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CIJE: Current Index to Journals in Education
Current Contents (in Dialog #440)
Humanities International Complete
Humanities International Index (formerly American Humanities Index)

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Appalachian Journal

A REGIONAL STUDIES REVIEW

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Toward a Genetic Profile of Melungeons in Southern Appalachia

DONALD N. YATES AND ELIZABETH C. HIRSCHMAN

Don Yates is the owner and principal investigator of DNA Consultants in Phoenix, Arizona. Born in Cedartown, Georgia, of Choctaw-Cherokee and Sephardic Jewish ancestry, he has a doctorate in classical studies from the University of North Carolina at Chapel Hill. He has a lifetime interest in Native American studies and genealogy research, and he worked for a decade at the biotechnology company Miles Laboratories (now Bayer Corporation). He has co-authored with Elizabeth Hirschman several books and articles, including Star, Crescent and Cross: Jews and Muslims in Colonial America (McFarland, forthcoming 2011), “Peering Inward for Ethnic Identity: Consumer Interpretation of DNA Test Results” (Identity, 8:1, Jan. 2008), and When Scotland Was Jewish: DNA Evidence, Archeology, Analysis of Migrations, and Public and Family Records Show Twelfth Century Semitic Roots (McFarland, 2007). His most recent work is Old Souls in a New World: Greeks, Jews and Egyptians in Native America, the story of a 3rd-century BCE Greek-speaking expedition from Ptolemaic Egypt that established the international dateline and coincidentally founded the Cherokee Nation. A member of Genealogical Speakers Guild, he is a frequent speaker and widely interviewed media spokesman on DNA testing for ancestry and ethnicity, especially autosomal DNA tests, and Native American genetics, particularly that of Old Cherokee families.

Beth Hirschman, professor of marketing at Rutgers University, has published more than 200 articles in marketing, consumer behavior, sociology, and semiotics. Her recent publications include “Bluegrass Revival: Marketing and Authenticity in the Hills of Appalachia” in Marketing the Arts (London: Routledge, 2010), “The Role of Marketing in Ancient and Contemporary Cultural Evolution” in The Sage Handbook of Marketing Theory (London: Sage, 2009), and “Suddenly Melungeon: Reconstructing Consumer Identity on the Other Side of the Color Line” in Research in Consumer Behavior. Vol. 11: Consumer Culture Theory (2007). She is co-author of Two Continents, One Culture: The Scotch-Irish in Appalachia (Overmountain Press, 2006) and author of Melungeons: The Last Lost Tribe in America (Mercer Univ. Press, 2005). She has made presentations on ethnicity and DNA testing at annual meetings of the Transformative Consumer Research Conference; the Consumer Culture Theory Conference; the International Conference on Diversity in Organizations, Communities, and Nations; the Society for Jewish Studies; and the Melungeon Heritage Association.

Introduction

Melungeons are an elusive and controversial subject in American social history (see e.g., DeMarce 1996; Hirschman and Yates 2007a; Hirschman 2003). Their population center is placed conventionally in the lower Appalachians in the contiguous region of southwestern Virginia, eastern Tennessee, southeastern Kentucky and western North Carolina (see e.g., Guthrie 1990). While often said to constitute a tri-racial isolate people, others have proposed that the Melungeons are descendants of early Portuguese, Spanish, Sephardic Jewish, Muslim Moorish, and/or Gypsy/Roma colonists in the southeastern United States (Kennedy 1997; Hirschman 2005; Price 1953). Still other researchers have questioned whether Melungeons diverge significantly in ancestry from other colonial-era settlers (DeMarce 1996). Despite these reservations, the so-called Melungeon Movement sparked by publication of N. Brent Kennedy’s book (1997) shows little sign of abatement today (see e.g.,

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Winkler 2004). There is a Melungeon Registry at the Wise County Historical Society, and genetic disorders such as familial Mediterranean fever (FMF) are being diagnosed and treated in Appalachian regional medical centers thanks to increased awareness and advocacy efforts. Although non-technical and non-academic in nature, books and articles continue to pour forth from members of the community (Alther 2007; Ball 1992; Elder 1999; Johnson 1997; Winkler 2004).

To help sort through the multiple suggested origins of the Melungeon people, we assembled a sample of 40 self-identified Melungeon descendants whose DNA we analyzed to provide additional information regarding their ancestral origins and ethnicity.1 This article reports the probabilistic predictive results of Melungeon ethnicity and ancestry from that study. We reach some tentative conclusions about genetic structure and demographic history that we hope will help stimulate further investigation into Melungeon ancestral origins and related sociocultural factors.

Subjects and Methods

Population Sample

A sample of 40 participants was selected for testing; persons were deemed eligible for the study based on self-identification of Melungeon ancestry, as has been the case in all prior published studies (see, for example, Guthrie 1990). While not a large number, this is an acceptable size for preliminary studies of sparse or isolated populations, such as American Indian tribes or diasporic ethnic groups such as the Amish. Most participants were current or prior subscribers to Nancy Sparks Morrison’s Melungeon Health e-mail discussion group, a focal point for dissemination of information about health issues and genetic screening of interest to Melungoens, or were related to a subscriber. A few were actively recruited for the study and had their tests paid for in the interest of gaining as many subjects as possible. All sample donors were either adults or children for whom a responsible parent signed, and appropriate informed consent was obtained in each case. Each participant was responsible for collecting a cheek swab sample and submitting it to the laboratory, Sorenson Genomics, Salt Lake City, Utah. The laboratory was unaware of the study or the purpose of the individual testing.

Of the participants, 21 were born in East Tennessee and had multi-gener-
ational roots there. The birthplace of about 20 percent was unknown. Most of the remaining came from states adjacent to East Tennessee, including North Carolina (3), Virginia (2), and Kentucky (2). Some individuals in the sample were closely related. Nine came from a single extended family represented by four generations from East Tennessee. There were 11 siblings and 11 parent-child pairings. Even those who were not closely related were often distantly connected. Surnames from participants’ genealogies were consistent with a list published by Kennedy (1997) posted on the Melungeon Health website. Those evidently of Melungeon association prima facie included Adams, Barnett, Caldwell, Carter, Collins, Cooper, Douglas, Elliott, Goode, Goodman, Goins, Hall, Jones, Kennedy, Mize, Ramey, Sparks, Starnes, and Stewart.

Background
The scientific stimulus toward using genetics to study human diversity and biological relationships occurred in the 1990s, when certain locations on the Y chromosome were identified as being of diagnostic use in typing male crime suspects (Butler 2006). The same characteristic repetitive chemical motifs on the genome of an individual, called short-tandem-repeats (STRs) or alleles (variations), were found useful for determining paternity or maternity, as well as other relationships (e.g., sibling, cousin).

A crystallizing event occurred when Karl Skorecki, a Canadian nephrologist of Ashkenazi (German, Polish, Lithuanian, Russian, or other Eastern European Jewish) parentage, attended synagogue one morning and noticed that a Sephardic (Spanish or Western European Jewish) congregant with the name Cohen seemed to have different physical features from the Cohens he knew. According to traditions of Judaism, Cohens are descended from the same male ancestor, the patriarch Aaron, brother of Moses, who was founder of the line of Old Testament priests. As such, men with the last name Cohen (or a form close to it, such as Cone) are regarded as members of the hereditary Jewish priestly caste. In temple services, they are called upon to come forth first to the pulpit and read from the Torah. Dr. Skorecki reasoned that if Kohanim (plural of Kohane, “priest” in Hebrew) were indeed the descendants of only one man, they should have a common set of genetic markers and might even preserve some family resemblance to each other. They would have the same Y chromosome signature as Aaron, since Y chromosomal genetic material is passed from father to son, virtually unchanged, generation after generation.

To test that hypothesis, Skorecki contacted Michael Hammer of the University of Arizona, a researcher in molecular genetics and pioneer in mapping global Y chromosome distributions from prehistoric human migrations. Their article in Nature (Skorecki et al. 1997) showed that a particular genetic pattern was indeed more likely to be present in Jewish men with Cohen-like surnames than in the general Jewish population or in Arabs and others who shared male descent from that branch of the human evolutionary tree. It came to be known as the Cohen Modal Haplotype.
Articles in scholarly publications, inspired by the success of Skorecki’s team, have since tackled such disparate subjects as the origins of the British people, the founding mothers of world Jewry, the North African legacy in Spain’s genetic history, the genetic footprint of the Mongols in history, and the peopling of the Americas (Oppenheimer 2006; Sykes 2006; Thomas et al. 2002; Bosch et al. 2003; Zerjal et al. 2003; Malhi 2001).

The techniques of tracing male and female descent are now generally accepted (Jobling and Tyler-Smith 2003; Sykes and Irven 2000; Richards and Macaulay 2001), with the nomenclature and phylogeny of male and female haplogroups becoming standardized (Semino et al. 2000; Y Chromosome Consortium 2002; Richards et al. 2000). For the present study, however, we used a more recent and potentially more powerful DNA testing approach—autosomal DNA analysis. This method of genotyping examines markers that are spread across the 22 human chromosomes not linked to gender. It has the potential of illuminating one’s total genetic inheritance, including deep, interwoven or hidden ancestry, and not just male or female demographic history. In genome-wide disease association studies, medical researchers today sequence hundreds or even thousands of such markers in an individual. On a smaller scale, genotyping technology in forensic science targets 14 sites, a standard adopted by the Federal Bureau of Investigation and termed Combined DNA Index System or CODIS markers. Autosomes or genome-wide genetic systems have been adapted, among other applications, to study why indigenous American populations were susceptible to European disease, to explain early Homo Sapiens’ triumph over Neanderthals, and even to set free wrongfully jailed prisoners and condemned inmates on death row.

Methodology

At the time this study was undertaken, there were two autosomal ancestry tests available and feasible for us to employ: an admixture test called AncestryByDNA 2.5 co-invented by researchers at Pennsylvania State University and DNAPrint Genomics of Sarasota, Florida (Halder et al. 2008; Frudakis 2005; Shriver and Kittles 2004) and the DNA Fingerprint Test, a product developed by DNA Consultants on the platform of a forensic database called OmniPop created by detective Brian Burritt of the San Diego (California) Police Department (Burritt 2006). The DNA Fingerprint Test was selected for several reasons. It was more recent, less expensive, and more informative than AncestryByDNA 2.5. Base measures of continent-specific admixture and biogeographical ancestry similar to those provided by AncestryByDNA already had been estimated for a sample of Melungeons in a previous DNA study using male and female haplotypes (Jones 2004). The DNA Fingerprint Test would yield more than just percentages of European, Sub-Saharan African, Native American, and East Asian ancestry, the four ethnicities that were the focus of AncestryByDNA. The DNA Fingerprint Test was capable of making probabilistic predictions about the relative contribution of sub-populations involved in all four of these broad
Figure 1. Sample lab report with CODIS scores

<table>
<thead>
<tr>
<th>Genetic System</th>
<th>Allele Designation</th>
</tr>
</thead>
<tbody>
<tr>
<td>CSF1PO</td>
<td>11, 11</td>
</tr>
<tr>
<td>D2S1338</td>
<td>16, 24</td>
</tr>
<tr>
<td>D3S1358</td>
<td>16, 18</td>
</tr>
<tr>
<td>D5S818</td>
<td>11, 11</td>
</tr>
<tr>
<td>D7S820</td>
<td>9, 10</td>
</tr>
<tr>
<td>D8S1179</td>
<td>12, 14</td>
</tr>
<tr>
<td>D13S317</td>
<td>9, 13</td>
</tr>
<tr>
<td>D16S539</td>
<td>9, 13</td>
</tr>
<tr>
<td>D18S51</td>
<td>15, 18</td>
</tr>
<tr>
<td>D19S433</td>
<td>13, 14</td>
</tr>
<tr>
<td>D21S11</td>
<td>30, 32</td>
</tr>
<tr>
<td>FGA</td>
<td>20, 21</td>
</tr>
<tr>
<td>TH01</td>
<td>6, 9</td>
</tr>
<tr>
<td>TPOX</td>
<td>11, 11</td>
</tr>
<tr>
<td>vWA</td>
<td>19, 19</td>
</tr>
</tbody>
</table>

As already mentioned, buccal cells were obtained from participants and viable specimens of their DNA were extracted. The samples were amplified by a process known as polymerase chain reaction (PCR) at the following 15 loci standardized in the FBI’s kit Profiler Plus: CSF1PO, D2S1338, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D19S433, D21S11, FGA, TH01, TPOX, and vWA. Results for an individual might look like this (see Figure 2).

In Figure 1, the scores in the column labeled Allele Designation represent pairs of values received from both parents. For example, in the locus known as FGA, where the allele reads 20, 21, the first number may have come from the mother, where it was part of her allele with another individual score (perhaps 20, 24) while the second number was inherited from the father (whose score on that allele may have been 21, 21). Alleles or variations at a given site combine to create an individualized DNA fingerprint. One’s DNA fingerprint is derived equally from one’s mother and father; theirs is derived in equal measure from their parents, and so on. Because of the process of recombination, the DNA Fingerprint reflects both the mother’s and father’s cumulative and combined genetic heritage, although it does not indicate what comes from which side or from any specific line in one’s genealogy. It is an overall, comprehensive analysis.

**OmniPop**

Most personal DNA profiles have a likelihood of one in one trillion of occurring in another randomly sampled individual. If populations are considered rather than individuals, each unique genetic profile produced by CODIS scores has a given mathematical probability of being present in a certain population, as defined in forensic studies. This statistic is termed its random match probability (RMP). The profile may be relatively common in one population, say among Portuguese people, and relatively uncommon in others, say in Scandinavian populations. By searching the population database (at the time, OmniPop 300.3, containing published genetic profiles gathered from over 300 modern-day populations), we can determine the primary populations ("matches") in which that profile is likely to have arisen in relatively high frequency over the past few centuries. From these matches we can infer geographical places of origin within a meaningful time depth.
ENSFI
In addition to OmniPop's worldwide samples, it is possible to compute statistically probable Europe-only ancestry through the database of the European Network of Forensic Science Institutes (ENFSI). This resource contains data from 24 populations in the European Union (n = 5,700 personal profiles). ENFSI incorporates a different array of CODIS markers than the U.S. standard, namely the AmpFLSTR SGM Plus kit adopted as a norm by the European Union. However, the reliability of the outcome is the same. As concerns validity, both approaches are approximately 80 to 90 percent accurate in predicting ethnicity (Burritt 2006). Granted, this is a rather modest confidence level, but autosomal ancestry testing is a field in its infancy. As the databases grow and additional populations with more complete and commensurate sets of markers are added, autosomal profiling is expected to gain in precision. Moreover, the 18 Marker Ethnic Panel enhancement introduced by DNA Consultants in August 2009 addressed several key "false negatives" or statistical noise issues. Improvements in the future are expected to isolate the country of origin of specific rare alleles inherited by individuals in a new product line featuring what might be called autosomal outliers, an ideal tool for Melungeon, Native American, Roma, and like studies.

To our knowledge, the only other genetic study on Melungeons within the past decade was conducted by Kevin Jones (2004). Unfortunately, the results of that study have never been published and the sampling protocol is unknown. The present study is the first to use autosomal DNA markers to analyze Melungeon ancestry. Older studies used either blood type systems or DNA haplotypes (see e.g., Guthrie 1990).

Findings
Across OmniPop and ENFSI, the top population matches (i.e., inferred biogeographical ancestry) showed notable levels of Jewish (both Ashkenazi and Sephardic), Middle Eastern, Native American, Sub-Saharan African, and Iberian ancestry within our Melungeon descendant sample. There were also intermittent indications of Roma/Gypsy in genealogies of certain individuals. We address each of these observations below.

Jewish and Middle Eastern Ancestry
Over the past two decades, much scientific and medical attention has been focused on Jewish genetics (Behar et al. 2003; Behar et al. 2004; Hammer et al. 2000; Motulsky 1995; Nebel et al. 2002; Thomas et al. 1998; Thomas et al. 2000; Thomas et al. 2002; Semino et al. 2004). ("Jewish," like Gypsy, Amish, and other designations, is used by geneticists, and is employed by us here as well, not as a religious denomination or cultural term but a name for a coherent, historical people with a common geographical origin and continuity of existence.) Most of these studies suggest that the presence of male haplogroups
J and E3b together with female haplogroups J and K, and occasionally H and U, are robust indicators of Jewish ancestry.

We were fortunate to have autosomal population data on both Sephardic and Ashkenazi Jews (Picornell et al. 2002 and Egyed et al. 2006). Comparing these data with our Melungeon subjects, we found significant indications of Jewish heritage. Twenty-four of our participants (60 percent) had strong matches with Sephardic Jews. Ashkenazi ancestry could be traced in 10 of the participants, or about one-fourth. Within the members of one large Melungeon family from East Tennessee, Ashkenazi ancestry was present alongside high levels of Sephardic Jewish, Spanish, Portuguese, North African, Middle Eastern and Roma/Gypsy. In others, Ashkenazi ancestry occurred together with salient amounts of Polish, Russian, Belarusian, Austrian, Sephardic, Algerian, and Tunisian. Several participants seemed to have fairly equal and comparable Sephardic and Ashkenazi Jewish matches. One sociocultural inference might be that the Melungeon population united otherwise disparate and separated elements of Sephard and Ashkenaz. To pursue this line of thought, one might venture to hypothesize that Melungeons practiced a syncretistic form of Judaism combining Sephardic and Ashkenazi customs. The impetus for such a fusion might have been the events following the inception of the Spanish Inquisition in the 15th century, when Sephardim were forced to flee Spain and Portugal and seek safe-haven with Ashkenazi Jews in Germany, France, and the Low Lands.

Several participants seemed to have Ashkenazic and Sephardic ancestry in conjunction with North African and Middle Eastern ancestries, particularly from Morocco, Tunisia, Algeria, Libya, Egypt, Syria, and Turkey. One participant had Ashkenazi as the strongest match, combined with Polish, Russian, Syrian, and Tunisian. This particular individual had a family origin story about Jewish ancestors that was ultimately confirmed through additional genealogical research and genetic testing. In another case, Ashkenazi Jewish was only a medium-strong match, although nearly all Arabic populations were represented in this individual's Top 20 world matches, particularly Egypt, Morocco, and Turkey, while Tunisia was No. 2. This suggested the possibility of Arab/Berber lines distinct from Jewish ancestry being present in the Melungeon population. In other words, this person's forebears may have carried ancestry originating within the Muslim world, as opposed to Christian Europe. A likely time frame for the blending of these populations falls in the 15th through 17th centuries, when the Islamic Ottoman Empire was in ascendancy on the world stage and attracted many Jewish refugees from Spain and Portugal.

**Middle Eastern**

Strong indications of Middle Eastern ancestry were present in the profiles of 20, or one-half, of the participants, often co-present with Jewish ancestry. A population classed as Middle Eastern ranked No. 1 in seven cases. These included Afghanistan (1), Algeria (2), Coptic/Egyptian (3), Saudi Arabia (1), and
Syria (2). Some of the Middle Eastern matches occurred in tandem with signs of Roma/Gypsy heritage.

**Roma/Gypsy**

The Roma (i.e., Romani, Sinti, Gypsies) have been studied extensively and there is little disagreement about their genetic origins (Iovita and Schurr 2004). Gypsy origins and migrations have been divided into three periods: 1) their migration out of predominantly Rajput and Punjabi populations in the Indian subcontinent westward into Islamic territory under the pressure of conquering Muslim generals like the Ghaznavids of the 12th century, until they reached Southeast Europe in about the 15th century, and thence into Northern and Western Europe; 2) 17th- and 18th-century expansion from Moldo-Wallachia and Hungary, and 3) a 19th- and 20th-century exodus from the Romanian Old Kingdom following the abolition of Gypsy slavery (Iovita and Schurr 2004 p. 279). More recently, scholars like Avraham Sándor have exposed the non-Indo-Aryan and Semitic sources of Gypsy culture and genetics in an original homeland partially retraced in their historical migratory routes and corresponding to Canaanite, Egyptian, and Hurrian populations in the ancient Middle East (Sándor n.d.a). With this background in mind, it is interesting to note that matches to one or more of the three Roma/Gypsy populations in OmniPop (Egyed et al. 2006; Havas et al. 2006; Novokmet and Pavcev 2007) occurred in high positions in one-fourth (10) of participants, usually alongside Indic matches, and Middle Eastern matches such as Egypt, Syria, Turkey, Iraq, and Afghanistan.

In one extended family, Romani matches appear to run through several generations, with Khandayat in northern India being the top match for one uncle, Turkish the top match for a father, as well as prominent in his children, and East Indian being the top match for the mother of the same. This geography replicates the trail of the Romani out of India into Asia Minor, their former homeland, and Southeast Europe, then part of the Ottoman Empire. For a prominent leader in the Melungeon Movement who requested anonymity, Gypsy ancestry was found combined with Indic and Arab matches. For another participant, the top matches were 1. Syrian, 2. Romani (Macedonian), 3. Macedonian, 4. Polish, 5. Romanian (Székler), 6. Romani (Croatia), 7. Oriya Brahmin (again, northern India...), 8. Hungarian (Eastern Romanian)... and 15. Rajput (northern India). If we search for the Gypsy origin in early American history, we might suspect a large influx of Gypsies from the 1720 effort of French finance minister William Law's agent, Elias Stultheus, to plant a colony in what became Tennessee, the so-called Mississippi Bubble.

**Berber/North African**

Matches to Berber and other North African populations (e.g., Saharan) were restricted to certain families and often were combined with apparent Jewish, Sub-Saharan African, Spanish, Portuguese, and Native American ancestries.
Paul Wexler in *The Non-Jewish Origins of the Sephardic Jews* (1996, pp. 12-13) maintains that modern-day Sephardic Jews stem primarily from ancient North African Berber proselytes who merged with later converts to Judaism on the Iberian Peninsula. This process took place in three phases: first, in North Africa in the 7th and early 8th centuries pursuant to the Arab settlement of North Africa; then, in the Iberian Peninsula between 711 and 1492 (the respective dates of the Muslim invasion and expulsion of the Jews from the Kingdom of Spain by its Christian monarchs); and finally, again in North Africa after 1391, where Iberian Jews began to settle in large numbers as a result of the nation-wide pogroms against the Jews in the Iberian Peninsula. We believe that the high incidence of Berber matches in our Melungeon sample echoes these events, although an alternative explanation might be to correlate Berber admixture to some other movement of populations, such as the influx of Africans to North America.

**Native American**

Native American populations figured as strong matches for all but five participants, i.e., 88 percent seemed to exhibit Native American ancestry. For nine of the participants, Native ancestry had the highest possible rank in the No. 1 position of world matches. As an aside, this does not mean that any of the nine was primarily or predominantly of Native American ancestry. The rank and number of matches in a high position cannot be equated to percentages of admixture. Nor can a match be said to indicate a specific tribe. Frequent Native matches found were Lumbee (a North Carolina tribe believed to have some ancestral overlap with the Melungeons, e.g., the surname Chavis is found in both groups) and Michigan Native American (Budowle et al. 2001 and Levedakou et al. 2001, respectively). Speaking anecdotally, it is our experience that these two matches often appear in test results of people claiming Cherokee ancestry. Such a correspondence might indicate that the main Native American group involved in Melungeon admixture was the Cherokees, but this is a probable assumption for admixed whites in general, especially in the Eastern United States, since the Cherokee are the most numerous indigenous nation and descendant group today. Moreover, they have always readily intermarried and assimilated with Americans of European origin.

**Figure 2. One participant's world scores**

1. Portuguese
2. Michigan Native American
3. Rwandan (Hutu)
4. Rwandan (Tutsi)
5. Brazilian Caucasian
6. Belgian (Flemish)
7. African American
8. Black Ecuadorian
9. Lumbee (Native American)
10. Hispanic
11. Florida African American
12. Native American
13. Moroccan Arabs
14. Azores
15. Caucasian
16. Serbian
17. Bhutia (India)
18. Tibet (Luoba)
19. Libyan
20. Argentinean
African
Sub-Saharan African matches were present in 13 participants, absent in 27, and No. 1 in 4 cases. Most common were African populations from Guinea and Rwanda, in other words, West Africa and Central Africa, the two main sources of colonial-era slaves (Salas et al. 2004). Yet three-quarters of the participants had no indication of Sub-Saharan African heritage, whatever. Based on our limited sample, Sub-Saharan ancestry would seem to be a common, but not universal, contributor to the Melungeon gene pool. Indeed, it seemed to be found in families rumored to have African heritage, such as Goins, but not in those lacking such a tradition. Thus, it appears to be a Melungeon genetic source similar to Gypsy—a frequent but not universal ingredient.

The top world matches of one participant shown in Figure 2 can serve as prototypical. As can be seen, the Melungeon community seems to be an amalgam of multiple races and ethnic groups. Based on the relatively shallow depth of the demographic history exposed by population genetics of this nature, we can postulate that 1) these characteristic Melungeon ancestries were present during the colonial time period of North American settlement, and 2) among these ancestries are several that are non-Western European. Persons having such origins would be those most likely to be classified as colored (and possibly non-Christian, see Hirschman 2005) by their neighbors, thus placing them in a position of lower social status and political power, and providing sociological support for the oft-cited discrimination against persons in the Melungeon community throughout their history (e.g., Kennedy 1997).

European
European ancestry was represented by matches to Caucasian-labeled populations (e.g., Alabama Caucasian) within the study sample, followed closely by Portuguese (Figure 3). (“Caucasian” is a term found in the original studies, where it defines all subjects not identifying themselves as black, Iberian, or American Indian.) However, populations labeled Caucasian ranked first for only three persons. Further, there were four participants for whom no Caucasian match appeared in the top entries. The relative weakness of Caucasian matches among our sample has as its corollary the presence of many non-Western European ancestries.

As touched upon earlier, OmniPop and ENFSI are based on different marker sets. They use the same formula to calculate probable frequencies, but the populations are delineated by different data and studies, with only partial overlap. ENFSI focuses on European Union countries and does not include

<table>
<thead>
<tr>
<th>Rank</th>
<th>Population</th>
<th>Weighted Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Scotland/Dundee</td>
<td>143</td>
</tr>
<tr>
<td>2</td>
<td>Denmark</td>
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<td>4</td>
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<td>5</td>
<td>France/Toulouse</td>
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<td>10</td>
<td>England/Wales</td>
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Hungary, Greece, Romania, and others. These differences notwithstanding, the following European motifs seem to have been salient among participants. In strict OmniPop comparisons, Portuguese matches were No. 1 in eight profiles (20 percent). Spanish populations were No. 1 in 13 (33 percent). Spanish sub-populations most often listed were Andalusian, Catalan, Balearic, Majorcan, and Minorcan—all on the Mediterranean side of the Iberian Peninsula. Strict ENFSI analysis indicated that the principal European countries and regions of likely ancestral origin for our sample on a weighted basis as seen in Figure 3 above.

Scotland was clearly dominant. Only three subjects lacked Scottish or Irish matches in their Top Ten most likely countries of European ancestry. Scotland or Ireland was the top match in one-fourth of participants. The lowest ranking countries were Germany (55) and Sweden (58). Of the two regions of Scotland covered by ENFSI, the Highlands (Dundee) outscored the Lowlands (Glasgow) by nearly double. Of the two Irelands, Ireland proper outperformed Northern Ireland, again by nearly double. Furthermore, of the two regions of France, it was the South (Toulouse) that won by a wide margin over the North (Lille). Note that England/Wales was at the bottom of the list, behind Spain, Portugal and Italy. Let us address these anomalies.

**Scots-Irish**

Population and emigration experts and American historians all agree that the Scottish element was remarkably influential in Britain’s American colonies, particularly in the backcountry of Appalachia (Fischer 1989 pp. 606-10, 634-35; Leyburn 1962 pp. 157-22; Miles 2006 pp. 330-36; Richards 2004 pp. 68-73, 100). The migration from Scotland and Northern Ireland from 1717 to 1775 brought an estimated 200,000 settlers to the New World (Hirschman, Brown, and Maclean 2006). Many of these colonists traveled down the Great Wagon Road to the Appalachian backcountry where they established permanent settlements and became the dominant ethnic group in the region. It is not surprising that Scotland is the leading European match for our Melungeon participants.

**Danish**

On a Europe-only basis, Denmark was indicated as the No. 1 ancestry in five cases. The high position of Danes is unexpected, perhaps, unless we reflect that the Normans who conquered Britain in the 11th century carried significant amounts of Danish blood. Moreover, the previous period of Scottish history had been subject to Danelaw, particularly in the north and east. “The Anglo-Norman presence in Scotland was very influential,” according to Oxford University geneticist Bryan Sykes (2006 pp. 184-85).

**French**

France/Toulouse or southern France was the top European ancestry indicated for three participants within the ENFSI database. If the Melungeons were true to Scots-Irish type, we would expect the closer lands of northern France (Lille)
to outweigh the Midi in importance, especially since the north was the immediate home of the Normans before their transplantation to Britain. Scotland always enjoyed close ties with France, but the connections tended to focus on the north of the country reached easily by sea.

One possible explanation of this evident gene flow from the south of France has to do with the Western European expansion of Jewish populations. As has been argued in detail (Hirschman and Yates 2007b), it is conceivable that the majority of Sephardic Jews came into existence with a large-scale conversion event in southern France circa 750–900 CE. This proselytizing movement is believed to have been centered on the establishment of a prominent Talmudic academy in Narbonne near Toulouse. An even more recent event is the Expulsion of Jews and Moors from Spain and Portugal during the late 1400s and early 1500s. As Kennedy (1997) has noted, this religious persecution dislocated tens of thousands of persons, some of whom made their way to the New World, while others settled in southern France. Thus, a strong genetic affinity between some Melungeon descendants and the current population of southern France would be expected.

Spain and Portugal

On average, these countries ranked No. 6 and No. 8 in the Europe-only comparisons. The question arises whether this reflects deep ancestry predating national identities or, in agreement with anecdotal evidence from the participants’ own family histories, proof of recent gene flow from Spain and Portugal. The latter possibility is supported by the presence of Spanish and Portuguese surnames, for example, Chavis, Perry, Steele (Castille), and Driggers (Rodrigues) within the Melungeon population. Oppenheimer, in his study of the origins of the British (2006), makes a good case that the colonists of the British Isles following the last Ice Age arrived from Iberia. However, because of the strength and consistently high position of Spanish and Portuguese matches in our sample, we believe that the Iberian ancestry among the Melungeons probably arose during the recent past, i.e., the time period from 1500 CE to the present.

Swiss and Italian

If we look at the remaining matches, we notice a pattern. The frequency of contiguous populations like southern France, Spain, Switzerland, Italy, Croatia, and Slovenia suggests relatively strong southern European or Mediterranean origins. If Melungeons were descended from ordinary Britons (Oppenheimer 2006; Sykes 2006; Wells 2006), their affinity with the Mediterranean, for instance, with Italian DNA, appears hard to explain. Could it come from the Roman occupation of England in ancient times? This is doubtful. Miles (2006 p. 154) remarks that the “vast majority [of Britons] were natives whose ancestors had lived in Britain for millennia.” He notes that in Roman Britain less than 5 percent of the inhabitants were actually “soldiers, administrators, merchants, slaves and craftsmen from the rest of the empire,” and that during the col-
lapse of the Italian presence in southern Britain in 450 (Roman rule had never extended to Scotland, Wales, or Ireland), many, if not most, withdrew to the Continent (p. 155). Thus, we cannot justifiably attribute the Italian genetic affinity apparently evident among Melungeons to either deep history or the four centuries when Britain was a Roman colony. We infer, rather, that it reflects Melungeons’ recent Mediterranean origins and is part and parcel with their already mentioned Jewish, southern French, and Berber roots.

**Validating the Study**

Because our study is based on a sample of 40 persons, it represents a modest and by no means comprehensive survey. One might well ask how it compares to larger samples gathered in earlier years. Fortunately, there is an excellent baseline for Melungeon genetic history and ethnic ancestry. In 1990, physical anthropologist and chemist James Guthrie analyzed blood samples collected from 177 Southern Appalachian Melungeons by Pollitzer and Brown in 1969. Using ABO blood groups, he compared the results to a worldwide database. The results are consistent—to a remarkable degree—with those in the present study. The leading matches found by Guthrie were Libya (North Africa), the Canary Islands (settled by the Spanish and Portuguese), Malta (a Mediterranean island population having Spanish, Italian, Portuguese and Arab ancestry), Portugal, Veneto (Italy), Ireland, Cyprus (an island off the coast of Lebanon), and Galicia (Spain). With the exception of matches to Gypsy populations (which were not available to him), Guthrie’s matches are quite consistent with our results. Taken together, the two independently conducted and differently conceived studies provide support for a multi-ethnic and multi-racial origin for the Melungeon population of Southern Appalachia.

**Summary**

The present study suggests that the Appalachian people known as Melungeons were not primarily drawn from ancestries in northwestern Europe but represent an amalgam of Mediterranean, Middle Eastern, North African, Sub-Saharan African, and Native American ethnic groups. It is possible that some founders carried South Asian and/or Gypsy/Roma ancestry as well. What they shared as physical attributes were darker coloring of their skin, hair, and eyes, and most likely exotic looking features which set them apart from northwestern Europeans. We believe this resulted in their being viewed as foreign, colored and non-white, and labeled in a stigmatized fashion.

On a sociocultural level of interpretation, we may infer that many or most of the original Melungeon founders probably were neither British nor Christian. Thus, they cannot be understood according to the four British folkways that cultural historian David Hackett Fischer perceives to be pervasively present in colonial America due to the planting of English regional cultures in Massachusetts, Virginia, Pennsylvania, and the Backcountry of the South (1989). Fundamentally different from the Puritans, Quakers, and other transplanted
Britons described by Fischer, the Native Americans and Sub-Saharan Africans contributing genes to the Melungeons would have held religious beliefs of an animistic form, likely invoking solar, lunar, water, earth, fire, and seasonal deities. Arab and Turkish-descended Melungeons probably shared Muslim traditions of a syncretistic blend of Sunnì and Shi'î theology. Iberian and Polish or Balkan Jews would have likely blended their Sephardic and Ashkenazic religious practices. If Gypsies were present in the early Melungeon population, they probably contributed Jewish and Zoroastrian religious traditions to the culture (see Sándor n.d.b). Perhaps most importantly, the present study supports the notion that colonial North America—at least in the Appalachian region—was inhabited by a multi-ethnic, multi-religious population from its inception. Greater recognition of the roles of these forgotten contributors to American culture is overdue.

Notes
1. We refrain here from pursuing any of the sociological ramifications or psychological aspects of identifying as Melungeon. For an article that examines some consequences of learning the results of DNA testing, we refer the reader to our 2008 article, “Peering Inward for Ethnic Identity: Consumer Interpretation of DNA Test Results,” Identity 8(1): 47-66.


3. It bears repeating perhaps that the language used to refer to different populations comes from the relevant source studies. There may be different definitions
involved. The names usually reflect present day geopolitical entities, not historical countries. We do not endorse one name over another.

4. A population in western Romania noted for its Gypsies.

5. It might be worthwhile to recall some of the known facts surrounding this lost chapter in America's frontier history. Under the scheme that came to be known as the Mississippi Bubble, the poor of Paris and Alsace—overwhelmingly composed of Jews and Gypsies, two groups often conjoined in history—were gathered up and sent as colonists to New France in 1720. The land agent was Etienne Stuteheus, a Jew. Parisians subscribed in a frenzy to the various stock issues. Fortunes were made on speculation. The first fleet of ships set sail and deposited their human cargo several hundred miles up the Mississippi between Natchez and Memphis. There the Jews and Gypsies, without arms or provisions, were supposed to hold the territory for France and combat the threat of Indian uprisings. After they realized they had been abandoned, however, many of them threw themselves on the mercy of the Natchez, Choctaw, and Chickasaw. Others became part of the Old Settlers in today's Northern (formerly Western) Cherokee Nation of the Old Louisiana Territory, later known as the Lost Cherokees. The crash at home came in 1721 when it was discovered that the finance minister's "junk bonds," as we would say today, were worthless. Law fell from grace and went into exile, giving up his titles and estates to resume a gambler's career in the casinos of Europe (Mackay 1898; Marcus 1973; Thiers 1859).

Gypsies still regard Memphis, the former capital of the Chickasaw, as their Jerusalem, making pilgrimages there and maintaining burial sites in Elmwood Cemetery. Under the name Half Breeds, their descendants helped Oglethorpe fight the Spanish and win Georgia for the English, being rewarded with land grants across the river from Augusta. Mixed Chickasaws, Jews, and Gypsies held these plantations until the 1970s, and North Augusta, S.C., is still a Gypsy mecca. The steamboat captain Job Adolphe Cramer in 1818 noted a town of Half Breeds still living at the ancient mound town of Chiska (now Ft. Pickering) where De Soto met his downfall, and where the French later built Fort Prudhomme in 1682. The strategic site, which split the French empire in North America in two after the Chickasaws formed an implacable enmity against the French and enforced a blockade of river traffic, was called by Mark Twain "the most beautiful vista on the Mississippi River." Disconnected from the road system and largely bypassed by time, it is being preserved as part of Memphis' future historic Riverwalk (information of Lauren T. Crews, Memphis, Tenn.).

6. Several scholars have suggested that Croatian settlers were present on the Eastern Seaboard since as early as 1449 and later formed part of the ethnic mixture that became known as Melungeons (Eterovich 2003; Prazak 1993). Slovenian-American author Louis Adamic wrote extensively on the subject, but almost entirely in Slavonic, so little of his work passed into the mainstream. We thank Nancy Morrison and Evelyn Orr for this information.

References


