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Mitochondrial and Y-Chromosomal DNA in the Analysis of Kinship: Methods, Current Practices, and Areas of Further Inquiry

Anne M. Cafer

Abstract: This paper examines the use of both mitochondrial DNA and Y-chromosomal DNA in the study of kinship groups, particularly those from ancient burial sites. The characteristics of both types of DNA that make them suitable for such endeavors as well as methods of application to kinship studies will be outlined. Additionally, specific examples from modern, ancient, and other non-human primate research will be discussed along with the implications of these studies. Finally, ethical concerns and areas of further study will be addressed. This paper is designed to assess the utility of a specific scientific method of analysis that can augment traditional approaches to the study of human and primate social structure, specifically the use of genetics in kinship analysis, rather than to suggest the superiority of biology or sociology in the study of human and primate social structure.

Introduction

As Robin Fox remarks, “kinship is to anthropology what logic is to philosophy” (Needham 2004:1). Needham goes on to note that kinship is often a study that students of anthropology pick up with little enthusiasm even though several prominent individuals including Levi-Strauss and Radcliffe-Brown made their mark by studying kinship (Needham 2004). Although Needham expresses his opinion that kinship is almost entirely a cultural phenomenon unexplained by current biological theory, many anthropologists and biologists have found it worthwhile to explore issues of kinship with both cultural and scientific frameworks in mind. This is particularly evident in the use of mitochondrial DNA and Y-chromosome sequences in the study of social structure and kinship. This inquiry will explore what makes mitochondrial DNA and the Y-chromosome appropriate mediums for the study of social and cultural norms, the various methods used by

researchers today, the applications and weaknesses of those methods, and finally the ethical issues that arise from this particular avenue of study. Its goal is not to promote the use of biology in the study of every cultural institution or simplify highly complex social structures to a few base pair sequences, but rather to discuss the applications of a specific scientific process to the study of social interaction and the implications those applications have.

mtDNA and Y-chromosome Properties

Before discussing the various applications of mitochondrial deoxyribonucleic acid (mtDNA) and the Y-chromosome in kinship analysis it would be beneficial to discuss the properties of these genomes that make them particularly useful to biologists, anthropologists, archeologists, and a host of other scientists.

The DNA located in the mitochondria is a circular double helix (as opposed to the linear DNA found in the nucleus of cells) composed of roughly 16,500 base-pairs (Sykes 2001), a fraction of what is found in the nuclear genome. The mtDNA has thirty-seven genes that function mostly in energy production such as the electron transport activities necessary for adenine-tri-phosphate (an energy storing molecule) manufacturing (Cann 1995), which explains the presence of multiple mitochondria in most cells. Because mitochondrial DNA allows the human “powerhouse” to function much like an independent cell with its own protein coding genes, tRNA, rRNA, and initiation codons (Anderson et al. 1981), it can replicate independently of nuclear control. Unlike the nuclear genome that has corrective measures for mutations that occur, mtDNA has no repair system. However, as mentioned above the body has many copies of mtDNA per cell which means the mutations that do occur are often tolerated (Cann 1995). Since the mutation rate in mtDNA is substantial compared to the nuclear genome (Behar et al. 2007) with a mutation approximately every ten thousand years (Sykes 2001). This makes mtDNA ideal for studying human evolutionary history. These mutations also tend to be stable, making them a more reliable tool for genetic analysis (Sykes 2001).

These properties, in combination with the method of inheritance of the mitochondrial genome unaltered by recombination, from mother to offspring and in particular from mother to daughter (Behar et al. 2007), make it ideal for use in the study of kinship, particularly mate-choice, long-term pair bonds (Cann 1995), family structure, and maternal lineages. According to Cann (1995:127), mtDNA is the preferred tool in the study of populations with different cultural norms.

Many of the same properties that make mtDNA such a successful tool in biological analysis of past and present populations’ social

structure are also found in the Y-chromosome. Ten percent of the Y-chromosome genome remains unaltered by recombination (Sykes 2001), which means it is easy to trace genetic lineages. It has relatively few base-pairs in comparison to nuclear DNA which makes significant mutations much easier to locate and sequence, and it passes in a direct line from father to son (Wei et al. 2004). As Sykes (2001) notes, the mutations found in the Y-chromosome are of the particularly useful sort—short tandem repeats (STR) which are easily identified and sequenced. The Y-chromosome is useful in studying social clusters as males traditionally stay near their parents (Chaix et al. 2004), in addition to family structure, pair-bonding, and paternal lineages.

It is important to define what exactly a haplogroup is, considering its paramount role in modern studies of human population development and kinship studies. A haplogroup is defined as a group that shares a common ancestor with a single nucleotide polymorphism mutation (Peters 2007), which simply means that one of the bases (A, T, C, G) has been substituted for another—i.e. the ancestral sequence may have read GGATCA and after a mutation a new haplogroup is formed where all the descendants will have a different sequence (e.g. GGACCA). Haplogroups are “discovered” by calculating the number of genetic mutations from the most common recent ancestor. Until 2002, scientists relied almost exclusively on the first hyper-variable region (HVS-1) located in the control region of the mitochondrial genome (Peters 2007) to assign haplogroups (Behar 2007). Today, with the complete genomes available, individuals and groups are placed into haplogroups based on analysis of HVS-1, HVS-2, the typing of twenty-two other sites (Behar 2007), a number of common mutations, and where those mutations occur. This allows for more precise screening and subsequently, more accurate placement of individuals into haplogroups. Haplogroups are also calculated in a similar fashion using various coding regions in the Y-chromosome.

It may be hard to imagine that over the tens of thousands of years of human evolution there is such a limited variability in mtDNA and Y-chromosome sequences making them so useful in studying modern populations’ ancestors. In fact, compared to other mammals humans have very little variability (Cann 1995). In 1980 Dr. Wesley Brown proposed his theory of a mitochondrial Eve—that a single human female is the “mother” of modern mitochondrial DNA sequences. He proposed this woman lived approximately 200,000 years ago (Cann 1995) and all modern day haplogroups branch off from her. For many, this is a hard concept to grasp, so Cann (1995) uses the example below to better illustrate the point:

Consider first that if we think about an individual today, we see the 32 distinct ancestors that individual had, going back

five generations. If we try to trace the person's nuclear alleles, we have to consider the probability of transmission in each generation... Yet, if we consider the person's mtDNA only, there is one and only one ancestor in this family pedigree. This is the maternal great-great-grandmother [Cann 1995:129].

This is to say that although there was only one contributor to modern day mtDNA sequences, mitochondrial Eve, she was certainly not the only female in her generation. The other females in this generation may have failed to produce daughters who would normally pass on their mtDNA. Even if the other females had daughters, at any point in the line to modern humans if a generation failed to produce a daughter then the entire mtDNA genome of that lineage is lost, and consequently that haplogroup disappears.

Jobling and Tyler-Smith (2000) points out a similar situation for paternal lineages. If a mutation (often the result of a single base mutation as previously mentioned) on the Y-chromosome codes for an adaptive phenotype then the corresponding sixty Mb (one thousand base-pairs) sequence will be positively selected for within the population. This positive selection can occur to the point of fixation (Jobling and Tyler-Smith 2000), at which point every male in the population carries the same Y-chromosome sequence.

Kinship: Anthropology v. Biology

Although this paper will address the use of biological methodologies in the analysis of traditionally cultural arenas, it is important to define terms relevant to the discussion that often lead to misinterpretations of conclusions when not clearly outlined. *Kinship* is a word used frequently in both biological and anthropological texts and research. Biologically, kinship usually refers to a genetic relationship independent of social or cultural practices. This is not a belief held exclusively by biologists: as Read, notes in a recent article WHR Rivers, a prominent British psychologist noted for his work on kinship terminology, describes kinship as a "...relationship which is determined, and can be described, by means of genealogy" (2001:2). This statement implies that the underlying principle in defining family is biological and physical in nature.

Anthropology, however, takes into account the social and cultural norms of a society when describing kinship and kin. Needham (2004) describes kinship as the transmission or inheritance of rights from one generation to the next (this does not necessarily require a direct biological connection, as with step-children). Pasternak et al. (1997) note that in some societies the sharing of a common ancestor is enough to mark individuals as kin. They may not even share a biological

ancestor—the relationship may be based on myth of descent. In cases such as these the use of Y-chromosome and mtDNA analysis can shed further light into the social infrastructure of a society as will be explored later in this paper. Also, it can be argued that defining kinship via genetic means implies that sex is a prerequisite for offspring and there are societies that do not view sex as a necessary custom for having children (Read 2001). This argument is somewhat weak in its opposition to the strict genetic view as there are few societies that do not associate, at least to a certain degree, the act of intercourse with the production of offspring (Pasternak et al. 1997). There are some anthropologists that take a more empirical view than a traditional approach of kinship, namely Hamilton and Maynard-Smith with their inclusive fitness and kin selection theories, respectively (Irons 1979).

In this analysis, kinship will be used in a strictly biological/genetic sense unless otherwise noted. Kin will be identified as those individuals who share a parent or grandparent or some recent ancestor and consequently either mitochondrial DNA or a Y-chromosome. Subsequently the term *relatedness* and its derivatives refer to the fraction of shared alleles (identical) between two individuals (Blouin 2003) rather than a social relatedness (i.e. a close friend of a mother or a woman related by marriage may be called an aunt, but have no biological connection and consequently no shared alleles; therefore the daughter and ‘aunt’ would not be related).

Identity by descent simply refers to descent of two alleles from an ancestor within a given population (Blouin 2003). *Likelihood*, according to Blouin (2003), is the probability that an estimation of population values is true given the current standards of observed data. Both terms will be useful when discussing the development and use of pedigrees to be discussed below.

Methods

Before the development of modern techniques that allowed scientists to look at an individual on the molecular level, excavators relied on the use of non-metric (Alt and Vach 1995) phenotypic traits (Schultes et al. 2000) to establish kinship within the burial site, also known as morphological traits. These morphological traits are often the result of several genes interacting and are not necessarily an indicator of relatedness, making conclusions drawn from them subject to error. This was the case in the excavation of a neonate graveyard that had been used from the twelfth to the nineteenth century in Aegerten, Switzerland (Kaestle and Horsburgh 2002). Several, individuals who were assumed to be stillborns were discovered, and based upon morphological indicators researchers initially concluded there were a disproportionate number of female fetuses (Kaestle and Horsburgh

2002). However, upon molecular analysis this conclusion was overturned as the fetuses were mostly male (Lassen et al. 2000), which was not expected given the traditionally higher rates of female infanticide. The detection of kinship requires a geneticist or other researchers to determine for a given set of traits the familiarity (Alt and Vach 1995) between two individuals. This requires both technical and theoretical approaches.

First a DNA source must be decontaminated (Kaestle and Horsburgh 2002). For current populations blood, hair, or skin cells are the favored choice but fecal samples are often used in primate studies. For extraction of ancient DNA (aDNA) techs must carefully collect samples from preserved bone matter such as teeth or long bones (Sykes 2001). These samples, particularly the bone and teeth, must undergo a variety of chemical treatments to remove possible contaminants but because the bones are often fragile, and the risk of degrading the DNA by traditional methods is high, scientists use a combination of approaches such as bleaching and UV radiation (Kaestle and Horsburgh 2002). Next the DNA must be extracted from the actual bone, tooth, blood, or other sample. The extraction process requires the source to be ground into a powder (Kaestle and Horsburgh 2002) if not already a liquid, then either exposed to an organic agent such as phenol (Kaestle and Horsburgh 2002) to remove all cellular components, or the technician can bind the DNA to a substrate such as silica and wash the organic components away (Kaestle and Horsburgh 2002).

After the DNA has been isolated it goes through amplification. This process, called PCR or polymerase chain reaction (after the enzyme that initiates it) takes the tiny amount of DNA extracted from the source and makes copies by heating and cooling the helix (Kaestle and Horsburgh 2002). After there is a sufficient amount of DNA to work with the sample is loaded into a gel and undergoes electrophoresis. During electrophoresis the gel and sample are subjected to an electrical current. The DNA, which naturally has a negative charge is attracted to the positive pole (Kaestle and Horsburgh 2002) of the electrophoresis chamber and the DNA fragments differentially migrate based on size (i.e. the smaller fragments composed of fewer base-pairs move faster, and are therefore closest to the positive pole). At this point the gel can be exposed to various stains so the fragments can be observed, photographed, and compared to other sequences. There is another method of staining which may occur during PCR (Kaestle and Horsburgh 2002); this method incorporates a dye during the PCR reaction so that it does not require staining later. However, the chemicals used in this process are more volatile and carcinogenic and require special handling.

Throughout this process the prevention of contamination is paramount. Normally those handling the DNA would take steps such as

gluing together bones, washing the bones with water, or X-raying the bones (to kill various bacterial agents), but these may further degrade the fragile mtDNA samples. To prevent this, technicians follow standard procedures to ensure that there is as little contamination as possible and ensure that if there is contamination it can be eliminated from the analysis. The first measure against false readings due to contamination is running a negative control (Kaestle and Horsburgh 2002) with the samples; so that if there is contamination it will show up in the control as well. Additionally, all individuals are typed (Kaestle and Horsburgh 2002) so that if contamination occurs the source can be identified. As a last measure it should be common practice that all samples are tested at other labs in addition to the host facility. If the host facility handles a variety of types of sample (animal, modern human, and ancient) a sample should be tested in a setting that has never been exposed to modern DNA if possible (Kaestle and Horsburgh 2002).

After the technical component of kinship analysis, anthropologists and biologists must use theoretical models in combination with the hard data to construct pedigrees and draw conclusions regarding social structure. There are roughly four theoretical approaches to constructing pedigrees. These approaches are used more for current populations due to their reliance on the cooperation of a complete community. The first approach, appropriately named exclusion, takes all the possible parents of a given set of offspring and excludes all but one set of parents from the sample (Jones and Arden 2003). This exclusion is based on number of alleles in common between parents and possible offspring. This result can be skewed if there are genotyping errors or null alleles (Jones and Arden 2003).

The next two approaches, categorical and fractional, are used when exclusion is not possible and calculate the probability of offspring belonging to a given male (Kaestle and Horsburgh 2002) by calculating the likelihood ratio (LOD score), which is the likelihood of an individual being the parent (alleles in common) divided by the likelihood of an individual not being related to the offspring (differing alleles) (Kaestle and Horsburgh 2002). In the categorical method the entire set of offspring are assigned to one male (Jones and Arden 2003). This method is preferred over fractional when the desired result is expected, in theory, to represent the biological truth. Fractional methods split the offspring among all possible fathers. This method is more useful in calculating an individual's reproductive success (Jones and Arden 2003) rather than parentage.

Parental Reconstruction, the final method to be discussed in this paper, uses parsimony to explain the allelic combination present in the offspring (Jones and Arden 2003). This method takes the potential

males and finds the combination of fewest males that explains the array of offspring.

All of these methods are subject to various sample collecting constraints and the appropriate technique should be used for the type of data being collected. These methods can be used independently or in concert. Ideally, the parents of the offspring are already known and the tests will simply verify that relationship (Jones and Arden 2003). However, in ancient burial sites this is rarely the case and unfortunately not all candidates are present in these sites, making the probability of success limited.

Today there are several computer programs that make the process of calculating kinship using the above methods much faster and more accurate. The program discussed here, KinGROUP uses the maximum likelihood approach to pedigree construction and group assignment (Konovalov et al. 2004). It is now used in most studies and is an improvement on many old programs. The program compares the alleles on the mtDNA and Y-chromosome (if applicable) of two individuals and determines the probability of relatedness by descent (Konovalov et al. 2004). After determining the relatedness the program places individuals in primary or subgroups depending on the number of alleles in common (Konovalov et al. 2004). This can also give rise to the loss of individual identification that will be discussed later in this paper. However, in some statistical packages, after sequencing several loci the indexes such as the Queller and Goodnight related index change little after eight or nine loci, which makes detailed analysis difficult (Girman et al. 1997).

Current Applications

After discussing the various methods of using mtDNA and the Y-chromosome in studying kinship and what makes these genomes good candidates for such analysis, it would be pertinent to discuss the practical application of these studies. The most significant application is in archeological excavations—multiple burials, mass graves, and in the identification of important historical figures (Alt and Vach 1995). As Schultes points out “...the identification of kinship is essential for understanding influences of biological relationships on social structure in ancient populations” (2000:38). The application of mtDNA and Y-chromosome analysis to archeological studies can be divided into three categories: individual, family, and local.

Examples of individual application include two sets of remains discovered in Japan. Two females were buried apart from the main coffin area with a large number of cone shells, which indicated to anthropologists that these females were probably a mother daughter pair of great importance (Kurosaki et al. 1993). However, upon testing

of the mtDNA this hypothesis was rejected, as the mtDNA did not match. This was also the case with the brothers Parthenio and Evmenios who founded a famous Greek church in the nineteenth century (Georgion et al. 2009). Parthenio's remains were preserved in the church but those of Evmenios were not. However, during church renovations a skeleton was found and it was assumed to be that of Evmenios but mtDNA showed four base pair differences, indicating that it was not the brother Evmenios (Georgion et al. 2009).

At the family level, mtDNA can be used to verify the relatedness of deceased family members, particularly in families of historic importance (as they often have more complete genealogical records). Researchers exhumed a family from their crypt at St. Margareth's in Germany and found that of the eight "males" buried there, two were genetically female (Haak et al. 2008). Researchers also showed that group burial did not necessarily determine relatedness, as the most recent male was not genetically related to the senior earls (Haak et al. 2008). This could be the result of a non-paternity event or a switching of bodies (the former being most likely), however, the females were determined to be a mother daughter pair of the earlship (Haak et al. 2008).

Locally, mtDNA can be used to distinguish common inheritance and residence patterns (Haak et al. 2008) of ancient populations. At another site in Germany, researchers excavated four burial mounds of the Corded Ware Culture from the Neolithic period around 2700 B.C. (Haak et al. 2008). Interpretations of the mtDNA and the Y-chromosome found in individuals at graves 99 and 98 allowed researchers to conclude that the nuclear family was prevalent in this society and that close proximity in burial—at least in this society—indicated a close biological relationship. This project showcases how the cooperative efforts of culture and biology come into play when analyzing ancient social structure. The mtDNA of the woman and both children from grave 99 showed they belonged to haplogroup K1b, and the Y-STR (short tandem repeat) showed that the man in the same grave and the boys belonged to the haplogroup R1a (Haak et al. 2008). The placement of this nuclear family in the grave was very intimate, indicating that families were often buried together. In grave 98 two of the three younger children were from the same haplogroup (X2) based on mtDNA and were most likely siblings, but the woman buried with them was of haplogroup H (Haak et al. 2008). Because of the familial relationship found in grave 99 scientists concluded that the woman buried with the children in grave 98 was most likely a paternal aunt or step-mother (Haak et al. 2008), someone close to the children.

Examples of analysis at the local level in archaeological studies include the excavation of the Ashkelon burial site in Israel and the Agerton church yard in Switzerland are two prime examples of

individual application of mtDNA and Y-chromosomal sequences. The Ashkelon site was the former sewer of a fourth to sixth century Roman bathhouse (cover for a brothel) where archeologists uncovered the skeletons of over a hundred neonates. Scientists, through mtDNA analysis and sex-typing, discovered the bodies of fourteen males and five females (Haak et al. 2008). Although the sample size was too small for the results to be statistically significant (Haak et al. 2008), researchers hypothesized that the abundance of males in the burial site was due to a desire for female babies that could be trained to take the place of their mothers in the brothel. Within the norms of this brothel culture, male infanticide was much more prevalent and daughters were a favored entity. In the Agerton site sex-typing and mtDNA confirmed that an initial conclusion of a disproportionate number of female neonates was indeed incorrect (Lassen et al. 2000) and there were more male neonates, as discussed above.

The variability of mtDNA and Y-STR present in an ancient population can also be very telling of its social structure. mtDNA analysis of the Jomon society of Japan from approximately 4500 B.C. showed seventy-five percent of all individuals fell into two major mitochondrial haplogroups (Haak et al. 2008). This lack of variability is usually associated with a society that defines itself matrilineally. Societies that trace lineages through the females tend to exchange the males for purposes of marriage to ensure a direct line of female descendents. This means all the women will be related to a common ancestral female and will possess her mtDNA; researchers will see fewer types of mtDNA in the remains.

Outside of ancient burial sites, mtDNA and Y-STR have been used in social behavior studies in higher primates, including humans. There are a variety of studies that use mtDNA and the Y-chromosome to study the social behavior of bonobos, chimps, macaques, and others. These studies mainly look at what drives association and nepotism within the group. One study of bonobos looked at the association of adults and noted that there was a high rate of exogamy because many of the females were not related suggesting early departure of females to other groups (Hohmann et al. 1999). This study also noted that the greatest proportion of close dyads in the society were mother-son pairs (Hohmann et al. 1999), where females were typically out of estrus, and therefore the likely driving force was the shared maternal genetics. This was also supported by a primate study that showed male chimps preferred to affiliate and cooperate with maternal brothers (Langergraber et al. 2007), although the impact of kinship was shown to be limited because a majority of highly affiliated individuals were unrelated (Langergraber et al. 2007). The sharing of mitochondrial DNA was also implicated as the reason for altruistic behavior of adult female Japanese macaques toward adolescent males. The females were

more likely to aid males that were either their great grandsons or brothers with kinship values of 0.125 (great grandmothers) and 0.25 (brothers) (Chapais et al. 2001). In addition, there may be more kinship factors at play, because aunts showed inconsistent altruistic behavior toward nephews even though the kinship value was the same as great grandmothers and great grandsons (Chapais et al. 2001).

It is also important to note that even though not all studies have the same findings or support the same theory, the use of mtDNA analysis can still be useful, even to support the idea that kinship is more than a biological phenomenon. Biologists researching chimpanzees in the Kanyawara community of Uganda sequenced their subjects' mtDNA as an index of matrilineal relatedness (Goldberg and Wrangham 1997), and their study revealed that chimps that nested together were not necessarily matrilineally related (Goldberg and Wrangham 1997).

Regarding human studies, the analysis has been somewhat limited outside the use of mtDNA and Y-STR for migration studies. One such study explored the tendency of traditional societies in central Asia to organize themselves into various lineages, clans, and/or tribes based on a common ancestor (Chaix et al. 2004). This common ancestor distinguished themselves from the rest of the population and united the group socially and economically (Chaix et al. 2004). However, upon mtDNA and Y-STR analysis, the researchers realized that this common ancestor was often mythical. The individuals may share a recent common ancestor, but there were no common haplogroups found throughout the lineage (Chaix et al. 2004). Like the last chimp study described, this supports the idea that kinship is more than a biological institution, and that tribes may be a conglomerate of clans who invented a mythical ancestor to strengthen group unity.

Strengths and Weaknesses

The application of mtDNA and Y-chromosomal analysis in a study of kinship strengthens a study's authority. As much as opponents of biological theory may dislike the application of genetic studies to cultural institutions such as child rearing and marriage, they cannot deny that empirical data strengthens the conclusions and assertions of a publication. For example, a study done on traditional whale hunting crews in Indonesia used interviews to calculate relatedness rather than mtDNA analysis, the application of which would have provided more substance to the study's conclusions that the hunting crews were more closely related than statistically expected (Alvard 2003). Although the application of genetics is not always appropriately applied to the study of social activities it still has its place in the field and will continue to play a large role in the understanding of social behavior, particularly as molecular testing improves and knowledge of genes and their functions

increases. As discussed above, mtDNA and the Y-chromosome have many properties that make them ideal candidates for use in kinship studies, but there are weaknesses as well that this paper will address in this section.

As already briefly mentioned, the actual process of collecting DNA and sequencing the genomes provides ample opportunity to contaminate the sample. Scientists take steps to ensure this does not happen, but it is an inevitability one must accept when working with DNA, and can cloud results if left unchecked.

Also, the haploid nature of mtDNA and Y-chromosome genomes make them sensitive to genetic drift, bottlenecks, and selective sweeps (Bamshad et al. 2001). This is not particularly problematic if one is studying human migration (a broad long term phenomenon). However, when looking for more time specific and detailed genetic information researchers must supplement mtDNA and Y-chromosomal analyses with independent autosomal loci (Bamshad et al. 2001). DNA extraction can also be highly destructive as bones must be ground into a powder and subjected to harsh chemicals (Kaestle and Horsburgh 2002). This gives rise to ethical concerns, discussed in a later section, but it also provides a technical challenge to laboratory workers as the different excavating conditions lead to a constant need to adjust the cleaning and extraction approach. DNA also has a “shelf-life” of approximately 130,000 years (Kaestle and Horsburgh 2002). This may seem like a long time, but this is only under optimal preservation conditions, in which bones are rarely found. The degraded nature of the DNA often makes analysis impossible. Even within the same crypt, some individuals may have enough DNA to analyze where others may not, which could result in false interpretation of social behavior.

Lastly, there is always human nature. Genotyping errors, contamination, and switching specimens can all lead to false interpretations of the data. When working with modern, living specimens this may not be particularly problematic as researchers can often return to the sources, but when dealing with aDNA researchers usually only have one opportunity, as Sykes (2001) discovered. Bones may be on loan from a site or museum and after extracting a sample, researchers must promptly return the specimen with no chance to make a second extraction. This is particularly true for institutions that study extremely old fossils, as there may only be a few bones and preservationists are loath to let even an expert drill into them.

Regardless of these weaknesses, mtDNA and Y-chromosomal sequences provide a wealth of information not available via morphological typing, autosomal sequencing, or ethnographies.

Ethics

Although the information obtained from conducting mtDNA and Y-chromosome analysis is invaluable there are very real political, social, and legal implications (Kaestle and Horsburgh 2002). The issues brought to light by these analyses fall into one of two core areas: legal and cultural rights of a historical area and individual/group identity.

As discussed above, the process of collecting the DNA used for analysis is often destructive to the skeletal remains from burial sites (Kaestle and Horsburgh 2002). Although scientists take steps to preserve the remains and ensure DNA collection is as noninvasive as possible, these new techniques raise the issues of respect and privacy of the individuals being studied. Does the potential wealth of information to anthropological, archeological, and biological institutions outweigh the sanctity of these burial sites? Kaestle and Horsburgh (2002) note that these are very real and serious issues that have yet to be formally addressed by federal and international laws in many countries, including the United States. As there are few laws outlining the process of obtaining consent for sampling aDNA, and rarely a surviving relative, individuals who are perceived to be culturally affiliated are asked to make these important decisions (Kaestle and Horsburgh 2002), even though they may not have a working knowledge of the culture or the best interests of those they are being asked to represent in mind.

Other cultural issues arise with mtDNA and Y-chromosome analysis of sites involving land claims and religious freedom. Kaestle and Horsburgh (2002) argue that showing the relatedness of modern populations to individuals in these burial sites can give rise to land claims by modern day peoples or requests to allow burial of modern individuals. Conversely, by showing that modern peoples are distantly related to individuals at a particular burial site (Kaestle and Horsburgh 2002) (misleading in some cases as not all individuals in a burial site can be analyzed because the DNA is too degraded), land rights may be restricted or denied. Kaestle and Horsburgh (2002) suggest that to be prepared for these issues scientists should work with local and native groups in the concerned area.

Juengst's (1998) article addresses another category of ethical dilemmas faced by researchers exploring DNA analysis in general. Humans have often used biology, and more recently the field of genetics in particular, to justify nepotism, tribalism, aggression, and racism (Juengst 1998). These ideas are sometimes afforded legitimacy in the medical and healthcare arenas. As genes are mapped and individuals are assigned to various genetic groups, there is less propensity toward seeing people as individuals (Juengst 1998). It is easier for a bureaucratic system (such as the current health care system in the United States) to pigeon hole individuals into broader categories

classified according to diseases and likelihood of maladaptive behaviors which carries serious implications for treatment and insurance costs. Juengst (1998) also makes the point that the assignment of groups could have long-standing legal complications. He uses the example of an individual who may not associate with a certain ethnic group but has the same mutation on his Y-chromosome, allowing him to demand the application of affirmative action in his favor (Juengst 1998). In addition, a female individual of the same ethnic group will not possess the mutation because she has no Y-chromosome. Although these are merely implications and as of yet not eminent concerns, a lack of cultural awareness and sensitivity when conducting research on mtDNA and Y-chromosome could make these very legitimate concerns for affected individuals in the near future.

Conclusion

This inquiry examines the role of mitochondrial DNA and the Y-chromosome in human and primate kinship studies and provides examples of the role biology plays in the reconstruction and interpretation of social structure, in not only ancient societies but in modern populations and other primate communities. The field of genetics allows anthropologists, archaeologists, biologists, and a host of other scientists to explore human origins, migration, and relationships within the context of social structure (Kaestle and Horsburgh 2002). The versatility of both mtDNA and Y-STR allow both genomes to be used in a number of situations and studies from birds, to wild dogs, and to higher primates including humans, past and present. Additionally, the use of these genomes is not limited to projects operating under a strictly biological perspective. As seen with the various primate studies, the use of mtDNA was used to negate the idea of a strict biological driver in social behavior.

The information scientists obtain from these studies is invaluable, but anthropologists must work to respect the dignity of individuals studied and promote an understanding of the results in such a way that individuals maintain their own identity and are not lost in scientific facts and figures that often overwhelm the literature.

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