Molecular anthropology: the judicial use of genetic data in archaeology

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A B S T R A C T

Anthropology has always been an unashamed scavenger discipline, acquiring and employing techniques developed in other physical, life and social sciences to apply to a holistic approach to studying humanity. In this regard, the adoption of genetic analyses into archaeological investigations has paralleled many previous adoptions including those of radiometric dating, stable isotope analysis and chemical analysis of material culture. Employing DNA data in reconstructions of prehistory, however, has been hampered particularly by the expense of generating the data — both financial and logistical — and, at least initially, by unwarranted resistance to take seriously molecular data. While the expense continues to rise as new techniques become available, there has been a reversal in the place of genetic data in that it is now privileged over other sources of data. This kind of molecular chauvinism leads to overreach in interpretation and is no less likely to hamper our progress. Moving forward we would do best be judicial in the use of genetic data alongside other independent archaeological evidence in reconstructing the past.

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1. Introduction

Modern and ancient DNA data are now routinely incorporated in reconstructions of the past. Ancient DNA (aDNA) loosely refers to any DNA that has degraded. The techniques employed in the analysis of aDNA are applied both to specimens of tremendous antiquity (e.g., Orlando et al., 2013) and those dead only a century (e.g. Miller et al., 2009). The DNA itself, as a consequence of its poor state of preservation, is both low quality and low quantity. Nonetheless, with ever improving technologies the field has gone from sequencing tiny fragments of DNA from museum specimens of preserved muscle tissue (Higuchi et al., 1984), to complete or nearly complete genomes of extinct human species (Briggs et al., 2009; Green et al., 2010; Lalueza-Fox et al., 2011; Reich et al., 2011; Reich et al., 2010). Just as there have been leaps forward in the technical ability to generate molecular data that is of interest to archaeology, there has also been a sea change in how it is treated within the field. In the late 1960s, the results of molecular anthropological studies were met with resistance and mistrust. Today, molecular data in general, and ancient DNA data in

particular, have been warmly embraced by prehistorians. The purpose of this brief review is not to use the benefit of hindsight to admonish archaeology's resistance to genetic data, but to highlight the growing problem of overreach. Genetic data is often placed above all other evidence, which is equally troubling, where a judicious use of molecular datasets would be more appropriate.

2. Anthropology's fraught relationship with molecular data

The incursion of molecular data into anthropology began in earnest when Vince Sarich and Allan Wilson published their immunologically informed phylogeny of the apes, including humans (Sarich and Wilson, 1967). Most startling to the paleoanthropological community was their conclusion that the common ancestor of humans and the other African apes lived about 5 million years ago. Most paleoanthropologists in the 1960s accepted 30 million years ago as a reasonable estimate of the age of the common ancestor (Pilbeam and Simons, 1965). So enormous a discrepancy meant that no one could see a way to reconciling the two reconstructions. Sides were taken. Heels were dug in.

Much of the vitriol surrounding the issue was voiced at conferences, but plenty made it into print. Sarich and Wilson were painted as outsiders without sufficient respect for the morphological data, with Simons (1968:328) carefully distinguishing them

from those who had done the hard work of studying the fossil record appropriately:

> Students of human origins will know, however, that the story of hominid[1] origins begins much earlier than this, since hominids of the genus *Ramapithecus* date back to the late Miocene, about 14 million years ago.

While Sarich and Wilson, though, were being chastised for their failure to appreciate the fossil record, many paleoanthropologists felt comfortable dismissing data they did not understand. Louis Leakey (1970:746–7), for example in 1970, wrote "I am not qualified to discuss the biochemical evidence…" but that "[t]he date of separation suggested by Wilson and Sarich, i.e., only five million years ago, is not in accord with the facts available today."

With the benefit of more than forty years accumulated history, it is too easy to paint Sarich and Wilson as the heroes, and the paleoanthropologists as the narrow-minded villains whose recalcitrance delayed advances in the field. Sarich and Wilson could, though, have done more to explain their methods and results. Sherwood Washburn, who had been Sarich's PhD advisor urged him to write a paper that would be accessible to the general anthropological community. Expressing frustration that such a paper would be necessary, Sarich responded, "That's all published. People should read what's published, and they should accept it" (described in Lewin, 1987). More recently, many molecular anthropologists have made considerable efforts to communicate with anthropologists not trained in molecular biology (e.g. Brown and Brown, 1992, 2011; Kaestle and Horsburgh, 2002; Matisoo-Smith and Horsburgh, 2012; Mulligan, 2006; O'Rourke et al., 1996, 2000), but none of these came soon enough to help the paleoanthropologists working 1960s and 1970s comprehend the new data and integrate them into their models of human evolution.

It took longer than it needed to, but paleoanthropologists did eventually come around and began integrating the molecular and fossil data. Slowly the dates attributed to the common ancestor of all the great apes slid away from 30 million years ago and closer to 15 million years ago. By 1984 David Pilbeam wrote that, "[t]he earlier debate between physical anthropologists and molecular biologists over the pattern and timing of hominoid evolution is now basically settled" and even self-deprecatingly asked "Why was the hominoid fossil record misinterpreted by dimmer paleontologists such as me?" He concluded that fragmentary fossil remains had been relied upon too heavily in the reconstruction of phylogenetic relationships; that the Miocene apes are taxonomically more diverse than are the extant apes as well as more morphologically heterogeneous rendering difficult the task of discerning relationships among the extinct species, and between the extinct and extant species.

3. The overcorrection

By the mid-1980s the resentment felt by paleoanthropologists at the infiltration of their field by biochemists, geneticists and molecular anthropologists had waned, and most embraced the

news lines of evidence as valuable contributions to the greater mission: the development of accurate, precise and rich explanatory models of human evolution. Where molecular data were once disregarded, we have now swung too far in the other direction, and people studying a human evolution from a genetic perspective have become as chauvinistic about their data as the paleoanthropologists ever were. I highlight a single quote here, but contend that the authors are not alone in their perspective:

> The best way to understand our evolutionary history as modern humans is comparing our own genome with those of our closest relatives. The genetic bases of the traits that we do not share with them are going to be those that define our singularity as a species (Sánchez-Quinto and Lalueza-Fox, 2015).

There are three fundamental problems with such a position: 1) DNA is not a blueprint for an organism; 2) important developments in human prehistory need not have been universally rooted in genetic change; and, 3) privileging the genetic data over all the other classes of data available impoverishes the nature of the reconstructions available to us.

3.1. The relationships between genotype and phenotype

The metaphor of DNA as a 'blueprint' or 'program' is an attractive and seductive one. Blueprints share a one to one correspondence with the object they specify; they always produce the same results. This is certainly not the case with DNA. Marks (1996) has described this perception of genetics as "high tech astrology" (p6) with genes being viewed as 'predisposers' in some sort of soft determinism. We are pretty good at looking at DNA and telling you if someone was lactose tolerant, or had sickle cell trait, or were bitter (PTC) tasters. We are terrible at looking at DNA and telling you if someone was musical, short-tempered, introverted, athletic, creative – that is, we are terrible at telling you most of the things that are likely to be of interest. The heritability of human height has long been the subject of research interest. As multiple studies make clear (Aulchenko et al., 2009; Gudbjartsson et al., 2008; Lettre et al., 2008; Visscher, 2008; Weedon et al., 2008), despite genome wide association studies (GWAS) in thousands of people, attempts to locate genetic variants strongly associated with variation in human height have proven underwhelming. Somewhat more than 50 variants have been identified that are associated with variation in human height. Combined, however, the variants can account for only 4–6% of the measured variation in human height. As Aulchenko et al. (2009) point out, if you want to predict the height of a person, you are currently better off employing the method that Galton published in 1886 (involving little more than averaging the heights of both parents and correcting for sex) than you are with a genome-wide survey of variation.

Other characteristics of importance are likewise poorly explained by existing surveys of genetic variants. A GWAS study attempting to located genes involved in the development of facial morphology was able to implicate five candidate genes (Liu et al., 2012). Just as in the studies of human height, however, the discovered variants contributed very little to the variation in human facial morphology. More recently an attempt to use genetic variation to calculate a predicted facial morphology (Claes et al., 2014). The study has been criticized on statistical grounds (Hallgrimsson et al., 2014). No correction was made to account for multiple comparisons, and further analyses showed that only one of the original 46 candidate genes was sufficiently significant to survive Bonferroni correction.

A final example I will offer here involves a GWAS in search of the genetic underpinning of personality traits. In the 1980s Cloninger

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[1] This discussion centers on the 1960s and 1970s, and so hominid is used to refer to humans, their ancestors and their closely related species since the divergence of our lineage from that of chimpanzees and bonobos. This older taxonomic scheme placed chimpanzees, gorillas and orangutans in the family Pongidae, and humans in the family Hominidae (hence, hominid). The taxonomy was revised to take seriously the notion that a taxon including chimpanzees, gorillas and orangutans but excluding humans is one constructed without reference to the biological reality that chimpanzees are considerably more closely related to humans than they are to gorillas and orangutans. See Wood and Richmond (2000).

(1986, 1987) developed a model describing three dimensions of personality which he measured with a questionnaire. The three original characteristics included were novelty seeking, harm avoidance and reward dependence and he later (1994) added persistence as a fourth dimension. Despite studying 5117 individuals and assaying 1,252,387 genetic markers, and with an analytical power of over 90% to detect variants that accounted for only 1% of the variability in each trait Verweij et al. (2010) were unable to detect a single contributing genetic variant. As they point out, it does seem reasonable to assume that variation in traits such a novelty seeking, harm avoidance and persistence seem likely to have been the subject of natural selection.

This phenomenon — the surprising difficulty that has been encountered when looking for genes that play a role in phenotypes we are particularly interested in — has been called missing heritability (Maher, 2008). With the benefit of hindsight, though, we perhaps ought not have been as surprised has we have been. Certainly, with more research we will come to better understand the implications of different patterns of genetic variation. The influence of particular genes depends on the genomic context in which it finds itself. This is known as epistasis, which is a term coined by William Bateson (1909) to describe when unexpected phenotypes were observed because of the combination of genes present, and when expected phenotypes went unobserved.

Genes are merely one of a number of causal factors at play during development that result in a particular phenotype, and furthermore they are involved in feedback loops in which they affect and are affected by the rest of the developmental system (Alberch, 1991; Pigliucci, 2010). The possible range of phenotypic outcomes from a given genetic complement is known as the norm of reaction. It is a concept designed to describe the tremendous complexity present in the interactions between genetic and environmental traits. The diet of rabbits, for example, has been shown to have a significant impact on the development of their facial skeletal morphology during development, and surprisingly also after skeletal maturity has been achieved (Scott et al., 2014).

Further complexity exists in the system as a consequence of epigenetic — that is, non-genetic — inheritance. It is likely that all the mechanisms involved in epigenetic phenomena have not yet been identified, but two major mechanisms are the chemical modification of the histone proteins, around which DNA is wound, and the patterns in which methyl groups (a carbon atom in the center of three hydrogen atoms) are bound to DNA. How epigenetic phenomena manifest are still being understood, but it is already clear that among other things, both diet and trauma can impact the patterns of DNA methylation in such a fashion that those altered patterns are inherited by offspring. And the offspring of those offspring. The variation in patterns of methylation result in variation in patterns of gene expression and have been shown to impact the likelihood of someone developing PTSD or major depressive disorders (Yehuda et al., 2014) and the coat color of mice (Waterland and Jirtle, 2003). Studies of DNA methylation patterns in ancient DNA have been undertaken (Gokhman et al., 2014; Pedersen et al., 2014; Smith et al., 2014). The efforts are hampered by poor preservation and the difficulties of interpreting patterns that vary on the individual, and even the tissue, level. Nonetheless, there is reason to be hopeful that more research in this line will prove fruitful.

3.2. The social and cultural complexities of studying humans

Implicit in assumptions that complete genomes hold all the important answers is the view that as humans are merely a particular instance of mammal, the same types of biological explanations that work for the rest of the animals will also work for humans. As noted above, complete genomes of any species won't tell you everything you want to know, but the issues are more complicated when the species at issue are humans and their immediate ancestors. Cultural and social inheritances are not merely a coat of paint on the surface of the interesting biological system. We have been producers of an archaeologically visible material culture for some 2.5 million years. We must take care not to underestimate the pervasiveness of the impact of cultural and societal variables on human development, phenotype and behavior.

Finally, not all the important developments in human prehistory need have been genetically driven. To take merely one example, there are several competing hypotheses to explain the development of modern human behavior. Modern human behavior is less often defined with an elegant description than it is with a list of archaeologically visible characteristics, the sum of which are taken to indicate modern human behavior — that is, behavior that would not look out of place in a present-day foraging context. The list varies a little between researchers, but generally contains a large, diverse and standardized artifact assemblage comprised of lithics as well as tools of bone, ivory, antler and shell; rapid innovation in tool technologies; art and jewelry; spatially organized camp sites with hearths; long distance transportation of raw materials; evidence of ceremony and ritual associated with human burial; enhanced fishing and birding technologies; seasonally driven mobility patterns; higher population densities implying more effective foraging techniques; and a move into cold, inhospitable environments (Henshilwood and Marean, 2004; Klein, 2009; McBrearty and Brooks, 2000). In one model the development of modern human behavior is seen as an abrupt change in the archaeological record signaling a change in neurological capacity (Klein, 1995). Whether the enhanced capacity is a generalized increase in cognitive capability or the development of a particular skill (e.g. sophisticated, grammatical language) is open, but the change is fundamentally genetic. The competing models point to a gradual development of modern human behavior as reflected in the archaeological record seen, for example, in the increasing standardization of blade manufacture during the Middle Stone Age such as in the Howieson's Poort tradition. Proponents of this gradualist model do not identify a biological change as the catalyst. There is not unified agreement about the identity of the catalyst, but hypotheses typically invoke either demographic or social change (Henshilwood and Marean, 2004). An increase in population density may have resulted in pressure to develop increased technological complexity for which the capacity, but not the need, had existed previously. Additionally, population pressure could force groups into marginal environments, which would also demand more intensive extractive technologies. The alternative, or parallel, catalyst to population pressure, is a change in the social landscape, perhaps the development of an extended family structure. The development of complex social categories of kinship that go beyond merely those reflecting the mother-offspring dyad could promote both increased division of labor, allowing both group-wide efficiency and the enhancement of personal expertise. Such a social structure could in turn promote economic and political cooperation fostering a feedback loop resulting in the kinds of technological and symbolic behavior we associated with behavioral modernity. My intention is not to arbitrate the debate on the origins of modern human behavior, but merely to offer an illustration of the significant role that non-genetic causes play in our models of human evolution.

3.3. Judicious interpretation

People engaged in research in molecular anthropology now confront substantial difficulty in analyzing and interpreting the

data they generate. This is in part because of the extraordinarily rapid improvements in DNA sequencing technologies. Moore's law describes the observation that the number of components that could be incorporated in integrated computer circuits was doubling approximately every two years, and the remarkably accurate prediction that "over the short term this rate can be expected to continue, if not to increase" (Moore, 1998). Moore's law has become a metric against which technological improvement is measured, such that it has become an aspirational rate of development. Since 2007 DNA sequencing technology has left Moore's law in the dust (Wetterstrand, 2015). The opportunities afforded us by the tremendous advances in DNA sequencing technology, and in particular by the ways in which they have allowed the access of ever more DNA from archaeological and paleontological specimens have been transformative. Analyses of these data, however, have remained difficult. Ancient DNA studies are especially hampered by small sample sizes. Recovering DNA from archaeological remains is expensive, time-consuming and fundamentally frustrating as significant portions of tested specimens fail to yield DNA. Conditions are consequently ripe for us to reach beyond our data. On the basis of mitochondrial DNA recovery from only six Neandertal individuals, for example, claims have been made for a patrilocal social system (Lalueza-Fox et al., 2011), the support for which is minimal at best (Vigilant and Langergraber, 2011).

Additionally, our abilities to effectively analyze and interpret even abundant modern genetic data now seem less secure than they once did. Recent simulation-based work, has shown that long supported models for the spread of human populations out of Africa are not better supported by the available data than other, very different, models (Pickrell and Reich, 2014). The observation that worldwide human genetic diversity decreases in an almost linear fashion with increasing genetic distance from Africa has long been interpreted as support for a serial founder effect model in which increases in local population density prompted small groups of people to venture out into regions previous unoccupied by people (Cavalli-Sforza et al., 1994; DeGiorgio et al., 2011; Deshpande et al., 2009; Harpending and Rogers, 2000; Liu et al., 2006; Prugnolle et al., 2005; Ramachandran et al., 2005). Under this model, splinter populations then had limited genetic interaction with the people left behind. Significantly different models, including severe bottlenecks and extensive admixture, and no bottlenecks and very ancient admixture, have been shown to result in the same smooth decrease in genetic diversity in increasing distance from Africa (Amos and Hoffman, 2010; DeGiorgio et al., 2009; Pickrell and Reich, 2014). In this specific case, archaeological data in combination with ancient DNA data, despite the inevitable limitations of small sample sizes, are the most promising road to resolution.

4. Conclusions

In the preface of 'The Human Career,' Richard Klein makes the case that the interpretations of the data we use to reconstruct human evolution should be modeled on the judicial system, "in which often limited evidence is weighed to determine which of two or more competing explanations or interpretations seems most reasonable" (1989, 1999, 2009). The incorporation of genetic data into models of human evolution were initially hampered by paleoanthropologists privileging morphological data over molecular. Successful synthesis took time, but it now seems clear that paleoanthropologists have worked harder at understanding the genetic data than other scientists have worked at understanding the morphological and archaeological data. To reconcile these lines of evidence it would be best for all concerned to place more value on a balanced approach rather than privilege genetics a priori in questions of human prehistory.

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