Interpreting intra-population variability from dental morphology and tooth dimensions of a modern Seminole Native American sample

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Introduction

Native American and Asian populations are typically grouped together in a single broad ancestry category despite their distinct population histories (Tallman 2016). Pooled Native American and Asian ancestry estimations are primarily based on the distant genetic relatedness of the two populations. This genetic connection stems from the Bering Strait Land migration event approximately 20,000-15,000 years before present. World-wide sea levels dropped, exposing land between large land masses, such as Asia and North America. The pooling of these groups in one ancestry category, however, does not account for thousands of years of separation or their post-Bering Strait migration population histories (Scott *et al*. 2016).

Examining intra-population variation and developing population-specific methods of Asian and Native American groups aid in redefining ancestry organization to better reflect the population diversity. Past research by the authors in a modern Japanese population reflect homogeneity within the sample, validating the utilization dental methods in ancestry discussions.

Dentitions are ideally suited to measure intra-population variability due to heritabilities of both their tooth size and dental morphological characteristics within populations. Harris (2003) and Hanihara & Ishida (2005) show that members of the same population are more related to each other than they are to members of a different population.

Materials and Methods

The Renee M. Menegas-Bock dental cast collection housed at The Ohio State University includes over 3,000 individuals. Within this collection, there are maxillary and mandibular casts, taken in the 1960s, from 347 living modern Florida Seminole individuals; *n*=80 of these individuals (f=45; m=35) were analyzed in the current study, ranging in age from 6-83 years at time of casting. To assess the intra-population differences, the Seminole group was compared to a modern Japanese sample from Jikei University curated in the 1960s to the 1990s; *n*= 201 Japanese individuals were analyzed in past research, ranging in age from 10-69 years at age of death, with 74 females and 127 males being represented.

Observations for 29 morphological dental traits were recorded on all available permanent teeth of the sampled individuals. Dental traits were scored using the Arizona State University Dental Anthropology System as described by Turner et al. (1991). A maximum of 63 characteristics were observed (maxillary=33; mandibular=30) per individual. Occlusal, buccal, and lingual traits were observed. Maximum crown diameter measurements were taken on all available teeth of an individual using a Mitutoyo digital sliding calipers that measures to the nearest 0.01 millimeter. Mesiodistal and maximum buccolingual measurements were taken for the maximum crown diameter. A maximum number of 64 measurements could be observed for each individual.

Intra-population differences were derived from comparative discriminant functions, descriptive statistics, t-tests, and ANOVAs were calculated in the SPSS statistical software package.

Results

Morphological trait score frequencies are presented for the sampled Seminole group.

Discriminant function models were made through comparative analysis with the previously researched Japanese population. Classification rates presented demonstrate the success in differentiation of the Seminole and Japanese groups. Multiple discriminant function equations were developed for increased utility of dental remains in ancestry estimations.

Table 1. Seminole Native American mandibular morphological trait frequencies.

Trait	Grade							
	n	0	1	2	3	4	5	6	7
Cusp Number M_1	47	0.000	0.000			0.085	0.383	0.426	0.106
Distal Trigonid Crest M_3	9	0.889	0.111						
Protostylid M_2	40	0.975	0.000	0.000	0.000	0.025	0.000	0.000	0.000
Cusp 5 M_1	47	0.085	0.000	0.074	0.404	0.383	0.085	0.000	
Cusp 6 M_1	48	0.500	0.083	0.375	0.021	0.021	0.000		
Cusp 7 M_1	47	0.894	0.021	0.085	0.000				

Table 2. Seminole Native American maxillary morphological trait frequencies.

Trait	Grade							
	n	0	1	2	3	4	5	6	7
Shoveling I[1]	56	0.054	0.232	0.393	0.196	0.036	0.089	0.000	
Labial Convexity I[1,2]	28	0.464	0.179	0.321	0.000	0.036			
Tuberculum Dentale I[1,2]	57	0.456	0.368	0.123	0.035	0.018			
Canine Mesial Ridge C	54	0.500	0.241	0.222	0.037				
Mesial/distal Acc. Ridge P[1]	61	0.984	0.016						
Mesial/distal Acc. Ridge P[2]	60	0.800	0.200						
Metacone M[1]	68		0.044	0.088	0.559	0.279	0.029		
Metacone M[2]	45		0.067	0.556	0.400	0.200	0.000		
Hypocone M[1]	65	0.000	0.015	0.015	0.167	0.446	0.246		
Hypocone M[2]	43	0.140	0.163	0.140	0.442	0.140	0.000		
Metaconule M[1]	68	0.956	0.000	0.015	0.015	0.000	0.015		
Carabelli's Cusp M[1]	68	0.265	0.103	0.132	0.132	0.132	0.118	0.118	0.000
Parastyle M[2]	45	1.000	0.000	0.000	0.000	0.000	0.000	0.000	

Table 3. Discriminant function analysis equation excluding molars one and two and results highlighting Seminole classification.

3 B-L	8 M-D	10 M-D	14 M-D	21 B-L	27 B-L
-45.503	26.030	8.843	20.597	9.355	25.038

Constant -260.741; Wilk's Lambda Significance = 0.002
Functions at Group Centroids: Seminole = -34.542; Japanese = 14.804
Original Classification: 61.5%; Seminole = 60.0%; Japanese = 62.2%
Cross-validated Classification: 92.3%; Seminole = 100.0%; Japanese = 88.9%

Table 4. Discriminant function analysis equation excluding all molars and results highlighting Seminole classification.

6 M-D	9 M-D	11 B-L	25 M-D	27 B-L	28 B-L	29 M-D	29 B-L
-20.623	18.699	3.337	68.952	38.752	-19.357	-5.891	-19.882

Constant -335.550; Wilk's Lambda Significance = 0.001
Functions at Group Centroids: Seminole = -55.162; Japanese = 27.581
Original Classification: 64.8%; Seminole = 63.2%; Japanese = 65.7%
Cross-validated Classification: 90.7%; Seminole = 100.0%; Japanese = 85.7%

Table 5. Discriminant function analysis equation utilizing anterior teeth and results highlighting Seminole classification.

8 B-L	10 M-D	10 B-L	11 M-D	11 B-L	23 M-D	24 M-D	26 M-D	27 B-L
-1.638	-2.096	-1.828	2.178	2.900	-2.651	2.666	6.532	-4.082

Constant -10.684; Wilk's Lambda Significance = 0.113
Functions at Group Centroids: Seminole = 4.788; Japanese = -1.524
Original Classification: 93.9%; Seminole = 83.3%; Japanese = 97.3%
Cross-validated Classification: 87.8%; Seminole= 91.7%; Japanese = 86.5%

Discussion and Conclusions

While the Seminole have undergone significant unifications and separations with other Native American groups over thousands of years and incorporated runaway slaves into their population, the isolation of the group in the Florida everglades contribute to the expression of unique dental phenotypes which may influence differentiation from other Native American groups. The relatively uniform composition of the modern Seminole population due to their isolated history in Florida may have factored into the general absence and presence dichotomy seen in the morphological scoring and the high classification rates seen in the discriminant function analysis models.

The similarities in population-wide uniform dental trait expression and measurements between the Seminole of this study and the previously investigated Japanese population corroborate the need for continued ancestry category refinement. The continued research of Native American sub-populations would provide further evidence of the dental expressions seen in this study. The continued sampling of populations and development of population-specific datasets and values would aid in the answering broad migration questions and discourage grouped Native American and Asian ancestry estimations.

Acknowledgements

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