

On the persistence and detectability of ancient Beothuk mitochondrial DNA genomes in living First Nations peoples

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ABSTRACT

Claims have long been made as to the survival to the present day of descendants of the Newfoundland Beothuk, a group generally accepted to have become extinct with the death of the last known member, Shanawdithit, in 1829. Interest has recently been revived by the availability of commercial genetic testing, which some claim can assign living individuals to specific Native American groups. We compare complete mitogenome sequences (16569 bp) from aDNA of eight distinct Beothuk lineages, including Shanawdithit's uncle Nonosabasut and his wife Demasduit, with three Newfoundland Mi'kmaq lineages and 21 other living Native Americans drawn from GenBank. A Newfoundland Mi'kmaq lineage in Haplogroup A is more similar to three Native Americans (1–3 SNPs) than to the most closely related Beothuk (24 SNPs). Nonosabasut in Haplogroup X is identical to a non-Beothuk Native American. Demasduit in Haplogroup C differs from three other Native Americans by 1–4 substitutions. Within a 2168 bp region of the HVS sequences available from living Mi'kmaq of the Miawpukek First Nation in Newfoundland, lineages in Haplogroups C, X, and A differ by 1, 4, and 8 substitutions, from the most similar Beothuk, and are more similar to other Native Americans. MtDNA genome sequences in living persons identical or similar to those of Beothuk do not necessarily indicate Beothuk ancestry. Mi'kmaq lineages cannot at this time be associated with any Beothuk lineages more closely than those of other Native Americans.

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Introduction

The Beothuk were a tribe of Maritime Archaic (MA) peoples in the 'Red Ochre' culture that inhabited the island of Newfoundland contemporaneously with an extant Algonquian First Nation, the Mi'kmaq, prior to and during early European colonization of the interior <1800. The Beothuk are generally accepted to have become extinct with the death of the last known member, Shanawdithit (1801–1829), preceded by the deaths of her uncle Nonosabasut (?–1819) and his wife Demasduit (?–1820) (Marshall 1996). Kuch et al. (2007) recovered, cloned, and sequenced a 406 bp portion of the HVS-1 mtDNA from the teeth of Nonosabasut and Demasduit, and assigned them to mitochondrial DNA (mtDNA) Haplogroups X and C, respectively. Where these haplogroups were also present in living Mi'kmaq, they took this as evidence of a 'close relationship' between the two tribes. However, Pope et al. (2011) concluded 'The Beothuk X HVS-1 motif differs from that of six other known eastern Mi'kmaq and (or) Gaspasian X haplotypes [from eastern Quebec] ... , and the Beothuk C HVS-1 motif differs markedly from the other known eastern Mi'kmaq C motif, such that a close relationship between the two First Nations groups is not supported Comparison of three additional Newfoundland Mi'kmaq C and X CR sequences confirms this (Collier 2010).'

More recently, Duggan et al. (2017) recovered aDNA and obtained complete or near-complete mitogenome sequences from a number of pre-historic persons on the island of Newfoundland, including MA and Beothuk dating from ca. 7700 BCE~1820 CE, including Demasduit and Nonosabasut. Questions as to the pre- and post-historical relationships of the Beothuk and Mi'kmaq remain. Here, we compare mtDNA sequences of Beothuk with those of Mi'kmaq lineages from Newfoundland and other Native Americans. These comparisons bear on questions of the utility of mtDNA sequence data in the association or assignment of living persons to extant or extinct Native American groups.

Materials and methods

Duggan et al. (2017) provide complete or near complete 16,579 bp mtDNA genome sequences (including indels) for 74 individuals, including 19 Beothuk, including Nonosabasut and Demasduit. The most ancient individual, designated 'L'Anse Amour,' is a member of the MA culture who dates to 7700 BCE. The MA and Beothuk cultures are disjunct by about 2K years (Duggan et al. 2017). These sequences were aligned with the 16569 bp revised Cambridge Reference Sequence (rCRS) by tacit removal of 10 indels. We also include the complete mitogenome of an individual of self-identified 'French'