

The importance of fine-scale studies for integrating paleogenomics and archaeology

Krishna R Veeramah



There has been an undercurrent of intellectual tension between geneticists studying human population history and archaeologists for almost 40 years. The rapid development of paleogenomics, with geneticists working on the very material discovered by archaeologists, appears to have recently heightened this tension. The relationship between these two fields thus far has largely been of a multidisciplinary nature, with archaeologists providing the raw materials for sequencing, as well as a scaffold of hypotheses based on interpretation of archaeological cultures from which the geneticists can ground their inferences from the genomic data. Much of this work has taken place in the context of western Eurasia, which is acting as testing ground for the interaction between the disciplines.

Perhaps the major finding has not been any particular historical episode, but rather the apparent pervasiveness of migration events, some apparently of substantial scale, over the past ~5000 years, challenging the prevailing view of archaeology that largely dismissed migration as a driving force of cultural change in the 1960s. However, while the genetic evidence for 'migration' is generally statistically sound, the description of these events as structured behaviours is lacking, which, coupled with often over simplistic archaeological definitions, prevents the use of this information by archaeologists for studying the social processes they are interested in. In order to integrate paleogenomics and archaeology in a truly interdisciplinary manner, it will be necessary to focus less on grand narratives over space and time, and instead integrate genomic data with other form of archaeological information at the level of individual communities to understand the internal social dynamics, which can then be connected amongst communities to model migration at a regional level. A smattering of recent studies have begun to follow this approach, resulting in inferences that are not only helping ask questions that are currently relevant to archaeologists, but also potentially opening up new avenues of research.

Address

Department of Ecology and Evolution, Stony Brook University, Stony Brook, NY 11790, USA

Corresponding author: Veeramah, Krishna R (krishna.veeramah@stonybrook.edu)

Current Opinion in Genetics & Development 2018, 53:83–89

This review comes from a themed issue on **Genetics of human origins**

Edited by **Lluís Quintana-Murci** and **Brenna Henn**

<https://doi.org/10.1016/j.gde.2018.07.007>

0959-437X/© 2018 Elsevier Ltd. All rights reserved.

Introduction

It is arguably Luigi Luca Cavalli-Sforza's work analyzing frequencies of classical genetic markers (blood groups and other protein allozymes) and some limited mitochondrial DNA (mtDNA) in modern populations from across the world [1–3], culminating in his opus *A History and Geography of Human Genes* [4], that first brought geneticists and archaeologist into conflict. By relating their data with information from other disciplines (linguistic phylogenies and distributions of archaeological culture), Cavalli-Sforza and colleagues attempted to reconstruct how people had colonized the world in past societies. However this work drew a number of critiques from researchers from other fields at the time [5–8], and, despite massive improvements in both the generating of genetic data (from uniparental markers, to SNP arrays, through to whole genomes) and its analysis, an intellectual tension has remained between human genetics and archaeology [9,10,11*,12*,13]. Until recently, it was somewhat easy for archaeologists to dismiss or at least question the work emanating from genetics, arguing that the results obtained from modern DNA (even using genomic-level data) relied on critical assumptions about how populations were distributed and structured in the past, while finding the estimates of timings of demographic events to have confidence intervals so wide (because of inherent uncertainty when modelling genealogical processes as well mutation rates and generation times) so as to be essentially useless.

However, the recent ability to reliably obtain ancient genomes from past people of interest (the field of paleogenomics), rather than extrapolating from modern populations, largely overcomes these issues, and now potentially confronts archaeologists with a paradigm shift.

Archaeologists can no longer take a back seat or avoid (not that they necessarily actively wish too) the findings arising from the field, as it is genetic data generated from their own samples that must now be interpreted, in particular the apparent evidence of substantial migration over the last 5000 years. In this paper, I first detail the major findings from human paleogenomics over the past five or so years and the major theme that these inferences fit into. I follow this with my opinion of why these results are not being readily accepted by the archaeological community, and finally detail a potential approach that will allow these two fields to work in a truly interdisciplinary fashion.

The arrival of paleogenomics

During the early period of paleogenomics, the primary focus of research was on sequencing archaic hominins such as Neanderthals to look for evidence of potential introgression with anatomically modern humans [14,15] and investigating to what extent hunter-gatherers in Europe had been replaced by incoming Neolithic farmers from the Near East [16–18], the very question Cavalli-Sforza and colleagues had attempted to examine in their early classical studies [1] and that had generated such debate for over 40 years using various type of genetic [19–23]. The general picture that emerged largely fit with the views of Ammerman, Cavalli-Sforza, Colin Renfrew and others of a large replacement during this transition (i.e. demic rather than cultural diffusion), with a clear shift in the genetic ancestry of individuals sampled from Europe within Paleolithic/Mesolithic versus Neolithic contexts. However, what was perhaps more surprising is that Early Neolithic individuals showed very little resemblance to modern Europeans, except Sardinians [16–18]. This left the question of what had happened since the Early Neolithic. To what extent were other migrations a factor in shaping the modern European gene pool [24], and might such migrations correlate in some way with particular archaeological cultures [25]?

Therefore the past three years has seen efforts shift towards better understanding the genetic ancestry of people sampled later in the Neolithic and into the Bronze Age (though work continues to be done elucidating the origins of the original farmers that moved into Europe [18,26–30]). The first major finding (discovered by two groups independently) was the identification of an additional genetic ancestry component introduced into Europe from Ukraine/Russia that was associated with the early Bronze Age Yamnaya steppe herder culture [31,32], who were later shown themselves to be a mixture of eastern and Caucasus hunter-gatherers and early Neolithic Iranians [33]. A similar genetic input was observed moving in an eastern direction into Central Asia, and it appears that at this point in time the major genetic ancestry types had been introduced such that later Bronze Age populations began to increasingly resemble modern

Eurasian population genetic structure. What has followed is a series of papers over the past two years sequencing individuals associated with different Late Neolithic, Bronze Age and Iron Age archaeological cultures in order to examine to what extent the proportions of putative ancestral genetic ancestry types are changing such that this may indicate some kind of migration (either connecting similar archaeological cultures in different regions or indicating a replacement of one material culture by another in the same region). In this regard, archaeology is very much a back seat driver in this process, acting simply as the a source of material for DNA extraction and providing some kind of hypothesis framework that geneticists can hang their models of migration, which is also likely responsible for some resentment between the disciplines.

An almost dizzying array of potential migrations, invasions and replacements have been described in Eurasia beginning ~5000 years ago using this general approach: eastern Caucasus-related ancestry into Minoans in Crete and northern steppe ancestry into Mycenaean Greeks; steppe ancestry related to the Beaker culture into continental Neolithic farmer individuals and then (with ~90% turnover) into Britain [34] and even Ireland [35]; eastern ancestry into post-Bronze Age Northern Europeans [36]; a Scythian expansion from the eastern to central steppes, followed by the Xiongnu-Hunnic invasion and replacement of Asian Scythians [37*]. This migrationist emphasis has recently been extended to more recent periods such as (perhaps not surprisingly) the European Migration Period (eastern Europeans moving into Bavaria [38], mainland Europeans moving into Britain [39,40]), as well as other continents (ancient Eurasian back migration into Africa [41], Papaun ancestry replacing indigenous East Asian ancestry in remote Oceania [42,43] and Neolithic and then Bronze Age migrants entering southeast Asia and replacing indigenous residents [44]).

Is paleogenomics as currently applied relevant to the work of archaeologists?

So what is it about this recent body of paleogenomics work that has archaeologists so on edge to the extent that it drew the attention of a recent Nature News article [12*]? Despite being hotly contested over decades, the finding of evidence of a population replacement of Paleolithic/Mesolithic hunter-gatherers by Neolithic farmers is not likely to be the key factor. The reason this topic has garnered such interest is there is substantial archaeological evidence that this population transition may have happened, and in many ways the genetic data has simply helped confirm one hypothesis over the other. Instead, it seems that it is the finding of evidence of so many new migration events in the Late Neolithic/Bronze Age and later that is proving most troubling (though not perhaps in the way geneticists may think). Formalized by Kossina and then Childe, archaeologist have historically been

Download English Version:

<https://daneshyari.com/en/article/8625632>

Download Persian Version:

<https://daneshyari.com/article/8625632>

[Daneshyari.com](https://daneshyari.com)