A106 Using Mitochondrial DNA (mtDNA) -Derived Maternal Ancestry to Assist in Forensic Anthropology Investigations of Deceased Unidentified Individuals From the United States-Mexico Border

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Learning Overview: The goal of this presentation is to demonstrate how mtDNA can be particularly useful for counties proximate to points of migrant entry along the United States-Mexico border, where the preliminary questions asked by investigators include whether the individual is an Undocumented Border Crosser (UBC) and an American citizen.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by demonstrating how forensic anthropologists and investigators can apply mtDNA in an alternative manner to both produce useful investigative leads and compare forensic anthropological estimates of ancestry.

MtDNA is commonly used in forensic cases of degraded DNA, such as at the Armed Forces DNA Identification Laboratory and Pima County Office of the Medical Examiner (PCOME), where unidentified individuals have been exposed to harsh or temporally elongated taphonomic processes. Because mtDNA is non-recombining, it is primarily used for exclusions of family reference samples in casework, as the sequence variants are not unique to a person but shared among maternally related individuals. Closely related mtDNA lineages with a shared evolutionary history are grouped into mitochondrial haplogroups. The geographic structuring of mtDNA haplogroups entails that certain haplogroups are in higher frequencies in specific areas than others. Population genetic studies have demonstrated a strong relationship between continental geography and mitochondrial haplogroups, such that an individual's haplogroup assignment can often be a proxy for maternal biogeographic ancestry.

Thus, mtDNA can be useful in some cases as an investigative lead by providing information about maternal ancestry.[1] The object of this presentation is to demonstrate how mtDNA can be particularly useful for counties proximate to points of migrant entry along the United States-Mexico border, where the preliminary questions asked by investigators include whether the individual is a UBC and whether they are an American citizen. UBCs are typically of Mesoamerican and Central American origin, with UBCs from the Caribbean and South America less common. More rarely, the border is a point of entry by individuals with ties to distant locations, such as the Middle East.[2] Current forensic anthropological ancestry estimation methods from the skeleton emphasize the vast range of cranial variation exhibited by Latino populations; thus, it is often difficult to accurately estimate ancestry from the skeleton alone, and having an additional data point such as maternal ancestry could produce a more definitive investigative lead.[3-6]

On average, Latino populations from common migrant-sending nations overwhelmingly exhibit mtDNA haplogroups of Native American origin, with approximately 2%–10% exhibiting haplogroups not native to the Americas.[7-10] By understanding the population histories and mtDNA variation of source populations (both common and uncommon) of UBCs, mtDNA haplogroups can assist investigators with their approach to an investigation. In this presentation, attendees will learn how mtDNA can assist an investigation in two ways: differentiating UBC from non-UBC cases and differentiating whether an individual is from a traditional or potentially non-traditional sending region. If hypothesizing that the majority of UBCs will have haplogroups native to the Americas, then those individual cases whose mtDNA haplogroups are non-native should be flagged for consideration as a non-UBC or non-traditional UBC case.

This study includes data on 340 cases from PCOME. Haplogroup calls were made using the European DNA Profiling Group mtDNA Population Database (EMPOP) and confirmed by a qualified analyst. Based on known haplogroup frequencies of Latino populations, the hypothesis that approximately 90%–98% of the PCOME UBC cohort will exhibit haplogroups native to the Americas was tested.[7-10] Forty-seven cases exhibit non-native haplogroups, the majority of which (n=36) are believed to be or identified as UBCs from Latin America. Therefore, approximately 10% of the entire PCOME sample exhibits non-native Eurasian haplogroups, supporting the hypothesis. This study also explored the proposed pipeline of flagging cases exhibiting non-native haplogroups as potential non-UBC or non-traditional UBC cases. Eleven of the non-native haplogroups belonged to cases non-UBCs and were all identified as or believed to be White American citizens. Five of the non-native cases had haplogroups of African maternal ancestry, and most of these were classified as UBCs, with forensic anthropological estimates of ancestry highlighting African or unsure ancestry. The cases with non-native haplogroups believed to be/identified as UBCs were not unexpected, as most of the haplogroups associated with these cases were documented in Spanish and/or Hispanic reference population samples by EMPOP; thus, regardless of the non-native haplogroup status, they are consistent with Latino population history, including Spanish gene flow. The study results provided in this presentation demonstrate how forensic anthropologists and investigators can apply mtDNA in an alternative manner to produce useful investigative leads.

The opinions and assertions presented hereafter are the private views of the authors and should not be construed as official or as reflecting the views of the United States government.

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