

Reconciling pre-Columbian settlement hypotheses requires integrative, multidisciplinary, and model-bound approaches

Achilli et al. (1) present unique evidence concerning human mitogenomes and argue that such data are sufficient to generate a consensus scenario for the first settlement of the Americas. Here, we challenge their statement of having achieved a reconciling model because it ignores coherent ideas recently proposed by many researchers.

To begin with, the results of Achilli et al. are presented as challenging the three-migration wave model (2), and a paper published by us (3) is cited as supporting this classic migration scenario. However, our article did not support simplistic scenarios, such as the three-migration model. Rather, we suggested—based on craniofacial data, as well as genetic, linguistic and archaeological evidence—that an initial major dispersal began after the Last Glacial Maximum (21,000 y B.P.). We also suggested that the biological and cultural characteristics of the first Americans that emerged—in part—during a standstill period in Beringia, were reshaped by recurrent trans-Beringian/circum-Arctic gene flow and local population dynamics. These processes altered the initial indigenous biological and cultural traits, especially in North America (3). Since the publication of our report, evidence from several disciplines has further validated our model (4, 5), and the distribution pattern and coalescence times of mitogenomes provided by Achilli et al. offer a remarkable additional support for this view.

To reconcile apparently conflicting views requires a completely different approach. In this context, integrative approaches can well be based on a three-step logic. First, a micro-evolutionary model is stated; second, the expected patterns of between and within-group variation are estimated for each kind of evidence (uniparental or autosomal markers, craniofacial traits, cultural remains,

and so forth); and third, the fit between observed and expected patterns is quantified in some way (a “model-bound” approach). However, the conclusions of Achilli et al. are based only on mitogenomes and a few cursory citations of results from some other genetic datasets, and no discussion of important evidence—such as phenotypic traits, archaeological sites, and linguistic patterns—is offered.

Furthermore, despite that some evidence was acknowledged by Achilli et al., the authors mostly disregard some important demographic aspects in their approach. This aspect is relevant because there are dramatically different consequences of initial dispersal events into uninhabited territories and subsequent dispersal events subjected to ecological (and cultural) constraints imposed by the first founders (e.g., density-dependent limiting factors). These ecological and evolutionary principles related to the pre-Columbian settlement of the Americas are of key importance for explaining the chronological and spatial patterns, such as the distribution of the four main lineages and multiple minor mtDNA lineages presented by Achilli et al. and others.

However, these patterns also need to be compared with different datasets to provide integrative scenarios. For example, in Fig. 1 we show the most recent Y-chromosome genealogy, along with craniofacial data summarized from figure 2 in our previous paper (figure 2 in ref. 3). Future approaches and solid integrative hypotheses require that the biological evidence be integrated with cultural, ecological, and paleoclimatic data (5), considering the explanatory constraints of each discipline, to generate a fully reconciling model of the indigenous settlement of the Americas.

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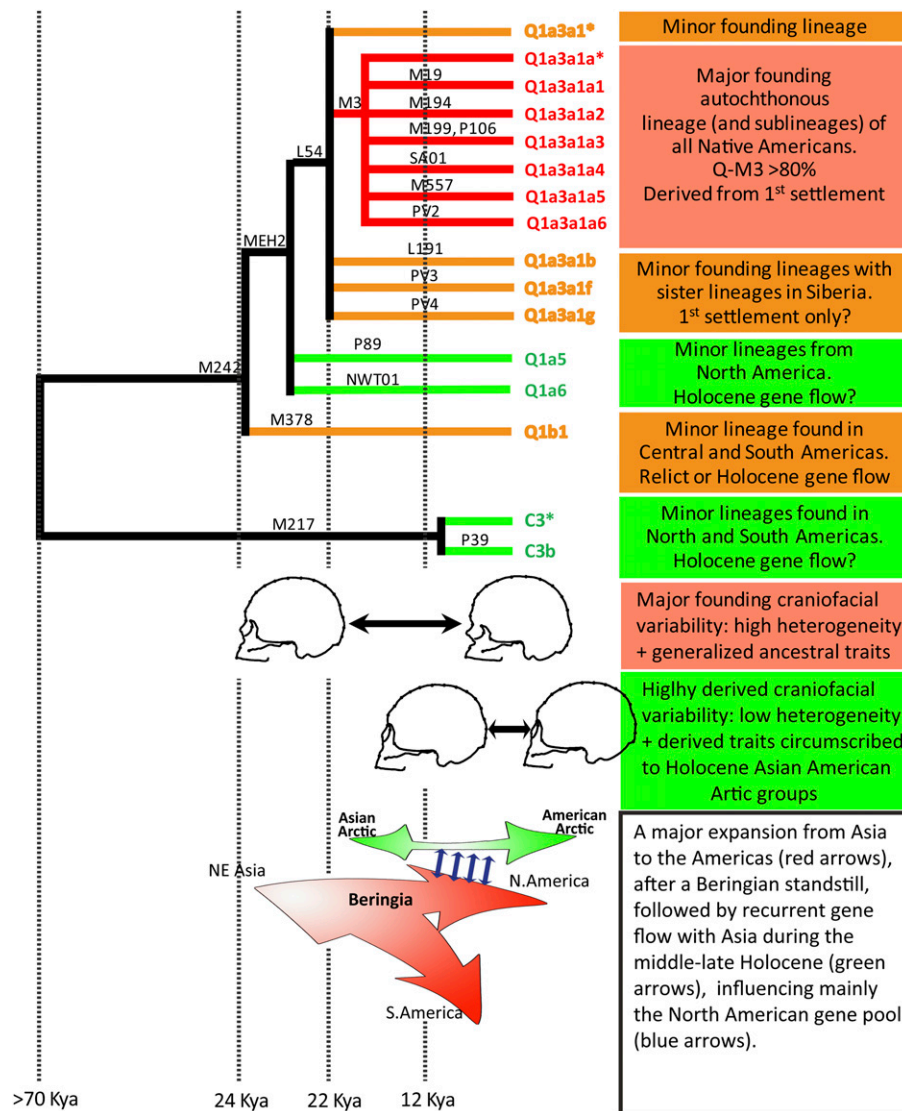


Fig. 1. A phylogeny of Native American Y-chromosome haplogroups, the main craniometric axes of variation in Asia–America, and a schematic scenario based on several lines of evidence. The only truly autochthonous Y lineage thus far identified is Q1a3a1a (or Q-M3) and its derivatives, which are found in all Native American groups. C3* is found in both North and South America, and C3b (or C-P39) is only found in northern North America. Although Q-M3 and Q1a3a1* (or Q-L54*) chromosomes are likely to represent descendants of the first settlers of the Americas, other lineages, such as Q1a5, Q1a6, and C3 (C3* + C3b) are most likely signals of Holocene circumarctic gene flow, although Q1b1 could be also parsimoniously explained as a relict lineage coming together with the first major Pleistocene arrival. This interpretation is in close agreement with craniometrical evidence presented in our model (3), which explains the large heterogeneity observed in ancient and modern Native American crania (including an array of ancestral and semiderived traits), and the evolution and dispersal across the Arctic of a set of highly derived traits (specially, extreme facial flatness) in the Holocene.