other Indian nation. The “real people” who said, “Wait a minute, that is not us” and challenged the experts years ago can celebrate the beginning of a new period of embracing their true history and not being misunderstood or dismissed by anyone.

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