The experiences of African and Indigenous descended populations in the Caribbean is informed by a limited number of ethnographic sources primarily from European chroniclers. While such sources provide some insight into the interaction between Indigenous Caribbean and African peoples, arguably, there are significant gaps in knowledge regarding the frequency and distribution of such encounters.

Ethno-historic Background

Western European colonization and the Trans-Atlantic slave trade during the late 16th to early 19th century profoundly affected the demography of Puerto Rico. Overall Puerto Rico did not have a large number of enslaved peoples relative to other Caribbean islands, however, at the time of emancipation in 1873, there were 29,335 enslaved peoples residing on the island (Fig. 1).

As a result of the effects of genocide, exploitation, and the purposeful de-population of the Indigenous population by European settlers, historical narratives suggest that the Indigenous population of Puerto Rico was eradicated by the late 16th century. To challenge this assumption, we examine the genetic maternal ancestry of Afro Puerto Ricans and other populations with indigenous maternal ancestry in North and South America, comparing the genetic nature of this ancestry and illuminating more about the histories of both Indigenous and African peoples in the wake of European colonization of Puerto Rico and the Americas.

Methods

Whole mtDNA sequences from 60 Afro-Puerto Rican samples were obtained via NGS. Whole-mito sequences from comparative populations with Indigenous mtDNA haplogroups were collected from GenBank. Comparative sequences from Argentina, Paraguay, Peru, Ecuador, and US Hanics, were run through Haplogrep 2.0 for haplogroup assignments. Summary statistics of each population were obtained via DnaSP. A median-joining network (MJN) of all individuals identified within the A haplogroup was created to examine possible genetic relatedness between the Afro-Puerto Rican sample and the comparative communities using PopArt and Fluxus NETWORK 10.0. Additional MJNs for the remaining haplogroups are forthcoming.

Results

We characterized the Indigenous mitochondrial ancestry of Afro-Puerto Ricans, also comparing the distribution of these mtDNA lineages across various other US, Central and South American populations.

Generally, Afro-Puerto Rican nodes in our network did not differ widely from each other, occupying the same general vector family. The MJN descriptive statistics showed a total of 336 segregating sites within the network and 142 parsimony-informative sites (Fig. 3). Two nodes on the MJN network were comprised of individuals from the Afro-Puerto Rican and US Hispanic populations. These were the only nodes with more than one population represented. Both of these nodes also each had closely-related nodes of an additional US Hispanic individual and an Afro-Puerto Rican with only a single sequence deviation to separate them (AFPR34, AFPR47, Fig. 2). In most other vectors, Afro-Puerto Rican nodes are separated from nodes of another population by at least 5 variations (Fig. 2). This distribution of Afro-Puerto Rican sequences within the A Haplogroup MJN suggests some level of homogeneity among the lineages in this haplogroup.

This distribution of Afro-Puerto Rican sequences suggest that the Indigenous ancestry of our sample population is similar to that observed in US Hispanic populations as opposed to the comparative populations. This could be the result of the possibility that the US Hispanic individuals in question had origins within Puerto Rico, which would partially explain the identical haplotypes. Another potential explanation is that Afro-Puerto Rican Indigenous ancestry had roots in regions of North America and Mexico. However, this is difficult to support because necessary identifying metadata about the comparative populations were not provided in GenBank. Regardless, this finding is unsurprising, given admixtures, migrations, and varied ancestries among US Hispanics in addition to historical parallels between the US and Puerto Rico.

In order to gain further data about the degree of genetic variation and relatedness between Afro-Puerto Rican and comparative populations, additional MJN analyses of the other 3 haplogroups should be performed. Supplementary data sets from North American Native groups as well as populations from Mexico and South America would help examine the hypothesis of relatedness between Afro-Puerto Rican Indigenous lineage to among the Americas.

Acknowledgements

Thanks to the Puerto Rican study participants, Lijuan Chen, Dr. Nicole Creanza, and the Vanderbilt School of Arts and Sciences.

References