

## 2 DNA AND ANCESTRY

### Basque Argosy

Isolated Populations as Treasures-Troves in Genetic Epidemiology: The Case of the Basques, by Paolo Garagnani et al., *European Journal of Human Genetics* 17 (2009): 1490-1494.

The Basques living on the western border between Spain and France are a unique population, one often considered as an exotic isolate. "Basques" often comes up as a match in people's DNA Fingerprint results, often because (as is widely believed, at least) a people resembling Basques helped repopulate the British Isles after the last Ice Age.

But Basques are not an isolate. This article proves they blend gradually together with and into their closest neighboring populations in Spain and France and, so, are not a candidate population, as the Finns are, for the study of disease associations.

"Basques do not show the genetic properties expected in population isolates," according to the authors. On the contrary, as many previous studies suggest, the Basques have so much diversity among themselves they were probably the source of population diffusions in prehistory, not a backwater trap for inbreeding.

October 22, 2009

### Population Turnover and the Etruscans

In a recent research article published in the journal *Molecular Biology and Evolution*, a team headed by Silvia Guimaraes of the University of

Florence documents how the Tuscans of the Middle Ages preserved Etruscan bloodlines while the contemporary inhabitants of the Italian state of Tuscany seem to have little or no connection with those mysterious antecedents from the Bronze Age.

It is an example of discontinuity in the mitochondrial DNA record. The paper is titled "Genealogical Discontinuities among Etruscan, Medieval and Contemporary Tuscans" (published online on July 1, 2009; you must have a subscription or pay to read the full text). The authors are on sure ground with their findings since they had access to ancient, medieval and modern DNA for comparisons.

It is often assumed that whoever lives in a place belongs to a population whose ancestors settled there thousands of years ago, and who created a sort of genetic bedrock beneath the present-day DNA landscape. The Italian study, however, disproves the applicability of this theory in a country famous for suffering many invasions but enduring and retaining its native population structure and composition. It was to be expected that the same mitochondrial lineages would be present today that were common in Italy thousands of years ago. Instead, some of them, selectively, just died out over time.

A similar situation was revealed in 2005 with the classification of mitochondrial DNA in 24 Neolithic skeletons from Germany, Austria and Hungary. One-fourth belonged to haplogroup G, a rather rare type today. In fact, today's Central Europeans have a 150-times lower frequency (0.2 percent) of this mtDNA lineage. The inference is that sometime between 7,500 years ago and the present day, large-scale population replacement or genetic influx took place in Europe. Today, it is haplogroup H that enjoys dominance. (The study is "Ancient DNA from the First European Farmers in 7500-Year-Old Neolithic Sites," by Wolfgang Haak et al., *Science* 11 310/5750: 1016-18.)

Cases of such discontinuities could be multiplied tenfold or more, especially in the New World. Haplogroup M, a common East Asian lineage, was found in the skeletal remains of two Paleo-Indians about 5,000 years old at the aptly named China Lake in British Columbia, although the message was lost on its discoverers (see R.S. Malhi et al. in *Journal of Archaeological Science* 20:1-7). A study by Pääbo et al. in 1988 proposed the existence of a previously unknown founding lineage on the basis of mitochondrial DNA extracted from a rare specimen of

7,000-year-old human brain matter in Florida. This discovery was almost immediately dismissed as "of no importance." An analysis of the bone remains of 25 pre-Columbian Mayas by Gonzalez-Oliver's group produced one type of mitochondrial DNA that could not even be classified. The Brazilian geneticist F. M. Salzano has remarked that of the 338 ancient cases investigated to date over two-thirds could not be assigned to the conventional six "Amerindian" haplogroups. Researchers found that among the remote Cayapa Indians of Ecuador, one-fifth of genetic variation was "other."

The Etruscan study shows that a whole population can turn over in a few centuries. It doesn't take thousands of years. If this is true, as it seems to be, then the story of the peopling of the Americas has many unwritten chapters. The revised standard version propagated in textbooks and anthropology departments is simplistic and reductive.

September 15, 2009

### **The Land Bridge to Nowhere**

Here we go again. A small number of Siberians crossed the Bering Strait when it was dry land 12,000 years ago and populated the entire New World.

I refer to the article in *PLoS* (Public Library of Science) *Genetics*, titled "Genetic Variation and Population Structure in Native Americans," by S. Wang et al. So far from vindicating a decrepit theory that had nearly drawn its last breath in anthropology circles in the late 1990s, the "new evidence" does nothing but perpetuate geneticists' circular reductionist logic again. Set up a survey the right way, and you will get the results you want.

First, the 678 markers the scientists investigated are those they have determined are associated with Native Americans in the first place. Surprise! They were found in high frequencies in the 29 Native American populations of the study—the very populations that have been studied to death since the 1980s. One much-cited study of alleged Siberian origins of Native Americans used only nine North American Indians, all from the tiny Papago tribe in Arizona. Most of the Indians were from South America. No study will touch an Indian with admixture,

although it is likely all Indians have some degree of admixture, at least in North America. Even the reservation-born and -bred Navajos, considered the "purest" have as much as 20 percent by one measure.

In every other population of the world except those in the New World, greater diversity equals source. Thus, geneticists established the "out of Africa" theory because Africa has the most genetic diversity.

But does it? Actually, the Americas have more. Rather than pointing to the source of migrations, the gradual increase in frequency of the 678 markers as we get closer to the Bering Strait could reflect a decrease in diversity as a result of genetic drift the farther removed populations became from a center situated, say, in Central America. The same phenomenon occurs on the fringes of the Atlantic, where one particular genetic type, the male lineage known as the Atlantic Modal Haplotype, reaches frequencies of over 80 percent in Connaught, Ireland. It did not originate in Ireland, though, but rather in Basque lands, which have a high amount of diversity, like Africa.

Geneticists set great store by a concept known as time to coalescence. This is a backtracking calculation of the age of a population according to how many mutations it has accumulated, usually in its mitochondrial DNA. Wind back the mitochondrial clock, and you get to zero hour. Nothing is wrong with this approach, but the geneticists go further and set the time together with theoretical migrations to arrive at a source—say Lake Baikal in central Siberia. They use theoretical migrations to prove theoretical migrations. For Native Americans, supposing even that they had one central origin, it could just as well have been in Panama. But for geneticists, it must be in Siberia or Mongolia because that is the only place it is allowed to be.

The search for one single source is illusory and reductionist anyway. Who would suggest that all Europeans came, say, from Tajikistan, 40,000 years ago?

Rather than keep attempting to reiterate Native Americans' lack of diversity, a colonial attitude with blinkers to begin with, geneticists should study how and why Native American diversity far exceeds that of the Europeans, Africans, Asians and all other world populations.

*November 23, 2007*

DONALD N. YATES and TERESA A. YATES

### **It's Always Darkest before the Dawn**

Some reviews of Nicholas Wade's *Before the Dawn: Recovering the Lost History of Our Ancestors...*

By far the best book I have ever read on humanity's deep history.

—E. O. Wilson

Tracing the history and the evolution of the human race from our common ancestor with chimpanzees 5 million years ago in a 300-page book was an ambitious undertaking, but Wade was clearly up to the task. If you are interested in human evolution and the history of mankind, this book is required reading.

—Searching for the Truth

Brings together a selection of early results (from genetics) to tell the story of modern man, *Homo sapiens sapiens*. We have known a good deal about this topic for decades, from investigations in archaeology, anthropology and comparative linguistics. However, our new, detailed knowledge of the human genome has clarified our understanding dramatically. A good analogy would be the results sent back by the first interplanetary probes, resolving what for centuries had been mere points of light or fuzzy blobs in our telescopes into actual landscapes of craters, volcanoes and dunes, while at the same time demolishing wishful-thinking fantasies (like those about Martian canals).

—National Review Online

More informative than *Nature via Nurture*, more readable than *The Blank Slate*, and proves (contra "The Emperor's New Clothes") that popularizations of population genetics don't have to be deceitful and revolting.

—Bookosphere

Wade's coverage includes the ancient near-extinction of humanity (DNA analysis shows at one point there were only 5,000 humans left after a mass die-off), human migration and intra-human relations

between Neanderthals and Homo sapiens. He also talks about the idea of race and the violent war-making nature of human society.

—World History Blog

While "race" is often a dirty word in science, one of the book's best chapters shows how racial differences can be marked genetically and why this is important, not least for the treatment of diseases.

—Publishers Weekly

And finally, a big slam from Wade's former employer *Nature* magazine!

Wade's explanations commit various well-known errors, such as equating correlation with causation and extrapolating from individual traits to group characteristics. ... Most of the scenarios he reports have not been rigorously tested, nor is it clear how they could be. The book has many internal inconsistencies, and one can easily find contrary evidence or readily construct alternative "just so" stories that invoke the same genetic scenario and the same kind of reasoning. ... Wade claims example after example of "genes for" traits.

Read the original review in *Nature* 441/7095 (15 June 2006): Kenneth M. Weiss and Anne V. Buchanan review *Before the Dawn: Recovering the Lost History of Our Ancestors* by Nicholas Wade (p. 813).

January 6, 2008

### When DNA Second-Guesses History

In a new article in the *European Journal of Human Genetics* (17/5:693), the enigmatic Etruscans of antiquity are again the subject of a DNA investigation. This time, the study, called "The Etruscan Timeline: A Recent Anatolian Connection," uses mitochondrial DNA to probe the ultimate origins of the people, who appeared on the stage of history in about the eighth century B.C.E. We know this time frame is fairly accurate because the Romans started their calendar in 753 B.C.E. with the founding of Rome and dated all records A.U.C. (Ab Urbe Condita,

"From the Founding of Rome"). Roman historians beginning with Ennius and Livy also recount how early Rome was conquered by the Etruscans and made subject to Etruscan kings for the first few centuries of its existence.

That is why it is strange that the present article estimates "an [sic] historical time frame for the arrival of Anatolian lineages to Tuscany ranging from  $1.1 \pm 0.1$  to  $2.3 \pm 0.4$  kya B.P." Based, then, on the retrospective coalescence of DNA, this calculates the Etruscans' migration from an original homeland in Anatolia (modern Turkey) to as late as 1200 C.E. and as early as 390 B.C.E. What is going on? The Etruscans were clearly seated in Italy 450 years before 390 B.C.E., and by 1200 C.E., they were long since gone as an entity. In fact, by the time of the emperor Claudius, who wrote a lost history of them around 1 C.E., the Etruscans were already considered historical oddities and their language dead.

Are geneticists trying to rewrite history? I think it is a case of a fundamental fallacy in their work. Calculation of a time to coalescence is obviously limited by the validity and reliability of the sample, but it is also very often illusory.

To take the example of Native Americans, just because geneticists arrive at a time to coalescence of 10,000 years before present, doesn't mean the *place* of coalescence has to be in Mongolia/Siberia, where they derive all Native Americans. It could just as well be in the Americas. DNA doesn't necessarily tell us anything about geography. But it is often pressed into service to prop up a theory about human migrations. Let us remember, though, that such constructs are just constructs, so DNA cannot be evidence, only confirmation of someone's historical or racial construct.

If one wishes to speak about evidence in a strict sense, however, it is interesting that the researchers (Francesca Brisighelli et al.) found, by mtDNA sequencing, a "novel autochthonous Tuscan brand of haplogroup U7." This can mean that the same U7 turning up elsewhere may be a sign of Etruscan movements.

November 2, 2009

## Armchair Archeology

The explosion in commercial archeology has brought a flood of information. The problem now is figuring out how to find and use this unpublished literature, reports Matt Ford in the current issue of *Nature* magazine.

"I became aware that what I was teaching would be out of date without looking at the grey literature (unpublished reports)," says one professor at the University of Reading in England.

A policy shift in 1990 required all construction projects to document archeological remains in Britain and generated an avalanche of findings that cannot be absorbed by the official academic field. The result is that our picture of the past is very much outdated. Academia is not likely ever to get caught up. Nor are academicians ever likely to warm to new theories of population genetics like diffusionism and transoceanic contact and colonization, since few of those theories ever received a hearing in the halls of academe in the first place.

Read the full story in *Nature*, "Archaeology: Hidden Treasure," vol. 464, pp. 826-27.

April 7, 2010

## Archeology Gets Its Feet Wet

American Schools of Oriental Research Annual Meeting: Tracking the Med's Stone Age Sailors

Andrew Lawler

Genetic studies are beginning to fill in the missing pieces in the history and prehistory of seafaring.

"By carefully sorting genetic data from living people, a researcher at this recent meeting covered in *Science* reported that around 6000 B.C.E., early seafarers indeed spread their seed—both agricultural and genetic—from their homeland in the Near East as far west across the Mediterranean as Marseilles, but no farther."

No farther? Could that be because they have looked no farther? Gunnar Thompson's new study, *Ancient Egyptian Maize*, whose first

print runs have already been exhausted apparently, builds a well-documented and persuasive case that "Indian corn blossomed with equal vigor along the shores of the Nile River and Gulf of Mexico at the very dawn of history."

You may say that Thompson is not a "real" researcher, but we would counter that 400 corncobs on ancient tombs and papyrus scrolls of Egypt and corncobs depicted with copper weapons on ancient ships are real enough to be remarked upon by anyone with eyes in their head and a brain to think.

"Male regents in the Middle East and India sent mariners overseas in search of the world's purest copper deposits. These were located in the Mediterranean Sea on the Island of Cyprus, in the Persian Gulf on Megan Island, and on Isle Royale in the Upper Great Lakes Region of North America. This worldwide exploration took place in approximately 6000 B.C.E. ... all the way to the shores of North and South America" (p.2).

December 9, 2010

### Gene Surfing in Canada

Gene surfing is a process in population expansion whereby certain variations become prominent and dominant in a short time, appearing to skip the slow, steady, uniform accumulation of variegation and diversification. According to a study of the population structure and genealogies of Saguenay Lac-Saint-Jean in Quebec, this type of drastic change accompanied the immigrant wave front that spread over the area in the 17th century. "Deep Human Genealogies Reveal a Selective Advantage to Be on an Expanding Wave Front" in *Science* magazine describes the resulting demographics.

**Abstract:** Since their origin, human populations have colonized the whole planet, but the demographic processes governing range expansions are mostly unknown. We analyzed the genealogy of more than 1 million individuals resulting from a range expansion in Quebec between 1686 and 1960 and reconstructed the spatial dynamics of the expansion. We find that a majority of the present Saguenay Lac-Saint-Jean population can be traced back to ancestors having lived directly on or close to the wave front. Ancestors located on the front contributed significantly more

to the current gene pool than those from the range core, likely due to a 20 percent larger effective fertility of women on the wave front. This fitness component is heritable on the wave front and not in the core, implying that this life-history trait evolves during range expansions.

So gene surfing in an expanding colonization phase can produce a genetic revolution whose effects will be felt for hundreds or thousands of years downstream in history. We wonder if the same wave front demographics might explain some of the following population phenomena:

- Large scale triumph of Norman male lineages following the conquest of England in 1066.
- Selective expansion of Middle Eastern genes in Tennessee (including Cherokee families, Jewish male and female lines and Melungeons)
- Relatedness among Jews and "Jewish diseases"
- Diversity-within-uniformity of Polynesians
- Population replacement of Old European (U, N) by Middle Eastern genes (T, J) in Europe as a result of the Neolithic Agricultural Revolution

Many students of history are puzzled why old populations have the allele frequencies and heterozygosity clines they have. Genetic drift is only part of the answer. Gene surfing and selection in deep history are the rest of it.

*November 27, 2011*

### **Obama's Melungeon Ancestry**

San Diego State University professor D. Emily Hicks has traced some common ancestry with President Barack Obama. According to the professor of Chicana/o Studies, she and the president share Melungeon roots. Obama is a descendant of Mary Collins of Orange County, Virginia, as well as of Nathaniel Bunch of Louisa County and John Bunch of New Kent—well-known "feeder" counties for what became the Melungeon settlement described in Brent Kennedy's book, *The Melungeons, The Resurrection of a Proud People*.

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Obama's Bunch line was found to carry E1b1a haplogroup, a sub-Saharan African male lineage. He is also supposed to have Cherokee ancestry in his mother's colonial genealogies.

Read the whole story, "President Obama and California Professor Share Melungeon Ancestry," at [www.prlog.org](http://www.prlog.org).

*September 21, 2011*

### Evolution and Ancestry: DNA Mutation Rates

As often happens in the annals of science, two research teams independently reached the same groundbreaking results, and publication to the scientific world occurred simultaneously. The breakthrough in the present case concerned the mutation rate of DNA and has profound implications for human evolution as well as for DNA Consultants' new offerings in autosomal DNA ancestry analysis, specifically our Rare Genes from History Panel. The following two studies are already much cited by geneticists, though they have garnered little attention in the press. They appeared in online versions on the same day, Aug. 23, 2012.

| Study or Source    | Type of DNA                       | Sample or Method                   | Rate per Generation | Time Depth in Years |
|--------------------|-----------------------------------|------------------------------------|---------------------|---------------------|
| Sun 2012           | autosomal microsatellites         | 2,477 mutations in Icelanders      | .001-.0001          | 25,000 to 250,000   |
| Kong 2012          | single nucleotide polymorphisms   | 4,933 mutations in Icelandic trios | 63.2 or .000000012  | Very great          |
| Butler 2009        | Core CoDIS STRs (microsatellites) | compiled from studies              | .0028-.0001         | 9,000 to 25,000     |
| Zhivotovsky 2004   | Y chromosome STRs                 | Y haplogroup comparisons           | .00069              | 36,000              |
| Heyer 1997         | Y chromosome tetranucleotides     | 42 males in forensic database      | .002                | 12,500              |
| FamilyTreeDNA 2004 | Y chromosome STRs                 | Estimated from customer base       | .004                | 6,250               |
| Brinkmann 1998     | STRs (CoDIS markers)              | 10,844 Father-son comparisons      | 0-.007              | 3,500 to Very Great |
| Parsons 1997       | mitochondrial DNA                 | 134 mtDNA lineages                 | .000029             | 862,000             |
| DNA Consultants    | Rare Genes from History           | average estimate across loci       | .001325             | 19,000              |

***DNA Mutation Rates.***

**Article sources:** James X. Sun et al., "A Direct Characterization of Human Mutation Based on Microsatellites," *Nature Genetics* 44/10 (October 2012): 1161-65. A. Kong et al., "Rate of *de novo* Mutations and the importance of Father's Age to Disease Risk," *Nature* 488 (2012):471-75.

From this, it can be seen that mutation rates vary from a low with SNPs to the high rate of Y chromosome STRs (as much as 0.4 percent per generation). DNA keeps surprising us by proving to be more stable than we would tend to expect, dutifully transcribing its original values from generation to generation without many mistakes or changes. Only Y chromosome seems to be highly changeable, depending on the father's age (Kong 2012). Autosomal STRs mutate at a rate between SNPs and the Y chromosome, between every 19,000 or 25,000 and 250,000 years. For our new autosomal ancestry markers, that is confirmation that the alleles we are examining on a statistical basis are pretty much unchanged for the past 20,000 years. That's about twice the length of what we call world history, hence a meaningful enough time frame for valid inferences about population patterns and ancestry of individuals.

**Definition:** *mutation* A change in a DNA sequence, either spontaneous within a generation or inherited, sometimes from a very distant ancestor. Mutations usually do not affect our health or cause any differences in our appearance. In other words, they are not genes proper and do not "code" for new proteins. Even though they are non-coding genes, though, they are useful in tracing lineages. From *A Glossary of Common DNA Terms*.

October 23, 2012

### Megapopulations

The dictionary defines megapopulation as a very large one, from the Greek suffix mega, the same element as in megabyte. In statistics, a population is the whole field from which you choose a sample or representative segment. Thus, to test American Hispanic/Latinos you might draw a sample of 400 people from a predefined population of everyone with a Hispanic surname in a telephone book. How reliable and valid your sample is depends on methodology. By combining

| Time Depth<br>in Years |
|------------------------|
| 25,000 to<br>250,000   |
| Very great             |
| 9,000 to<br>25,000     |
| 36,000                 |
| 12,500                 |
| 6,250                  |
| 3,500 to<br>Very Great |
| 862,000                |
| 19,000                 |

populations you can study a metapopulation (all related populations, for instance North *and* South American Latin or Iberian populations) or megapopulation (all populations with Iberian ancestry in the world). Going from the small to the large, we have, then, individual, sample population, metapopulation, megapopulation, universe.

In a census, the sample and population coincide; everyone is counted.

In population statistics, this hierarchy might look like this: John Doe, Arizona Hispanic study (n=104, that is 104 persons in the sample), U.S. Hispanics, North American Hispanic, Iberian American, Iberian or Part-Iberians in the World.

At DNA Consultants, megapopulations are the broadest ethnic category calculated and reported to you. We look at metapopulations, too, but only as a control measure. Our database coverage is described as follows.

#### **Megapopulation Names and Number of Populations**

|                        |    |
|------------------------|----|
| African                | 17 |
| African-American       | 28 |
| American Indian        | 24 |
| Australoid             | 3  |
| Austronesian           | 6  |
| Central Asian          | 39 |
| Central European       | 13 |
| East Asian             | 39 |
| East European          | 8  |
| European American      | 24 |
| Iberian                | 32 |
| Iberian American       | 61 |
| Jewish                 | 3  |
| Mediterranean European | 20 |
| Melungeon              | 1  |
| Middle Eastern         | 36 |
| North Asian            | 3  |
| Northern European      | 15 |
| Romani                 | 4  |
| South Asian            | 35 |
| Southeast Asian        | 12 |

**Beyond Megapopulations: Percentage of Total Populations**

These categories correspond roughly to what people used to think of as "race," a now-discredited notion. They are continent-specific, with African and Caucasian extended to African and European populations in North and South America.

|           |     |     |
|-----------|-----|-----|
| African   | 45  | 11% |
| Amerind   | 24  | 6%  |
| Austral   | 9   | 2%  |
| Asian     | 67  | 17% |
| Caucasian | 255 | 64% |

**Another Calculation**

We created these totals to see what kind of white versus non-white coverage the database has.

|           |                 |     |
|-----------|-----------------|-----|
| White     | 255             | 64% |
| Non-white | 145             | 36% |
| Total:    | 400 Populations |     |

And that's all you need to know about megapopulations!

*April 9, 2012*

**Rare Genes from History**

DNA typing has gone from successes in the criminal justice system and paternity testing to new heights in mapping genetic diseases and tracing human history. John Butler in the conclusion to his textbook *Fundamentals of Forensic DNA Typing* raised an important question about these trends: How might genetic genealogy information intersect with forensic DNA testing in the future?

"At DNA Consultants that new chapter in DNA testing arrived several years ago," said Donald Yates, chief research officer and founder. "As we approach our tenth anniversary, examining human population diversity continues to be the whole thrust of our research, and it just gets

more and more exciting."

The company's DNA database atDNA 4.0 captures and puts to use every single published academic study on forensic STR markers, the standard CoDIS markers used in DNA profiles for paternity and personal identification. In 2009, the company introduced the first broad-scale ethnicity markers and created the DNA Fingerprint Plus test.

But its innovations didn't stop there. In October 2012, the company announced the launch of its Rare Genes from History Panel.

### **Why CoDIS Markers?**

"Theoretically," noted Butler in 2009, "all of the alleles (variations) that exist today for a particular STR locus have resulted from only a few 'founder' individuals by slowly changing over tens of thousands of years."

How true! Hospital studies have determined that the most stable loci (marker addresses on your chromosomes) have values that mutate at a rate of only 0.01 percent. That means the chance of the value at that location changing from parent to progeny is once every 10,000 generations.

The autosomal clock of human history ticks at an even slower quantum rate than mitochondrial DNA. Like "mitochondrial Eve," its patterns were set down in Africa over 100,000 years ago when anatomically modern humans first appeared on the stage of time.

Though the face value of the cards in the deck of human diversity never changed—and all alleles can be traced back to an African origin—as humans left Africa and eventually spread throughout the world, alleles were shuffled and reshuffled.

Humanity went through bottlenecks and expansions that emphasized certain alleles over others. Genetic pooling, drift and selection of mates produced regional and country-specific contours much like a geographic map.

By the 20th century, when scientists began to assemble the first genetic snapshots of people, it was found that nearly all populations were mixed, some more than others. The geneticist Luigi-Luca Cavalli-Sforza at Stanford University proved that there is almost always more diversity within a population than between populations.

If there is no such thing as a "pure" population—a control or standard—how are we to make sense of any single individual's ancestral lines? Statistical analysis provides the answer. And rare genes are easier to trace in the genetic record than common ones. Their distinctive signature stands out.

### **It All Began with the Melungeons**

About the same time as DNA Consultants' scientists were cracking the mystery of the Melungeons, a tri-racial isolate in the Appalachians, they became aware of certain very rare alleles carried by this unusual population in relatively large doses. The Starnes family, for instance, in Harriman, Tennessee, was observed to have a certain rare score repeated on one location in the profiles of members through three generations. The staff dubbed it "the Starnes gene."

Soon, company research had characterized 26 rare autosomal ancestry markers—tiny, distinctive threads of inheritance that reflected an origin in Africa and expansion and travels through world history. Genes in this new generation of discoveries were named after some distinctive feature associated with the pattern they created in human genetic history—for instance, the Kilimanjaro Gene after its source in Central East Africa. The Thuya, Akhenaten and King Tut genes were named for the royal family of Egypt whose mummies were investigated by Zahi Hawass' team in 2010. The Starnes Gene became the Helen Gene. Because of its apparent center in Troy in ancient Asia Minor and predilection for settling in island populations, it was named for "the face that launched a thousand ships," in the famous phrase by Christopher Marlowe.

All 26 of DNA Consultants' new markers are rare. Not everyone is going to have one. But that's what makes them interesting, according to Dr. Yates. Coming from all sections of human diversity—African, Indian, Asian and Native American—they are like tiny gold filaments in a huge, outspread multicolored tapestry, explains Phyllis Starnes, assistant principal investigator and wife of the namesake of the first discovery. But does that mean that her husband has a connection to Helen of Troy? The markers don't work on such a literal level, but it does imply that Billy Starnes shares a part of his ancestral heritage with an ancient Greek/Turkish population prominent on the page of history.

Over the past two decades, geneticists have worked out the macrohistory and chronology of human migrations in amazing detail and agreement. The Rare Genes from History Panel is another reminder—in the words of an American Indian ceremonial greeting—that “We Are All Related.”

These rare but robust signals of deep history can act as powerful ancestral probes into the tangled past of the human race as well as unique touchstones for the surprising stories of individuals. For more information about the science of autosomal DNA ancestry testing, visit [dnaconsultants.com](http://dnaconsultants.com) or check out its Twitter or Facebook page.

September 30, 2012

### Witches in the Attic

Three of my ninth great-grand-aunts were accused of witchcraft. Not exactly what I was looking for, but it is colorful. These were the famous Towne sisters depicted in “The Crucible.” All three were accused of witchcraft, and two were hanged. Only one escaped. Of course, neither Sarah Towne Bridges Cloyce, nor her two sisters, Rebecca Towne Nurse and Mary Towne Easty, who were executed, were witches. They just happened to live in a town caught up in a lunacy as bizarre as “The Walking Dead.” Except this was real. Rebecca Nurse was hanged for witchcraft July 19, 1692, and Mary Easty was hanged Sept. 22, 1692, as cited by Frances Hill in *The Salem Witch Trials Reader* xv. Sarah alone escaped the collective madness.

Various theories have been discussed as the source of this madness. According to Mary Jane Alexander in her *Los Angeles Times* article, “Family History Proves Bewitching,” the truth is probably more complex than hysterical teenagers or hallucinations brought on by ergot-tainted, moldy bread. That image is National Lampoon movie madness—albeit with Puritan clothes. She blames family rivalries and acrimonious land disputes. And some of these theories may have led in varying degrees to the Salem witch trials. But the Indian wars and the perception of Indians as heathens has largely been an ignored, albeit important, factor.

For instance, what of the Indian “witch” cake? One of the famous preachers of the day, Samuel Parris, preached a sermon laying a large part of the blame on a church member, Mary Sibley, who asked an

Indian named John to make a "witch cake," Hill writes. Puritans believed Indians willingly participated in devil worship, according to Elaine G. Breslaw in her *Tituba: Reluctant Witch of Salem: Devilish Indians and Puritan Fantasies*.

Breslaw makes the case that despite many incorrect references to Tituba as an African, there is ample evidence that she was referred to as Indian along with her husband at the time of the Salem witch trials. Like her husband, she was an Indian slave from Barbados who lived in the Parris household. When questioned, she made up wild tales and confessed to witchcraft no one could provide evidence for. For what motive? Survival. I am sure there was little to no love lost between an Indian slave and her white captors who called her a witch.

And the Puritans believed her story because it fit what they thought of American Indians. Though she was not executed, it spun a web of fear that went out of control. That fear was based on a fear of American Indians and their beliefs. Hill says, "That credibility was reinforced ironically by the continued association of Native Americans with witchcraft and a refusal to fully integrate Indians into Puritan society." Indians were considered heathens.

According to a 2004 article, "Salem Witch Trials," in the *Sun Journal*, the Indian wars were a contributing factor as Puritans believed God was punishing them because of the wars—attacks from the Wabonaki and other tribes along the coast: "... It was around this time that the girls started to have fits, believed to be the act of the devil. Since the devil could not do anything without God's permission, the Salem villagers thought that God was punishing them for not being Christian enough. To show that they were truly Christen (sic), they would kill all of the devil's sidekicks to show that when attacked by the devil, they would remain true to God and prove their faith. So, you see, without the Indian war, the Salem witch trials could not have happened."

It is an interesting theory. Of course, that does not mean Tituba and John are completely blameless. Tituba and John's confessions and accusations contributed to the Salem witch trials. But that does not make them witches. They stirred up a lot of trouble in fear of their own fates and accused people left and right. John accused Sarah in court. Sarah (Towne Bridges Cloyce) famously called him out when he testified she was a witch to the court by saying, "Oh, you are a grievous liar,"

according to Alexander in her *Los Angeles Times* article.

How did it turn around so? It is odd. The court called Tituba a witch after the incident of the "witch cake." But they were not prepared for her powers of storytelling, and she began to point fingers at others. Because the court believed so much in the truth of her testimony that she was a witch, they did not question what else she said or who else she accused. Then it all fell apart like in Yeats' poem, "The Second Coming": "Things fall apart/ The centre cannot hold."

At the core of their belief in her testimony was that an American Indian is a heathen. Until recently, this belief had not completely gone away—if it has now. The song, "Witch Doctor" was released in 1958. "Witch doctor" was a slur for a Native American healer who healed with plants and herbs—properly known among his people as a "medicine man (or woman)."

This slur has been in use for some time though it actually meant the reverse—an aboriginal healer working to protect against witchcraft. The Oxford English Dictionary states that the first use of the term "witch doctor" to refer to African shamans (medicine men) was in 1836 in a book by Robert Montgomery Martin (1803–1868). But evidently the idea that they were evil has been around for a lot longer.

So, how did Sarah escape? On an Easter Sunday, she slammed the door to the church when the preacher, Samuel Parris, insinuated her sisters were witches. Accused shortly thereafter, she was imprisoned and shackled, Hill says. However, her brother, my ancestor Jacob, a lawyer, and other friends spirited her away, and "she surviv(ed) the winter in nearby caves," according to the article "Witch Trials-Victims" on the Miner genealogy website. Later, she and her husband, Peter Cloyce, built their home in a nearby town until she was declared innocent. Eventually, she returned to receive three gold crowns from the town for the persecution of herself and the execution of her sisters.

Sarah's story is depicted, fictionally, as Goody Cloyse, a witch, in Nathaniel Hawthorne's short story, "Young Goodman Brown." She is also portrayed in the movie *Three Sovereigns for Sarah* with Vanessa Redgrave receiving the coins from Salem.

In conclusion, I am in good company being related to three accused witches. Three presidents—Taft, Ford, and Arthur—are "also descended from one of Salem's executed witches or their siblings [as well as] Clara

Barton, Walt Disney, and Joan Kennedy," Alexander says in her article. But no wonder this has been hidden until recent times. It was not until 1957 that "the General Court of Massachusetts resolve(d) that 'no disgrace or cause for distress' be borne by descendants of witch-trial victims." This was about the time I was listening to "Witch Doctor" on the radio.

*April 11, 2013*

### **New Euro Test**

DNA Consultants' new Euro DNA Fingerprint Test is an analysis of your European DNA in terms of statistical living population matches. Other methods before it generally fail to break down European heritage into meaningful national components.

"For a long time there simply weren't enough data in the literature to support such a product," said Principal Investigator Donald Yates. "European scientists have a different marker standard from the U.S. and that made comparisons difficult. Fortunately, after several years of work by our statistics team, we now have 71 European populations in our database — complete coverage of countries of Europe, including so-called foreign populations like Gypsies."

Like the company's other autosomal line of tests, Euro DNA Fingerprint Test matches your unique DNA profile with populations reported in academic studies. For this, it uses the computer program atDNA.

Other methods of assessing your ancestry are limited by the approach known as "haplotyping." A male or female can take our tests because the markers we look at are genome-wide, and none is located on a sex chromosome. The standard used in this test is the same set of identifying profile adopted by forensic institutes and law enforcement in the European Union, that is European Network of Forensic Science Institutes, or ENFSI.

"Even though there are some tests out there that purport to give you percentages of world or European ancestry," said Yates, "there have been and continue to be fundamental flaws in the methodology."

Most genetics studies, he noted, are still fixated on male or female lineages, those that can be determined by haplotyping.

DONALD N. YATES and TERESA A. YATES

"If you go back 10 generations," he says, "you have a thousand lines, not just two—no Y chromosome or mitochondrial sex-linked test can tell you anything about your father's mother or mother's father." Autosomal testing has the advantage over sex-linked testing of providing a more complete picture.

*May 31, 2013*

### **Cherokee New Year**

As Jews conclude a week of Rosh Hashanah and mark Yom Kippur beginning at sunset today, Cherokees worldwide are gearing up to celebrate their own cycle of fall festivals, including a New Year or Great Moon Gathering, which, like the Jewish High Holy Days, appears to begin earlier this year than in the past.

The Alabama Echota Cherokees, for instance, are holding their 16th Annual Festival Sept. 28-29. It will take place at the Oakville Indian Mounds & Park in Danville, Ala.

The Cherokee Nation of Oklahoma got the season off to a gala start with its 61st Annual Cherokee National Holiday on Labor Day weekend. This group of Cherokee descendants traces its roots in Oklahoma back to the days of Indian removal in the 1830s and is recognized by the U.S. Federal Government as a sovereign nation under Indian treaties from the 19th century. It boasts 300,000 card-carrying members today and is frequently in the news for rancorous lawsuits against other Cherokee groups. Their main "rival" is the United Keetoowah Band, also federally recognized and also headquartered in Tahlequah, Oklahoma. A third federally recognized group is the Eastern Band of Cherokee Indians in western North Carolina. This Indian nation's website claims a history of 11,000 years and original territory of 140,000 square miles covering eight present-day southern states, centered on Tennessee, although it has been granted official status only since 1924.

The Echota Cherokee Tribe of Alabama is smaller and quieter than the Big Three. It is one of nine Indian groups or tribes along with Choctaw, Shawnee and two other Cherokee recognized by the Alabama Commission of Indian Affairs. The Echota still live close to the land and maintain tribal property in their communal name to this day, with several thousand families scattered statewide around Falkville, Alabama. When

they have a homecoming, it is an emotional event.

We are happy to see that the Echota have an active women's society, and that their current principal chief is female, Charlotte Hallmark. We wish them and their members a joyous New Year. Jews have been celebrating their peoplehood on this date for 5,774 years, but Cherokees can point to many more thousands of years of existence.

*September 13, 2013*