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Genetic Heritage and Native Identity of the Seaconke Wampanoag Tribe of Massachusetts

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ABSTRACT The name "Wampanoag" means "Eastern People" or "People of the First Light" in the local dialect of the Algonquian language. Once extensively populating the coastal lands and neighboring islands of the eastern United States, the Wampanoag people now consist of two federally recognized tribes, the Aquinnah and Mashpee, the state-recognized Seaconke Wampanoag tribe, and a number of bands and clans in present-day southern Massachusetts. Because of repeated epidemics and conflicts with English colonists, including King Philip's War of 1675–76, and subsequent colonial laws forbidding tribal identification, the Wampanoag population was largely decimated, decreasing in size from as many as 12,000 individuals in the 16th century to less than 400, as recorded in 1677. To investigate the influence of the historical past on its biological ancestry and native cultural identity, we analyzed genetic variation in the Seaconke Wampanoag tribe. Our results indicate that the majority of their mtDNA haplotypes belongs to West Eurasian and African lineages, thus reflecting the extent of their contacts and interactions with people of European and African descent. On the paternal side, Y-chromosome analysis identified a range of Native American, West Eurasian, and African haplogroups in the population, and also surprisingly revealed the presence of a paternal lineage that appears at its highest frequencies in New Guinea and Melanesia. Comparison of the genetic data with genealogical and historical information allows us to reconstruct the tribal history of the Seaconke Wampanoag back to at least the early 18th century. Am J Phys Anthropol 142:579–589, 2010.

For thousands of years, the Wampanoag occupied a territory that encompasses present-day eastern Rhode Island and southeastern Massachusetts, including Cape Cod, Martha's Vineyard, Nantucket, and the Elizabeth Islands (Fig. 1). Archeological evidence suggests that the first Native Americans appeared in what is now New England between 10,000 and 12,000 years ago when the glacial ice sheets had started retreating. However, at that time the climate was still harsh and indigenous groups likely occupied the Great Lakes region from western North America before expanding across eastern North America. Thus, the major settlements in the region were established only between 10,000 and 3,000 years ago, as the environment grew warmer and became more favorable for the inhabitants of New England (Siebert, 1967; Fiedel, 1992; Snow, 1994; Bragdon, 1996).

It is now believed that, before European contact, there were more than 67 separate Wampanoag communities in the region residing in the places that now bear their names, including Aquinnah, Patuxet, Nantucket, Suconesset, and Mashpee. All spoke different dialects of the Wampanoag language, which belongs to the Algonquian language family, within its northern branch including the Massachuset, Nauset, and Narragansett languages (Michelson, 1917; Bushnell, 1922; Siebert, 1967; Goddard, 1978; Potter, 1993). During this time, the area representing the traditional territory of the Seaconke Wampanoag was simply called Seekonke (also Seeconk and Seecunk) (Bowen, 1997).

In the decades following the establishment of the Plymouth Colony, the English colonies and villages of the Wampanoag people developed an uneasy but interdependent relationship (Bragdon, 1996; Lepore, 1998; Philbrick, 2006). However, in the face of the colonists' increasing encroachment on Wampanoag lands and in retaliation for the death of his brother at the hands of the English, Massasoit's son Metacomet, or Philip, initiated the liberation uprising against the English, known as King Philip's War. This conflict ultimately led to the defeat of Wampanoag tribes (Schultz, 2000; Philbrick, 2006).

Available historical sources indicate that, following contact with Europeans, Wampanoag tribes underwent a severe decline in population due to the introduction of pathogens, devastating "virgin soil" epidemics and war (Abbott, 1903; Cook, 1973a,b; Salisbury, 1984; Speiro and Spiess, 1987; Snow and Lamphere, 1988; Bragdon, 1996; Lepore, 1998; Philbrick, 2006). King Philip's War, in particular, resulted in a dramatic reduction in the Wampanoag population—from over 5,000 to less than 400 individuals (Cook, 1973a,b; Fickes, 2000; Schultz, 2000). Those who survived were either enslaved/indentured to the English or tribes hostile to the Wampanoag for a period of years, shipped out of the colonies to be sold overseas as slave labor, or were driven deep into hiding

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Fig. 1. A map of New England with the traditional locations of New England Native American populations indicated on it (based on *The Pequots in Southern New England*; modified after map available at www.dowdgen.com/dowd/document/pequots.htmlsource).

among neutral Indian tribes (Moore, 1866; Travers, 1957; Cook, 1973b; Boussevain, 1976; Mayo, 1986; Doughton, 1997; Lepore, 1998; Fickes, 2000; McBride, 2001; Newell, 2001; Kolchin, 2003; Olexer 2005). Less subtle and more insidious means employed by the English to obliterate Wampanoag culture included outlawing all use of the Massachusetts language and tribal names, enacting colonial laws prohibiting the Wampanoag from organizing or forming tribal assemblies, and converting the New England natives to Christianity (Moore, 1866; Abbott, 1903; Salisbury, 1984; Philbrick, 2006).

Despite these circumstances, the Wampanoag people maintained certain aspects of their culture that could be shared and practiced in private, turning to clan and family as their sources of knowledge. Yet, without a focal cultural center and the ability to congregate and share information, traditional Wampanoag society began to disintegrate. Eventually, shared history, education, and language slipped away as older generations passed on. By the early 1700s, what had once been a viable thriving culture began its descent into obscurity.

During this same period, European powers introduced African slave labor into New World society (Curtin, 1969; Blank, 2002). To expand economically, the English required more than what a weakened and dwindling native population could provide (Cook, 1973b; Bossevain, 1976; Lepore, 1998; Fickes, 2000; Newell, 2001; Kolchin, 2003). The introduction of African slave labor paved the way for the creation of a new culture in the margins of colonial New England. Members of this emerging slave class, while highly visible and indispensable in shoring up the structural and economic vitality of the communities of southern New England, were viewed as outcasts because of their historical and cultural make up and also their skin color (Calloway, 1997; Karttunen, 2005).

Although the remnants of existing Wampanoag families were now technically free, the effort to maintain their independence did not occur without some cost. Whereas most African slaves lived on or near the work place of their owners, the Wampanoag, with their poor socioeconomic status, lived on the outskirts of towns in family enclaves, in less than adequate housing (Annawan Historical Society, 1993; Vaughan, 1995; Calloway, 1997). Over time, the few Wampanoag people who survived began marrying people of African descent. In general, the reduction of Indian males through war, infectious diseases, and slavery led to significant intermarriage between native women and African males in the 18th century and afterward (Lepore, 1998; Newell, 2001; McBride, 2001). In addition, albeit less common, Wampanoag individuals began marrying into colonial families. By the 18th century, a new culture that embraced English, Wampanoag, and African elements was born out of necessity, resulting in the hybridized successive generations we see today.

Well into the 20th century, the descendants of the Seaconke Wampanoag continued to work the farms in and around what is today called Bristol County, MA. In 1925, the First Free Methodist Church was built to bring Christianity to the few native families still residing in Seekonk, MA (Fig. 2). It is written in the excerpt of the 50th anniversary of this church that many of the Seekonk people were of Indian descent (First Free Methodist Church, 1975). After 1925, with tribal families marrying into those of the surrounding community and advancing in education, assimilation into society became the norm.

However, the community also began the necessary reconciliation with its once-existing culture, which had remained hidden for generations. This effort culminated in the reorganization of the people comprising the Sea-

Fig. 2. A photograph of the Seaconke Wampanoag Tribe, circa 1925 (from collection of Michael Markley).

conke Wampanoag into a modern tribal organization in October 1996 (The Providence Journal, 1996a,b; Seekonk Star, 1996). Later, in February 1997, in the first Wampanoag public assembly held on the Seaconke Plain—the former Pokanoket territory—in 321 years, the citizens of all the Wampanoag Nation celebrated this rebirth (House of Representatives of the Commonwealth of Massachusetts, 1997; The Providence Journal, 1997; The Sun Chronicle, 1997; Town of Rehoboth, 1997). Despite centuries of difficulty, the Wampanoag managed to preserve many of their cultural traditions, including special celebrations and events in their towns, such as the annual powwow (www.seaconkewampanoagtribe.org). Unfortunately, it has not been possible to fully recover information about their cultural practices, languages, and genetic diversity that is lost since the late 17th century.

Therefore, to investigate the influence of the historical past on their biological and cultural identity, University of Pennsylvania (Penn) researchers joined the Seaconke Wampanoag Tribe in a study of genetic variation in its members. This analysis involved the characterization of both mitochondrial DNA (maternal) and Y-chromosome (paternal) haplotypes from study participants. When viewed in the context of genealogical and historical information, this analysis reveals a complicated picture of genetic ancestry in the tribe, and facilitates efforts to reconstruct the unique tribal history of the Seaconke Wampanoag Tribe back to at least the early 18th century.

METHODS

Participants

In summer 2005, Penn researchers visited the Seaconke Wampanoag tribe in Seekonk, MA, to undertake this genealogical and genetic study. Blood and buccal samples along with family history information were obtained from 28 members of the tribe following informed consent, and with approval of the University of Pennsylvania IRB. The majority of the participants shared common ancestors and were related either through maternal or paternal descent self-assigning themselves as "Citizens" to the tribe. Several other participants lacked a familial connection to other members of the tribe but had formally been accepted as "Friends."

Historical and genealogical data

To better understand New England Indian history, we carefully assessed historical documents, ethnological publications and archival materials that discussed indigenous populations of the region. We also reviewed written genealogical records and oral histories about the Seaconke Wampanoag that were provided by tribal members. This information provided the essential genealogical context in which to interpret the genetic data obtained from mtDNA and Y-chromosome analyses.

Mitochondrial DNA analysis

To elucidate the maternal genetic ancestry of the Seaconke Wampanoag, we examined mitochondrial DNA (mtDNA) variation in both male and female participants through single nucleotide polymorphism (SNP) analysis and direct sequencing. Through this approach, we identified phylogenetically important mtDNA lineages, as well as delineated maternal haplotypes in these individuals. The SNP analysis involved screening the samples for markers (C3594T, A8701G, T9540C, T10873C, C12705T, and G14783A) that identified the basal portions of the mtDNA phylogeny (L, M, N, and R). These markers were analyzed using TaqMan® assays (Applied Biosystems), and read on an ABI 7900HT Fast Real-Time PCR System. Once assigned to one of these basal lineages, the samples were screened for markers that define African haplogroups or their subbranches (A7055G = L1; C7256T = L1/L2; C13650T = L1/L2; A13803G = L2a; G3693A = L2d; T2352C = L3e) and West Eurasian haplogroups (G1719A = I/W; C7028T = H; G8251A = I; C14766T = H/V), using both TaqMan assays and PCR-RFLP analysis (Gokcumen et al., 2008; Rubinstein et al., 2008). All samples were screened for the G10398A and C10400T markers that help to delineate the basal portion of the mtDNA phylogeny, using PCR-RFLP analysis (Schurr et al., 1999).

In addition, for each sample, the hypervariable segment 1 (HVS1) of the control region was directly sequenced using published methods (Gokcumen et al., 2008), while hypervariable segment 2 (HVS2) was sequenced using the primers indicated in Table 1. All sequences were read on an ABI 3130xl Gene Analyzer in the Department of Genetics Sequencing Core Facility, and aligned and edited with the SEQUENCHER 3.1 soft-

TABLE 1. Primers used for PCR amplification and sequencing of the HVS2 region

	Primer sequence	Function	Primer coordinates
1	5′-CCTAAATAGCCCACACGTTC-3′	Amplification/sequencing	16527–16556
2	5′-GGTGAACTCACTGGAAGGGG-3′	Amplification/sequencing	725–705
3	5′-GATCACAGGTCTATCACCCT-3′	Sequencing	1–20
4	5′-CTGTTAAAAGTGCATACCGCC-3′	Sequencing	429–409

Primer coordinates are indicated according to the rCRS (Andrews et al., 1999).

ware tool (Gene Codes Corporation). The combination of SNP and HVS1 + HVS2 data allowed us to define maternal haplotypes in these individuals.

Y-chromosome analysis

We also investigated the paternal genetic ancestry of the Seaconke Wampanoag by screening male samples for phylogenetically informative SNPs in the nonrecombining portion of the Y chromosome (NRY) that define major paternal lineages. These lineages, or haplogroups, and the subbranches within them, were tested in hierarchical fashion according to published information (Y Chromosome Consortium 2002; Karafet et al., 2008). The markers analyzed include LLY22g, M2, M3, M9, M12, M19, M20, M33, M35, M45, M69, M70, M75, M81, M89, M96, M102, M107, M123, M124, M130, M148, M168, M170, M172, M173, M174, M191, M194, M199, M201, M207, M230, M242, M253, M267, M285, M304, M343, M346, M410, P15, P25, P37.2, P215, P297, and PN2. These markers were analyzed using custom TaqMan assays and scored on an ABI 7900HT Fast Real-Time PCR System.

In addition, paternal haplotypes in the male samples were defined by analyzing diversity at 17 Y-STR loci available in the AmpFlSTR® Y-filer PCR Amplification Kit (Applied Biosystems). A separate multiplex reaction was used to characterize six additional fragment length polymorphisms and two additional Y-STRs (M17, M60, M91, M139, M175, M186, DYS388, and DYS426). PCR products were run with GeneScan™ 500 LIZ® Size Standards (Applied Biosystems) and sized using GeneMapper ID v.3.2 (Applied Biosystems) on an ABI 3130xl Gene Analyzer. The combination of SNP and STR data allowed us to define paternal lineages in these individuals.

RESULTS

Genealogical data

Using available recorded and oral tribal history, we were able to reconstruct a tribal genealogy that included all of the participants. For most persons, the genealogy coalesced to a few founder individuals, with these persons thought to share significant native Wampanoag heritage. Overall, the genealogy information provided by participants was consistent with the reckoning of their genetic ancestry.

mtDNA diversity

On the basis of coding region SNPs and control region sequences, we identified a total of 15 distinct mtDNA haplotypes in the 28 Seaconke Wampanoag participants. These haplotypes belonged to African and West Eurasian lineages, with African haplogroups encompassing the majority of their mtDNAs (Table 2, Fig. 3a,c).

Among the haplotypes belonging to African maternal lineages, haplogroups L0, L1, L2, and L3 were represented. L0a haplotypes have been observed in populations from various parts of Africa as well as groups from the Near East (Salas et al., 2004; Behar et al., 2008), while L1c and L2a haplotypes are widely distributed among populations from West and Southwest Africa (Alves-Silva et al., 2000; Salas et al., 2002, Rosa et al., 2004; Cerný et al., 2007; Behar et al., 2008) but also seen in North African groups (Córte-Real et al., 1996; Krings et al., 1999; Kivisild et al., 2004). Overall, mtDNAs belonging to sub-Saharan African mtDNA haplogroup L are prominent in African–American populations, comprising up to 86% of the mtDNAs in them (Salas et al., 2002, 2004, 2005; Behar et al., 2008). Similar patterns were also observed in studies of mtDNA, Y-chromosome, and autosomal genetic markers in Caribbean populations, reflecting the impact of the Trans-Atlantic slave trade in 16th through 19th centuries (Martinez-Crusado et al., 2005; Benn-Torres et al., 2007; Simms et al., 2008).

On the basis of comparisons of the genealogical and genetic data, we determined that the mtDNA of the main female ancestor of the tribe, a Wampanoag woman, belonged to L3e. In general, L3e haplotypes occur at significant frequencies in sub-Saharan African populations (Bandelt et al., 2001; Salas et al., 2002, 2004; Kivisild et al., 2006). However, while not especially common, this particular haplotype (no. 13) was similar to those previously reported in African–American and African populations (Bandelt et al., 2001), and most closely resembled haplotypes originally seen in Bantu-speaking Yao and Ronga groups in Mozambique (Salas et al., 2002). In fact, all tribal members who traced their direct maternal ancestry to this Wampanoag female ancestor shared this haplotype, confirming written and oral genealogical records of the tribe.

A minority of the Seaconke Wampanoag individuals had mtDNAs belonging to West Eurasian haplogroups H and I. Most of them belonged to haplogroup H, the most common maternal lineage in European populations (e.g., Achilli et al., 2004; Loogväli et al., 2004).

Y-chromosome diversity

The analysis of NRY SNPs and STRs revealed 8 distinct haplogroups and 13 haplotypes in the 17 male participants (Tables 3 and 4). Similar to the mtDNA data, the paternal gene pool consisted of predominantly African and West Eurasian lineages (Fig. 3b,d).

However, we also detected a small number of Native American haplotypes that belonged to haplogroup Q1a3a, which is widespread among Amerindian populations (Bortolini et al., 2003; Zegura et al., 2004; Bolnick et al., 2006). A detailed evaluation of tribal genealogical data revealed that the Q1a3a haplotype (no. 9) had likely been introduced through intermarriage with an individual having Cherokee ancestry several generations

TABLE 2. mtDNA control region sequence and coding region SNP data

No.	Hg	N	HVS1 (+16,000)	HVS 2	G1719A	T2352C	C3594T	C7028T	A7055G	C7256T	G8251A	A8701G	T9540C	T10873C	A10398G	C12705T	C13650T	A13803G	C14766T
1	H	1	CRS	263-309.1C-315.1C															
2	H	1	129-311	263-309.1C-315.1C															
3	H	1	366	55-57-263-309.1C-315.1C															
4	H	1	295	263-315.1C															
5	I	1	129-172-223-311-391	73-199-203-204-250-263-315.1C	+			+			+				+	+			+
6	L0a1	1	129-148-168-172-187-188G-189-223-230-311-320-362	93-185-189-200-236-247-263-315.1C			+	+	+	+		+	+	+	+	+	+		+
7	L1c	1	129-187-189-223-278-293-294-311-360	73-151-152-182-186A-189C-247-263-265-315.1C-316			+	+	+	+		+	+	+	+	+	+		+
8	L1c3	1	129-163-187-189-223-278-293-294-304-311-360	73-151-152-182-186A-189C-195-247-263-315.1C-316			+	+		+		+	+	+	+	+	+		+
9	L2a	1	086-183C-189-192-223-278-294-309-390	73-146-152-195-263-315.1C			+	+		+		+	+	+	+	+	+	+	+
10	L2a	1	189-223-278-286-294-309-390	73-143-146-152-195-263-315C			+	+		+		+	+	+	+	+	+	+	+
11	L2a	3	189-223-278-286-294-309-390	73-146-152-195-263-315C			+	+		+		+	+	+	+	+	+	+	+
12	L3b	1	129-209-223-288-292-295-311	73-189-200-263-309.1C-315.1C	+			+			+	+	+	+	+	+			+
13	L3e	11	172-183d-191.1C-192.1C-223-320	73-150-195-263-309.1C-315.1C		+		+				+	+	+	+	+			+
14	L3e	1	189-223-311-327	73-150-189-200-204-263-309.1C-315.1C		+		+				+	+	+	+	+			+
15	L3e	2	172-183C-189-223-320	73-150-195-263-309.1C-309.2C-315.1C		+		+				+	+	+	+	+			+

Note: Mutation positions and nucleotide substitutions are indicated according to the rCRS (Andrews et al., 1999), with the numbers for the HVS1 starting from np 16,000 (e.g., 129 = 16,129) and ending at 16,400. Those for HVS2 begin at np 50 and end at 372. The G3693A, C10400T, and G14783A mutations were not present in any of the samples.

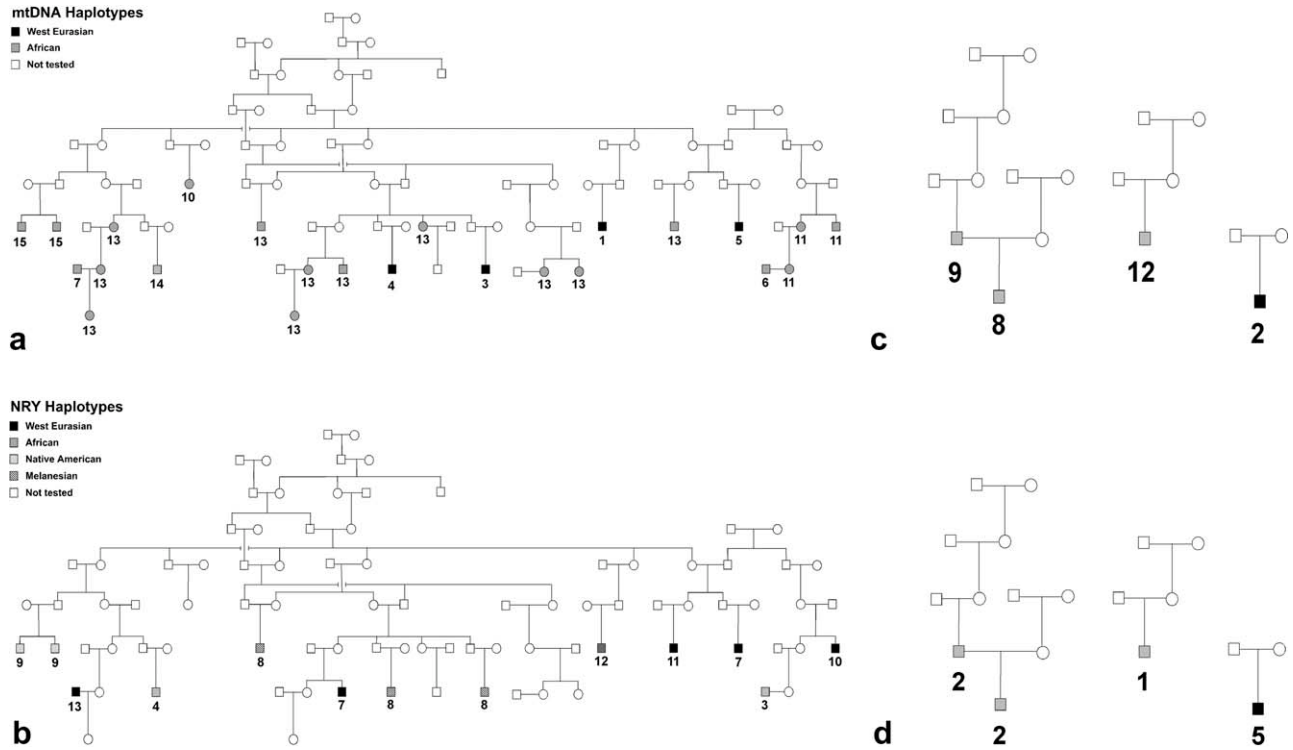

Fig. 3. The distribution of maternal and paternal haplogroups in the Seaconke Wampanoag tribe. The colors of the symbols indicates the general geographic region from which the haplotypes are thought to have originated; the numbers of the haplotypes shown below the individual symbols correspond to those indicated in Tables 2, 3, and 4; (**a**) Citizens mtDNA haplogroups; (**b**) Citizens Y-chromosome haplogroups; (**c**) Friends mtDNA haplogroups; (**d**) Friends Y-chromosome haplogroups.

ago. Further comparison of the STR profile of this Q1a3a haplotype with those from other North American Indian populations confirmed the existence of closely related haplotypes in the Cherokee, Chickasaw, and Seminole populations from the US Southeast (see Bolnick et al., 2006).

Surprisingly, one of the NRY Seaconke haplotypes (no. 8) that represented a primary male ancestor of the tribe possessed the M230 marker, which indicated that it belonged to haplogroup S [formerly K-M230] (Karafet et al., 2008) (Tables 3 and 4). Haplotypes from this paternal lineage are commonly observed in different populations from Papua New Guinea and Melanesia (Kayser et al., 2003; Karafet et al., 2005; Friedlaender et al., 2006; Scheinfeldt et al., 2006; Hudjashov et al., 2007), but have not previously been reported for Native American populations. According to the Seaconke Wampanoag genealogical records, this male ancestor was an 18th century sailor from Australia who settled in the New England area, and married a Wampanoag woman. Based on this information, it had been assumed that this individual was of European descent. However, in light of the new information about his Y-chromosome haplotype, this man clearly appears to have had Melanesian paternal ancestry.

Several individuals had Y-chromosomes that belonged to African haplogroup E1b1a, while another's belonged to E1a (Tables 3 and 4). These haplogroups are among the most common paternal lineages seen in African populations (e.g., Underhill et al., 2001; Semino et al., 2004), with the highest frequencies of E1b1a being found in Bantu-speaking groups (Knight et al., 2003; Rosa et al., 2007). These findings are consistent with the history of slave importation from West, Southeast, and Southwest Africa. They also reflect the tendency of members of isolated Indian communities to intermarry with members from other marginalized societies in North America (Abbott, 1903; Salisbury, 1984; Newell, 2001; Philbrick, 2006).

The remaining NRY haplotypes belonged to West Eurasian lineages. Haplogroups E1b1b1, G2a, and J2a were represented by single haplotypes, and R1b1b2 was detected in four paternally unrelated tribal members, whose haplotypes differed by their STR profile (Tables 3 and 4). R1b1b2 (formerly R1b3) is delineated by the presence of M269 marker, and is a common lineage in Western Europe ([haplogroup 1 in Scozzari et al., 2001]; Cruciani et al., 2002; Tambets et al., 2004; Karlsson et al., 2006), although it appears at its highest frequencies in the Iberian Peninsula and Ireland (Alonso et al., 2005; Moore et al., 2006). By contrast, haplogroup G occurs frequently in the Caucasus, Turkey, and Near East (Semino et al., 2000; Al-Zahery et al., 2003; Nasidze et al., 2003; Cinnioglu et al., 2004), while J2 is ubiquitous in the Near East and Mediterranean region (Al-Zahery et al., 2003; Behar et al., 2004; Cinnioglu et al., 2004; Zalloua et al., 2008).

In an effort to ascertain the possible source areas of the R1b1b2 Y-chromosomes, we searched the Y-chromosome Haplotype Reference Database (YHRD; www.yhrd.org) to find matches with our STR haplotypes. When using the full 17-STR profiles presented in Tables 3 and 4, we found no matches. However, after reducing the number of STRs being used to define the haplotypes to seven loci (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, and DYS393) to compare our data to

TABLE 3. Y-chromosome haplotypes defined by SNPs

No.	N	Hg	M139	M168	M96	M33	PN2	M2	M35	M89	M201	P15	M304	M172	M410	M9	M230	M45	M242	M346	M3	M207	M173	M343	P25	P297	M269
1	1	E1a	+	+	+	+																					
2	2	E1b1a	+	+	+		+	+																			
3	1	E1b1a	+	+	+		+	+																			
4	1	E1b1a	+	+	+		+	+																			
5	1	E1b1b1	+	+	+		+		+																		
6	1	G2a	+	+						+	+	+															
7	1	J2a	+	+						+			+	+	+												
8	3	S	+	+						+						+	+										
9	2	Q1a3a	+	+						+						+		+	+	+	+						
10	1	R1b1b2	+	+						+						+		+				+	+	+	+	+	+
11	1	R1b1b2	+	+						+						+		+				+	+	+	+	+	+
12	1	R1b1b2	+	+						+						+		+				+	+	+	+	+	+
13	1	R1b1b2	+	+						+						+		+				+	+	+	+	+	+

TABLE 4. Y-chromosome haplotypes defined by STR alleles

No.	N	Hg	DYS19	DYS385	DYS388	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS426	DYS437	DYS438	DYS439	DYS448	DYS456	DYS458	DYS635	Y_GATA_H4
1	1	E1a	18	13-16	12	12	30	22	10	12	12	11	16	10	11	19,20	15	15	20	11
2	2	E1b1a	15	15-18	13	14	31	22	10	11	13	11	15	11	12	21	15	15	22	10
3	1	E1b1a	16	16-16	14	12	30	21	10	11	14	11	14	10	11	22	15	17	21	12
4	1	E1b1a	15	15-17	12	12	29	21	11	11	13	11	14	11	13	22	15	17	21	12
5	1	E1b1b1	13	17-19	12	13	31	24	10	11	13	11	14	11	12	18	16	15	22	11
6	1	G2a	16	14-15	12	12	28	22	10	11	14	11	16	11	11	21	15	16	20	13
7	1	J2a	15	13-18	17	13	29	23	09	11	12	11	14	09	11	21	15	14	22	13
8	3	S	14	12-19	11	13	30	22	10	13	13	11	15	09	11	16	15	17	22	12
9	2	Q1a3a	13	15-16	12	13	31	23	10	14	14	12	14	11	11	21	14	14	22	12
10	1	R1b1b2	14	11-14	12	13	29	25	11	13	13	12	15	12	12	19	16	16	23	11
11	1	R1b1b2	14	11-14	12	13	29	22	10	13	13	12	14	12	13	18	17	17	23	11
12	1	R1b1b2	14	11-15	12	13	29	23	11	13	13	12	15	12	12	19	18	17	23	11
13	1	R1b1b2	14	11-15	12	13	29	24	11	13	13	12	15	12	11	19	16	18	23	12

Note: The nomenclature for haplogroups follows the conventions established in Y-chromosome Consortium (2002) and Karafet et al. (2008). The following Y-SNPs were assayed but are not present in this population (LLY22g, M12, M17, M19, M20, M60, M69, M70, M75, M81, M91, M102, M107, M123, M124, M130, M148, M170, M174, M175, M186, M191, M194, M199, M253, M267, M285, P37.2, P215).

a greater number of samples/populations in the YHRD, we found matches between our R1b1b2 haplotypes and those seen in Western Eurasia. Unfortunately, these matches were not specific to any region or country, thereby preventing us from identifying the specific geographic origin of these haplotypes.

DISCUSSION

Genetic ancestry of the Seaconke Wampanoag

Genetic analysis of members of the Seaconke Wampanoag Tribe, who claim ancestry from Indian populations that traditionally inhabited New England, reveals a complex mixture of maternal and paternal lineages of Native American, Melanesian, African, and European derivation. The high frequency of nonnative haplotypes in this population, along with the paucity of Native American haplotypes, reveals the substantial changes in the genetic composition of the Seaconke Wampanoag Tribe in post-contact American history. This pattern has also been observed in other Native American tribes of North America (e.g., Santos et al., 1996; Huoponen et al., 1997; Malhi et al., 2003; Bolnick et al., 2006).

While our study did not find any maternal Native American lineages in the Seaconke Wampanoag tribe, we did detect a Q1a3a paternal haplotype in this group. How closely this Q1a3a haplotype resembles those originally present in Wampanoag groups or other Algonquian populations is not entirely clear, as the individual possessing this haplotype had male descendants from a Cherokee community to the south. Both cultural and linguistic evidence indicate that the Cherokee recently migrated to southern Appalachia from the lower Great Lakes region, where Algonquian populations reside (Bushnell, 1922; MacNeish, 1952; Goddard, 1978; Snow and Lamphere, 1988; Potter, 1993; Snow, 1994). Unfortunately, other NRY studies of Algonquian populations did not analyze their Y-chromosomes for the same 17-STR panel that we used, making an exact comparison of their haplotypes with those observed in the Seaconke Wampanoag difficult. In any case, the shift in the genetic composition of Indian tribes from the northeastern US may reflect both the demographic impact of European colonization and historical admixture involving marriage with persons from nonnative communities, resulting in the replacement of Native American mtDNA and NRY lineages with nonnative ones (e.g., Karttunen, 2005).

In contrast, the Seaconke Wampanoag have a unique indigenous background relative to other Indian populations from the region based on the presence of NRY haplogroup S in some of its male members. This paternal lineage has a strong geographic focus in Indonesia and Melanesia, and the haplotype of one of the main paternal ancestors is clearly linked to those seen in that region (Kayser et al., 2003; Karafet et al., 2005; Friedlaender et al., 2006; Scheinfeldt et al., 2006; Hudjashov et al., 2007). Such a finding attests to the demographic impact that European colonization had on both the Americas and Australasia, including the mixing of persons of geographically separated indigenous communities through slavery, employment in the shipping and whaling industries, and other colonial economic activities, which brought people from various different continents into contact with one another (Howe et al., 1994; Gray, 1999; Vickers, 2000; Equaino, 2007).

The prevalence of sub-Saharan African maternal and paternal haplotypes in this group undoubtedly reflects the influence of the Trans-Atlantic slave trade on the genetic make-up of colonial America and the emergent United States, and the removal of people from different areas of West Africa (e.g., Bandelt et al., 2001; Salas et al., 2002, 2004, 2005). It also points to historical intermarriage between natives and enslaved or freed African slaves, a practice that became increasingly common in Northern states after emancipation acts were passed, beginning in Massachusetts in 1780 (Moore 1866,; Belz, 1978; Jones, 1999; Blank, 2002). Similar historical shifts in genetic composition have been shown for other Native American populations, most of which experienced significant bottlenecks following the colonization of Americas (e.g., (Mulligan et al., 2004; Schurr, 2004; Bolnick et al., 2006).

Similarly, the presence of West Eurasian mtDNAs and Y-chromosomes in the Wampanoag gene pool likely reflects the influence of continuous European contact with Indian tribes of New England since the 17th century, during which time these lineages were introduced into them. The increased frequency of these haplogroups likely reflects the degree of intermarriage between members of native and nonnative communities, especially since the 19th century. It further supports Seaconke Wampanoag tribal history, which indicates that Indian individuals had married into colonial European families.

Overall, the observed pattern of genetic diversity in the Seaconke Wampanoag tribe indicates that most of its NRY haplotypes and all of its mitochondrial haplotypes are nonindigenous in origin. However, in this regard, it should be noted here that the genetic markers used in this study survey only a small fraction of the total human genome for variants that are useful for reconstructing human phylogeography. The remainder of the genome that was not examined also provides information about individual and population histories, as do written records and oral traditions. Thus, while providing insights into the familial and genetic histories of Citizens of the Seaconke Wampanoag tribe, the uniparentally inherited marker systems used in this analysis do not completely define them, biologically speaking, nor provide a full picture of their population history. In this respect, the investigation of autosomal variation in this community may reveal new details about the genetic contribution of indigenous ancestors.

At the same time, the genetic data clearly support the extensive genealogical information and tribal records gathered by the Seaconke Wampanoag Tribe. Some of these genealogical records indicate Native American ancestry in past generations that would not appear through the analysis of mtDNA and Y-chromosome variation because direct maternal and paternal links to indigenous ancestors had been lost due to population loss or admixture. Together, these sources of information have allowed us to trace the familial connections of the Seaconke Wampanoag community back to the early 18th century. Our data also reflect the profound impact of historical factors on the cultural, linguistic, and genetic make-up of Indian communities in New England. They further highlight the complexity of indigenous identity of tribes from this region, and underscore the importance of honoring the distinct peoples and cultures that historically inhabited North America.

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