# CRANIOMETRIC INDICATORS OF ANCESTRY AMONG FRENCH AMERICANS

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**ABSTRACT.** The accidental discovery of human remains washed out of the Wabash River bank in northwestern Indiana has led to attempts to identify them. The individuals are thought to be associated with Fort Ouiatenon, a historic French fur trading post constructed in 1717. The contents of the site (12T1198), found approximately 1.6 km from the fort, include human remains and associated coffin nails. The human remains studied (n = 3) were fragmented and incomplete. This study attempts to determine ancestry of the individuals using metric indicators, following procedures laid out in Standards for Data Collection of Human Skeletal Remains (Buikstra & Ubelaker 1994) and analyzed utilizing SPSS version 23. The study built a database of individuals of French, non-French European, and African ancestries. Analysis was conducted using discriminant function analysis to cluster and predict ancestries. The results of the study were successful in differentiating French ancestry, but the individuals of 12T1198 could not be confidently placed within this group. However, post priori analysis suggests a large amount of gene flow occurring early in the Americas causing individuals of French American ancestry to plot within different groups. The individuals of 12T1198 align with this discovery by plotting into multiple groups. The ultimate designation of these burials as European points to a possible association with Fort Ouiatenon, meaning they may be among the first French settlers in the area.

Keywords: Ancestry, craniometrics, French American

#### INTRODUCTION

In 2011, human remains were discovered washed out of the bank of the Wabash River in Tippecanoe County, Indiana, approximately 1.6 km from Fort Ouiatenon. Recovery efforts, conducted by the Indiana University-Purdue University Archaeological Survey (IPFW-AS), discovered four individuals in various levels of completeness, as well as historic coffin nails. Deemed site 12T1198, the remains were sent to the University of Indianapolis for bioarchaeological analysis.

The question quickly arose, are these individuals associated with the fort? If so, they would represent some of the oldest historic remains in the state of Indiana. The analysis that followed sought to extract as much information from the remains as possible, including age, sex, and ancestry. However, when attempting to determine ancestry, it was not enough to state whether these individuals were European; a more precise designation was necessary. This was done by collecting craniometric data from French, non-French European, and African populations. Discriminant function analysis (DFA) was con-

<sup>1</sup> Corresponding author: Heidi E. Miller, 740-704-3978 (phone), hemiller740@gmail.com. ducted to determine if groups could be separately classified. The DFA classification was applied to the individuals from 12T1198 to determine if the individuals classified as French.

**Determination of ancestry.**—One of the fundamental concerns for those who study skeletal remains is the establishment of the biological profile, which includes age, sex, ancestry, stature, and other idiosyncrasies (Reichs 1986; Byers 2011; White et. al. 2012). The term ancestry refers to one's biological heritage and used to be termed "race." However, while the term race sees continued use, especially in the general public, it is considered antiquated by anthropologists because it refers to both ethnic and anatomical indicators of heritage.

The concept of race may also be conflated with geographic variation (Caspari 2010). Anthropologists agree that variation exists across geographic areas, but the question is whether these variations can be seen in the phylogeny of local and regional populations. Livingstone (1962) argues that variation is best understood through clines and the distribution of individual morphologic and genetic traits, as opposed to racial categories which display a non-concordance of many traits and obscures the migration and gene flow that causes the observed variation.

Unfortunately, the concept of race still exists due to the social categorization of people and the visible physical characteristics on which these racial categories are assigned by the public. To aid the public in understanding the problems with the concept of race, the American Association of Physical Anthropologists (AAPA) issued a statement declaring that all humans belong to a single species (Homo sapiens) and, while regional populations exist, all groups descend from a common ancestral group (AAPA 1996). Additionally, the AAPA states there is more genetic diversity within, than between, populations. The AAPA then goes on to add that there are obvious physical differences between groups living in different parts of the world with varied traits that researchers have sought to classify for centuries.

Carl Linnaeus performed some of the earliest classification when he divided humans into four subspecies: *Homo sapiens europaeus, Homo sapiens asiaticus, Homo sapiens afer*, and *Homo sapiens americanus* (Blumenfield 2011). Generally, biological anthropologists today designate races within three major groups: White, Black, and Asian/Native American. It is within these three groups that the most research has been conducted. However, these racial categories continue the problem of conflating ethnic and anatomical indicators (DiGangi & Hefner 2013). Thus, herein, the term ancestry will be used in place of 'race' since race is not a biologically useful term .

Anthroposcopy, defined as the "visual inspection of the human body... for the purpose of identifying traits of a qualitative nature" (Byers 2011, p. 14), became the basis for the earliest studies to differentiate between groups (Giles & Elliott 1963). These studies have since been reworked and built upon and the use of anthroposcopic traits is still commonly used to determine ancestry in unknown remains (Buikstra & Ubelaker 1994; Gill 1998; Byers 2011; White et. al. 2012). However, researchers are often frustrated by the ambiguity of anthroposcopic traits, especially as form is seen as variation across a continuum, as opposed to discrete groupings. This has led to efforts to quantify anatomical differences using standardized measurements of the skeleton (Brues 1990).

One of the earliest studies, conducted by Giles & Elliott (1963), sought to differentiate between Whites and Blacks. The study focused on

American White and Black crania from the Hamann-Todd collection and used nine measurements to establish discriminant function equations able to separate unknown individuals into one of the two ancestral groups. W.W. Howells (1973) expanded on these early studies by analyzing crania from around the world. Howells (1973, 1989) observed the variation among populations and sought to record measurements of groups from Europe, Africa, Asia, Oceania, North America, and South America.

French Colonial history in North America.— In 1534, Jacques Cartier was sent by the French king to explore the coast of Newfoundland and the St. Lawrence River, prompting fur traders and settlers to begin immigrating to these areas (Gascoigne 2001). In 1608, Samuel de Champlain founded Quebec, then Montreal three years later, thereby establishing the region that would become New France. After the founding of the city of Montreal, immigration was primarily composed of French citizens, especially single males (Vigeant 2012). After 1680, immigration to New France shifted and, while France retained the majority of arrivals, immigrants from the British Isles and other European countries were not uncommon.

In the 1670s Louis de Buade, Comte de Frontenac et de Palluau was appointed governor general of New France (Eccles 1983). Frontenac made it his personal mission to expand both the area controlled by France and the fur trade. He began by building forts within the areas already controlled by New France, which would provide protection for French traders in the region. Then, in 1673, Louis Jolliet found the mouth of the Mississippi River, opening up vast new areas to the French and the fur trade.

In 1717, Fort Ouiatenon was established on the Wabash River near the present-day city of West Lafayette, Indiana (Tippecanoe County Historical Society, No Date). Named for the Ouiatenon (Wea) Native American village located nearby, the trading post became an important site for the regional fur trade.

Territorial disputes between the French and English led to the French and Indian War in 1754. At the conclusion of the war, the French lost all their lands in North America, including Fort Ouiatenon, which was soon garrisoned by English troops. However, a lack of trust in the English and a growing number of settlers streaming across the Appalachian Mountains, caused the Native American groups to rebel. In 1763, an Ottawa uprising led to the capture of eight frontier posts, including Fort Ouiatenon. It was here that the opposing groups met to discuss a peace treaty.

Terms of the treaty allowed the British to peaceably maintain forts in the West, but all settlers had to return east of the Appalachian Mountains. The British abandoned Fort Ouiatenon and the post returned to a small, French settlement until after the Revolutionary War when Native American groups again became alarmed at the increasing number of white settlers and skirmishes broke out across the region. Fort Ouiatenon became a staging ground by Native Americans for raids into the surrounding area. Fearing for their lives, the remaining French settlers abandoned the post in 1780. Efforts to secure the fort proved fruitless and, in 1791, President Washington ordered the post to be destroyed and the Native groups dispersed. Over time, the fort was obliterated from the landscape and, eventually, forgotten. Then, in 1967, after decades of searching and mistaken locations, the fort was rediscovered (Noble 1982, 1991).

In 2011 excavations were conducted by IPFW-AS after human remains were discovered washed out of the bank of the Wabash River in Tippecanoe County, Indiana, approximately 1.6 km from the fort (Williams-Draeger, Pers. Comm.). The site, 12T1198, contained the remains of four individuals as well as associated historic coffin nails. After excavation, the remains were sent to the University of Indianapolis Indiana Prehistory Laboratory, where they remain today. Analysis of the individuals was conducted by the author (H. Miller) and the three individuals complete enough for analysis were determined to be males of young to middle adult age (Miller 2014, 2015).

Anthroposcopic and craniometric ancestral analysis were conducted on two individuals, Burial 1 and Burial A, but was deemed inconclusive as a preponderance of indicators could not be achieved. In an effort to estimate ancestry and determine if the individuals are associated with the fort, a study was designed to utilize cranial measurements to predict French ancestry. The authors recognize that France is a European country and not a homogenous racial, ethnic, or ancestral group. However, based on the previous discussion of clinal variation (Livingstone 1962), the authors hypothesized that France may be a distinct enough population, with variation from both peninsular separation and access to Mediterranean trade, to create a statistically distinct group. This could allow discrimination between and prediction into groups utilizing DFA.

## MATERIALS AND METHODS

Sample and data.—Measurements were chosen for analysis based on the availability of data within the samples used. Measurements were chosen to keep the highest number of individuals in the sample. As a general rule, 7-10 measurements are typically used in DFA. Therefore, seven measurements were selected to keep a meaningful sample size. In the case of all samples, reported measurements were transferred into the measurement system used in Standards for Data Collection from Human Skeletal Remains (Buikstra & Ubelaker 1994) to promote consistency and allow for comparison among groups. The seven measurements used were Maximum Cranial Length (GOL), Maximum Cranial Breadth (MCB), Nasal Height (NLH), Nasal Breadth (NLB), Orbital Breadth (OBB), Orbital Height (OBH), and Frontal Chord (FRC). Groups were created based on data collected and mined from a number of archaeological sites and databases.

Materials.—The first Montreal parish church, the Notre-Dame church, began construction in 1672 with church records indicating the cemetery was in use from 1691 through at least 1796 (Vigeant 2012). The majority of individuals from Notre-Dame cemetery were of French ancestry, with more than half being born in Montreal. The Ville of Sainte-Marie was founded in 1736 (Municipality of Sainte-Marie 2014). The religious parish was founded just after the city in 1737 with the burial ground in use from 1748 to 1879. The Notre-Dame and Sainte-Marie collections are housed at the University of Montreal with analysis led by Dr. Isabelle Ribot. In addition, a Parisian sample was used that represents 19<sup>th</sup> century Parisians. This database was shared by Dr. Marie Danforth of Mississippi State University and originally came from Dr. Alain Frement at the University of Maryland.

Fort Biloxi was established in present day Mississippi in April 1699 (Carter et. al. 2004; Danforth 2011) and became the capital in 1719. Full excavation of the Moran site began in May 2007, led by Dr. Marie Danforth of Southern Mississippi University. Analysis conducted on the burials determined the individuals to be European, with French ancestry as the mostly likely ancestral determination based on skeletal analysis, diet, and analysis of associated artifacts.

The use of comparative samples is essential for the aims of this research and the data collected by Howells (1973, 1989, 1995) establishes an extremely useful database from which to begin. Two European groups were chosen: Norse and Berg, as well as two African groups: Egypt and Dogon. The data used were compiled by Howells between 1965 and 1980 and the authors acquired it from the William W. Howells Craniometric Data Set provided by the University of Tennessee, Knoxville (Auerbach 2014).

Excavations began in 1990 on the west side of Chicago to save what was left of the earliest Dunning Cemetery (Grauer & McNamara 1995; Grauer et al. 1998). The portion excavated was believed to be associated with the Cook County poor farm, the almshouse, and the insane asylum. Historical resources suggest this portion of the cemetery was in use from 1851 until 1869. Sex estimation indicated the presence of 19 adult males with osteological analysis conducted by faculty and students at Loyola University in Chicago with data provided to the authors by Dr. Anne Grauer. Ancestral analysis was conducted by the author (H. Miller) utilizing FORDISC (Ousley & Jantz 1996) to assign individuals to an ancestral category. A posterior probability of 0.80 was chosen for a confident designation. Of the 19 adult males, three were confidently assigned to the European ancestral group and two were assigned to the African ancestral group and placed in the West African sample. The remaining individuals were not used in analysis due to a lack of recordable craniometrics and confident ancestral designation.

The Wright and Rhoads cemeteries were excavated as part of cultural resource management mitigation projects near Indianapolis, Indiana (Nawrocki et al. 1998, 2010). Osteological analysis of both cemeteries was conducted at the University of Indianapolis Archaeology Forensic Laboratory led by Dr. Stephen Nawrocki. Historical research of the Rhoads cemetery determined that the property was owned by the Rhoads family from either 1821 or 1822 until sometime after 1906, but before 1928. Excavations uncovered 46 burials and one cremation urn within the delineation of the cemetery. Excavation of the Wright/Whitesell/Gentry [Wright] cemetery uncovered 33 burials. Available indicators of individuals from both cemeteries suggest the interred are of European ancestry.

In sum, the sample consists of 316 individuals separated into four groups: French, non-French European, North African, and West African populations. The French group (n = 85) consists of individuals from the Notre Dame and Saint Marie cemeteries of Montreal, and the Moran site from Biloxi, Mississippi, as well as measurements mined from the Parisian craniometric database. The non-French European sample (n = 124)consists of individuals from the Dunning Poorhouse Cemetery, the Wright and Rhoads Cemeteries, and Howells' Norse and Berg populations. The North African sample (n=58) is comprised of Howells' Egypt population, and the West African sample (n = 49) is comprised of Howells' Dogon population plus two individuals from the Dunning Poorhouse. For the purposes of this study, only adult males with positive ancestral determination were used.

Methods.—For the sample used in this study, linear discriminant analysis was conducted using SPSS version 23. Initial analysis was conducted to test whether individuals of French ancestry could be classified as a group separate from the non-French European ancestry. The four groups: French, European, North African, and West African were chosen as the grouping variables with cranial measurements chosen as the independent variables. A second analysis was conducted to observe where the individuals from 12T1198 would plot into the groups created in the DFA. The individuals from 12T1198 were added to the database as ungrouped cases thereby excluding them from the analysis to create groups, but allowing group membership to be predicted.

Validation of classification was accomplished in two ways. First a leave-one-out cross-validation test was conducted during the initial DFA. Second, a quadratic discriminant analysis was conducted using the statistical language R.

## RESULTS

**Discriminant function analysis.**—The total sample consisted of 316 individuals, with 32 individuals excluded from analysis due to missing discriminating variables (craniometric measurements) for an analysis sample size of 264 individuals. The assumption of homogeneity of covariance was assessed using a Box's M Test with an alpha level used in this analysis of 0.001. The *p*-value of this test is 0.000, meaning there is no evidence of difference between the covariance structures (Table 1). This violates

Table 1.--Results of the Box's M Test of Homogeneity.

Box's M		500.166
F	Approx.	5.658
	df1	84
	df2	104417.285
	Sig.	0.000

the assumption of homogeneity. However, this test is sensitive to departure from normality. Due to the violation of assumption and the sensitivity of the test, a quadratic discriminant analysis was conducted to confirm the linear discriminant analysis (see below).

The analysis of Eigenvalues proves the functions created are effective (functions 1 and 2) and moderately effective (function 3) at discriminating between variables (Table 2). In addition, the Wilks' Lambda Test of Assumptions displays a *p*value of less than 0.001 for all the functions, thus rejecting the null hypothesis that the functions have no discriminating ability (Table 3).

The discriminate functions were then used to classify individuals into groups based on the grouping variables (Table 4). Of the original groupings, 89.7% of French individuals, 66.7% of non-French European individuals, 70.7% of North African individuals, and 93.6% of West African individuals were correctly placed into the predicted groups (French, European, North African, and West African, respectively). Overall, this analysis saw 77.5% of original grouped cases correctly classified into Predicted Groups. The bottom half of the table displays the results of the leave-one-out cross-validation test. This test is conducted to confirm the classification performance of the analysis. Overall, 76.1% of crossvalidated grouped cases were correctly classified.

As mentioned previously, the quadratic DFA (Table 5) was conducted after the results of the Box's M test came back significant, indicating there was evidence of differences between covariance structures. The top portion of the chart displays the prior probabilities, the bottom portion of the chart displays the classification

table. When compared against the output from SPSS, the data were almost identical. Thus, the quadratic discriminant analysis was successful in correctly classifying individuals into the predetermined groups, thereby confirming the linear discriminant analysis.

**Output 2.**—A second analysis was conducted to observe where the individuals from 12T1198 would plot into the groups created in the original DFA. All classification groups remained the same. The individuals from 12T1198 were added to the database as ungrouped cases thereby excluding them from the analysis to create groups, but allowing group membership to be predicted. Since the individuals of 12T1198 were not included in the classification, the underlying output (Table 6) is almost identical to that of the first analysis and will not be further discussed.

The individuals from 12T1198 were analyzed as ungrouped cases and are placed into predicted groups based on the groups created from the other samples. In the result of interest, one 12T1198 individual was placed in the Predicted European Group, and one was included in the Predicted North African Group.

#### DISCUSSION

By saving the classification results to the dataset, it can be seen that Burial 1 was classified as North African and Burial A was classified as European. Interestingly, this is the opposite of what was expected. Burial 1 displayed anthroposcopic traits more often associated with Europeans while Burial A displayed highly mixed traits, including a guttered nasal sill and wide nasal aperture displayed often in individuals of African ancestry. This surprising classification could reflect the anthroposcopic ancestral assessment which saw an amalgamation of traits in both individuals. It could also be attributed to the presence of admixture.

However, when referring back to the classification output, some French individuals were also classified as North African, with others classified as non-French European and West African. These same misclassified individuals were primar-

Table 2.—Results of the Analysis of Eigenvalues.

Function	Eigenvalue	% of variance	Cumulative %	Canonical correlation
1	1.801	51.7	51.7	0.802
2	$1.384^{a}$	39.8	91.5	0.762
3	0.296 <sup>a</sup>	8.5	100.0	0.478

Test of function(s)	Wilks' Lambda	Chi-square	df	Sig.
1 through 3	0.116	598.769	21	0.000
2 through 3	0.324	312.974	12	0.000
3	0.772	71.884	5	0.000

Table 3.—Results of the Wilks' Lambda Test of Assumptions.

ily from the French populations in North America. Therefore, a new hypothesis was posed that the individuals of 12T1198 would plot to the same group as French American individuals. In a third analysis, the individuals of French American ancestry were removed from the French group and left uncategorized to test into which group they would be classified (Table 7). In this classification result five of the nine uncategorized individuals were classified as North African, with only one as European, and three as West African.

Why are these individuals being classified as North African? This may be due to the atypicality of the North African group, comprised solely of Egyptian individuals from the Howells dataset and dated to 600–200 B.C. This dataset, as we learned after our initial analysis, has potential issues with inclusion of individuals from other areas of the world, including Greece. Thus, the Egyptian dataset was excluded from further analysis and interpretation.

After removing the North African group from analysis, all of the uncategorized individuals that were previously classified as North African were then classified as non-French European (Table 8). In addition, the percentage of correctly classified grouped cases rises to 95%, with 94.1% of crossvalidated grouped cases correctly classified.

The DFA confidently discriminated between ancestral groups and accurately placed individuals within predicted ancestral groups. In particular French ancestry could be determined through craniometric analysis. Furthermore, the post priori tests indicated that the individuals of 12T1198 and the French American individuals computed very similarly, first as North African and then as non-French European. Further analysis showed that French Americans, while a small sample size, do not create a homogenous group, instead clustering into multiple groups. This is likewise reflected in the individuals of 12T1198.

Perhaps DFA is detecting the disappearance of French traits in the Americas. This hypothesis has been posed previously by Gore (2008), who posited that geography and genetic drift were more influential on facial morphology and biological variation than genetic ancestral groups.

				Predicted G	roup Members	hip	
		GroupComb	French	European	N. African	W. African	Total
Original	Count	French	61	1	4	2	68
		European	4	74	31	2	111
		N. African	3	10	41	4	58
		W. African	0	0	3	44	47
	%	French	89.7	1.5	5.9	2.9	100.0
		European	3.6	66.7	27.9	1.8	100.0
		N. African	5.2	17.2	70.7	6.9	100.0
		W. African	0.0	0.0	6.4	93.6	100.0
Cross-validated	Count	French	61	1	4	2	68
		European	4	71	34	2	111
		N. African	3	10	41	4	58
		W. African	0	0	4	43	47
	%	French	89.7	1.5	5.9	2.9	100.0
		European	3.6	64.0	30.6	1.8	100.0
		N. African	5.2	17.2	70.7	6.9	100.0
		W. African	0.0	0.0	8.5	91.5	100.0

Table 4.—Classification Table showing predicted classification of individuals.

77.5% of original grouped cases correctly classified.

76.1% of cross-validated grouped cases correctly classified.

	French	European	N. African	W. African
Prior probabilities of groups:	0.2394366	0.3908451	0.2042254	0.1654930
Predicted Group Membership				
French	61	4	4	0
European	0	68	5	1
N. African	4	37	47	1
W. African	3	2	2	45

Table 5.—Output of Quadratic DFA using R.

This hypothesis is most clearly reflected at the Moran site, where all three complete individuals were categorized as West African, despite firm genetic evidence that categorizes them as European.

The results from the 12T1198 site may be illustrating a mixing of characteristics due to the amount of gene flow between groups that occurred within a few hundred years of the appearance of Europeans in the Americas. In this analysis, we can see the individuals from site 12T1198 and those from the French American samples were classified into a variety of groups (Table 9). This is not surprising as the dates of the cemeteries used for the French American group would have allowed time for genetic flow to occur, but could still represent more recent immigration patterns. This analysis supports our hypothesis that gene flow in the Americas worked to remove distinct European and French traits, thereby

				Pre	Predicted group membership			
						N.	W.	
			GroupComb	French	European	African	African	Total
Cases Selected	Original	Count	French	61	1	4	2	68
			European	4	74	31	2	111
			N. African	3	10	41	4	58
			W. African	0	0	3	44	47
		%	French	89.7	1.5	5.9	2.9	100.0
			European	3.6	66.7	27.9	1.8	100.0
			N. African	5.2	17.2	70.7	6.9	100.0
			W. African	0.0	0.0	6.4	93.6	100.0
	Cross-validated	Count	French	61	1	4	2	68
			European	4	71	34	2	111
			N. African	3	10	41	4	58
			W. African	0	0	4	43	47
		%	French	89.7	1.5	5.9	2.9	100.0
			European	3.6	64.0	30.6	1.8	100.0
			N. African	5.2	17.2	70.7	6.9	100.0
			W. African	0.0	0.0	8.5	91.5	100.0
Cases Not	Original	Count	French	0	0	0	0	0
Selected			European	0	0	0	0	0
			N. African	0	0	0	0	0
			W. African	0	0	0	0	0
			12T1198	0	1	1	0	2
		%	French	0.0	0.0	0.0	0.0	100.0
			European	0.0	0.0	0.0	0.0	100.0
			N. African	0.0	0.0	0.0	0.0	100.0
			W. African	0.0	0.0	0.0	0.0	100.0
			12T1198	0.0	50.0	50.0	0.0	100.0

77.5% of selected original grouped cases correctly classified.

76.1% of selected cross-validated grouped cases correctly classified.

				Predicted g	roup members	hip	
		GroupComb	French	European	N. African	W. African	Total
Original	Count	French	61	1	1	0	63
C		European	5	72	32	2	111
		N. African	3	10	43	2	58
		W. African	0	0	3	44	47
		French American	0	1	5	3	9
	%	French	96.8	1.6	1.6	0.0	100.0
		European	4.5	64.9	28.8	1.8	100.0
		N. African	5.2	17.2	74.1	3.4	100.0
		W. African	0.0	0.0	6.4	93.6	100.0
		French American	0.0	11.1	55.6	33.3	100.0
Cross-validated	Count	French	60	2	1	0	63
		European	5	71	33	2	111
		N. African	3	10	41	4	58
		W. African	0	0	4	43	47
	%	French	95.2	3.2	1.6	0.0	100.0
		European	4.5	64.0	29.7	1.8	100.0
		N. African	5.2	17.2	70.7	6.9	100.0
		W. African	0.0	0.0	8.5	91.5	100.0

Table 7.—Results of Classification Analysis of French American sample.

78.9% of original grouped cases correctly classified.

77.1% of cross-validated grouped cases correctly classified.

creating a more homogenized 'American' ancestral group.

The aims of this project sought to understand ancestry of the individuals at 12T1198. Instead, we stumbled across evidence regarding morphological changes in the Americas. This research can help improve our understanding of variation in the Americas, especially that of French Americans. The historical background proves that French individuals had significant contact with disparate groups in the new world, and we, as researchers, must consider gene flow from French, Native America, African, and other European groups when assessing morphological variation in the Americas.

Utilizing craniometrics and discriminant function analysis, we were able to successfully separate French individuals from the European macro-

Table 8.—Results of Classification Analysis without North African group.

			Prec			
		GroupComb	French	European	W. African	Total
Original	Count	French	61	2	0	63
C		European	4	103	4	111
		W. African	0	1	46	47
		French American	0	6	3	9
	%	French	96.8	3.2	0.0	100.0
		European	3.6	92.8	3.6	100.0
		W. African	0.0	2.1	97.9	100.0
		French American	0.0	66.7	33.3	100.0
Cross-validated	Count	French	61	2	0	63
		European	5	101	5	111
		W. African	0	1	46	47
	%	French	96.8	3.2	0.0	100.0
		European	4.5	91.0	4.5	100.0
		W. African	0.0	2.1	97.9	100.0

95.0% of original grouped cases correctly classified.

94.1% of cross-validated grouped cases correctly classified.

			F	Predicted gro	oup membersh	nip	
		GroupFinal	1.0	2.0	4.0	5.0	Total
Original	Count	Fr. American	2	0	1	2	5
C		Parisian	0	61	2	0	63
		European	0	4	103	4	111
		W. African	0	0	0	47	47
		12T1198	0	0	2	0	2
	%	Fr. American	40.0	0.0	20.0	40.0	100.0
		Parisian	0.0	96.8	3.2	0.0	100.0
		European	0.0	3.6	92.8	3.6	100.0
		W. African	0.0	0.0	0.0	100.0	100.0
		12T1198	0.0	0.0	100.0	.0	100.0
Cross-validated	Count	Fr. American	1	0	2	2	5
		Parisian	0	61	2	0	63
		European	0	5	101	5	111
		W. African	1	0	1	45	47
	%	Fr. American	20.0	.0	40.0	40.0	100.0
		Parisian	0.0	96.8	3.2	0.0	100.0
		European	0.0	4.5	91.0	4.5	100.0
		W. African	2.1	0.0	2.1	95.7	100.0

Table 9.—Results of Classification Analysis of American groups.

94.2% of original grouped cases correctly classified.

92.0% of cross-validated grouped cases correctly classified.

group. In addition, site 12T1198 was found to be not inconsistent with French, especially American French individuals. More importantly, we uncovered morphological variation within American French and non-French European groups that points to rapid gene flow within the Americas. The individuals of site 12T1198 appear to reflect this complex gene flow.

## LITERATURE CITED

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