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LEHIGH UNIVERSITY

The Applications of Archaeogenetics:

Assessing the Nutrition Profiles of Native American
Groups

Sophia Dent

Modern geneticists have made great strides in identifying the genetic factors underlying nutritional disorders. In the context of the nutritional disorders that affect Native American groups, this paper explores the potential of archaeogenetics in identifying the extent to which these genetic markers are preserved in ancient DNA and the subsequent information that they can provide regarding the etiologies and dispersal patterns of such disorders.

At the core of our existence, beyond our musculoskeletal system, beyond our tissues, organs, and even cells, lies an exceedingly complex, highly organized molecule that is mere nanometers in size. This molecule is DNA, which encodes the vital information that directs the functioning of our bodies, and, along with RNA, comprises our hereditary information, or genome. The genome of *Homo sapiens* consists of three billion DNA base pairs, which, remarkably, are 99.9% identical among human individuals. Despite this near identical similarity, however, there are vast physiological, physical, and cultural differences among our species. The underlying factors of these differences are single nucleotide polymorphisms (SNPs), which manifest as heritable single nucleotide changes within a chromosome (Boccia 2010:38; Thaler et al. 2010). SNPs, minute and seemingly benign, can cause the chromosome to take an altered state, thereby conferring slightly different expression and functions. Given that there are several million SNPs within a genome, the additive effect can be significant, resulting in the great amount of variation among individuals of a single species and likely playing a causative role in the 3-4 billion cases of nutrition-related diseases worldwide (Boccia 2010:38, Nabhan 2011:32).

One of the major factors influencing SNPs is, logically, what we most frequently put into our bodies—the nutrients and dietary chemicals that fuel our daily activities. Yet considering the great percentage of the human population that suffers from nutritionally-based disorders and diseases, it is clear that there are a multitude of complex factors at play in regulating these SNPs and thus one's genetic response to dietary chemicals. The consumption of certain chemicals can lead to mutations, differential selection, altered genetic expression, and, ultimately, the reactions that we see among many individuals within our species (Nabhan 2004:58). Further investigation into these different reactions has shown a pattern among regions and cultures, supporting the notion that the factors affecting different ethnic groups are derived from the diets of their

ancestors. These diets were shaped by adaptations to availability, disease-resistance, social structure, and cultural predilections. Therefore, through comparative studies between and within ethnic groups, nutrition genomics and archaeogenetics can attempt to identify the genes and SNPs that underlie different reactions to foods. An important aim of nutrition genomics is to “understand the functional interaction between bioactive food components and the genome at the molecular, cellular, and systemic level in order to understand the role of nutrients in gene expression and, more importantly, how diet can be used to prevent or treat disease.” (Castle et al. 2007:3). Accordingly, this paper will examine the potential of the burgeoning field of archaeogenetics, in tandem with the genomics of modern ethnic groups, patterns in nutritional disorders, and comparative studies of ancestral versus modern diets, to address questions of differential genomic expression in our ancestors and how it affects the dietary health of the human population today.

This particular research will focus on the use of nutrition genomics and archaeogenetics to address the health of Native American groups. With their history of long-term isolation from all other racial groups, the study of Native American groups provides an opportunity to examine the effects of nutrition and environmental conditions on the changes and continuities of genetic expression throughout a lineage (Sievers & Fisher 1981:192). Their isolation enables a comparative assessment of the effects of environmental conditions versus heredity on genetic expression. This could be accomplished through comparing the genetic profiles of Native American groups from regions of different climatic conditions, or comparing the profiles or unrelated groups from similar climate conditions.

Native American ethnic groups also have a suite of nutritional disorders that plague a large percentage of their population, making them well suited for examining genetic, ancestral,

and environmental patterns. A study by the Indian Health Service (2004-2006), reports that the percentage of the death rates caused by diabetes was 68.1% in the American Indian and Alaska Native population compared to 24.6% in the total US population. The percentage that was alcohol-induced was 43% in the American Indian and Alaska Native population compared to 7% in the total United States population. In addition, Native American populations have very high rates of lactose intolerance and cardiovascular disease (Indian Health Services 2011). While much genetic diversity among Native American populations does exist, the focus of this paper is the broader patterns of nutritional health disparities and the degree to which they are derived from common ancestry.

Examining the composition of common ancestral diets and their effect on the adaptation of genomes holds major implications in the examination of nutritional disorders and the ways in which human evolution proceeds. It is of major significance that American Indians, even when following the same diet as other ethnic groups, are at greater risk of developing metabolic diseases. The genetic basis of this discrepancy can be addressed through analyses of present-day Native American population genetics and genome analyses derived from the remains of their ancestors. While this approach is not without challenges, the increasing amount of information that the human genome can provide us with, together with vastly improved techniques in the relatively nascent field of archaeogenetics, can provide valuable information on nutrition-related diseases and disorders.

Native American Nutrition-Related Disorders

Diabetes

Geneticists studying modern populations have identified several sites of genetic alterations they believe could play key roles in causing diabetes. These sites of mutation and alteration have been identified in the insulin receptor (chromosome 10p13), the glucagon receptor (17q25), the glucagon synthase gene (19q13), and genes encoding fatty acid binding proteins (4q) (Kahn et al. 1996:513). Genomic alterations have also been seen in studies of the mitochondrial DNA of those affected by diabetes. Diabetes is likely a polygenic disease with multiple genetic factors underlying its heterogeneous causes and complex symptoms (Kahn et al. 1996:510).

There are certain groups within the Native American population that are particularly affected by diabetes, including the Hopi, Papago, Navajo, and Pima (Nabhan 2004:163). The Pima are especially of note, with as much as 50% of the Pima adult population affected by diabetes (Castle et al. 2007:19; Centers for Disease Control 2012). The Pima have traditionally lived in a desert-like region of Central and Southern Arizona, where the ancestral subsistence base consisted of hunting and gathering, supplemented by some agriculture. Many of their dietary staples had a very low glycemic index, meaning that the constituent glucose was released and absorbed over a longer period of time (Lieberman 2003:363). As a result, the metabolism and culture of the Pima adapted and evolved to accommodate such low levels of glucose intake. Therefore, when given the same amount of glucose as a group of individuals of European descent, Pima insulin levels skyrocketed to three times that of the Europeans, who are genetically predisposed for the metabolism of simple sugars and carbohydrates (Diamond 2003:600).

This significantly different reaction to glucose could be explained by James Neel's "thrifty gene" hypothesis (Neel 1962), a widely accepted theory which postulates that occupants of desert areas have an oligogenetic mechanism for maximizing insulin derivation from glucose-poor foods. This "thrifty gene" would have conferred an advantage to the Pima ancestors by enabling them to obtain more nutrients and store more fat during times of food availability, which would better increase their chances of survival during times of famine. After all, for groups such as the Pima, adequate nutrition was hardly regularly available; if such a "thrifty gene" did exist, it would be logical that it would have been subject to positive selection (Diamond 2003:600, Draper 1977:311, Nabhan 2004:600). Positive selection could have then perpetuated this gene and served as the driving force for its fairly rapid spread through the population. According to this theory, a rapid change in diet would have been detrimental to the Pima; "untethered from the foods to which their metabolisms are best adapted," (Nabhan, 2004:32) such as slowly-digested, pectin-rich foods, the Pima quickly succumbed to a number of nutritional disorders—especially diabetes—when faced with a glucose and simple carbohydrate-rich diet.

Obesity and Cardiovascular Health

In broader studies of Native American health, diabetes is frequently considered to be an element of a larger syndrome: "Syndrome X." The other elements of this hypothetical syndrome include high blood pressure, high triglycerides, and obesity (Nabhan 2004:132). Like their heightened response to glucose, Native Americans increased risk for obesity and weight gain when following the same "Westernized" diet as other neighboring ethnic groups. This could be

associated with the famine-resistant functions of the “thrifty gene,” providing further support for its influence on multiple disease etiologies (Diamond 2003:600).

A genetic basis for the predisposition for obesity has also been identified in the human genome. On a genetic basis, an amino acid substitution in the intestinal fatty acid binding protein (FABP2) on chromosome 4q has been suggested to cause an increase in fatty acid sequestration. An even more significant gene variant is (R230C, rs9282541), which is unique to Native Americans. This genetic variation is located on the cholesterol transporter gene and is associated with high levels of cholesterol efflux (therefore increased intracellular cholesterol storage), diabetes, and obesity (Acuna-Alonzo et al. 2010:2878, Kahn et al. 1996:523). Thought to be a result of SNPs, such a mutation would have been very advantageous to maintaining energy stores despite the dynamic food availability characteristic of ancestral diets. With its strict distribution among Native American ethnic groups, this genetic alteration has potential to increase the understanding of ancestral life and how to better mediate the lasting effects of ancient lifestyles present in the genomes of descendent groups.

Lactose Intolerance

Another nutritional disorder that is differentially expressed among ethnic groups is lactose intolerance (Watts 1981:20). The prevalence of this disorder among Native American groups is particularly pronounced as nearly 100% of the adult population is affected by lactose malabsorption (Nabhan 2004:8). Like the genetic predispositions to diabetes and obesity, the genetic basis for lactose intolerance also elucidates the subsistence strategies of ancestral populations, enabling inferences to be drawn regarding the social nature of the group. It is possible that mobile egalitarian groups and agricultural, socially stratified groups could have

very unique genetic signatures as a result of their different nutritional sources and caloric requirements. For example, let us explore the phenomenon of lactose tolerance, the distribution of which is very limited. Lactose tolerance is an autosomal *recessive* disorder, which raises the question of what would impose such strong selective forces to perpetuate it within an ethnic group (Sievers & Fisher 1981:213). Patterns of lactose tolerance distribution suggest that groups with long histories practicing agriculture and raising livestock have higher rates of lactose tolerance (Hipkins & Rutkowski 2005, Nabhan 2004:18). Considering the opposite case, in groups with long histories of mobility and hunting and gathering, lactose tolerance would not have been advantageous. Instead, it would have proved beneficial for a child to lose the lactase enzyme at a younger age, so as to reduce the caloric demand on the mother, as mobile hunting and gathering imposes high caloric requirements on individuals (Nabhan 2004). The question remains whether lactose intolerance was the result of a mutation deleterious to all but agriculturalists, or whether it was a mutation that arose in response to higher levels of lactose exposure. Attempting to identify the presence or absence of lactose intolerance in ancestral groups could begin to address this.

Gene variants identified through modern genetics and suggested to be causative factors of lactose intolerance are evident in hereditary markers. Using these modern genetic markers as a proxy, ancient DNA studies can subsequently be applied to identify lactose tolerance or intolerance in ancestral populations (Brown & Brown 2011:10; Elmadfa 2010:8; Vergeres 2010:127-140). This holds the potential to reveal significant information about the subsistence strategies and social structures of past populations, as well as the heredity and persistence of the genetic basis of nutritional disorders such as lactose intolerance.

Alcohol Metabolism

Although alcohol metabolism isn't necessarily a nutritional issue, it provides a nice compliment to the ways in which dietary compounds are variably expressed across different regional and ethnic populations. Like lactose tolerance, it is hypothesized that genetic alterations influencing the overproduction and reception of alcohol dehydrogenase were positively selected for in populations that adopted agriculture as a subsistence base early in their history. Such populations had limited access to clean water, due to contamination resulting from agriculture and raising livestock, and thus adopted the practice of fermentation (Nabhan 2004:29). In addition, genomic analyses have led to a hypothetical connection between decreased alcohol metabolism, diabetes, and obesity. Genes encoding alcohol dehydrogenase have been identified on chromosomes 11 and 4q, the latter of which has also been postulated to be involved with diabetes and fatty acid sequestration. Given that alcohol is a fermented sugar, it is likely that this is more than a mere coincidence. It would be of interest to investigate further whether alcoholism is another element of the multiple disorders, mostly nutritionally-based, that appear to be inherited together (Edenberg 2006: 1539; Nabhan 2004:27).

Applications of Archaeogenetics

It cannot be overlooked that individual responses to dietary compounds are not derived solely from genetics; rather the response to different foods is likely a result of the complex interplay of environmental factors, culture, and reaction to disease with genetic factors. As long as these complicating factors are taken into consideration, however, archaeogenetics can still reveal valuable information about different populations and their reactions to foods. The vast array of ethnic cuisines provides a great example of how genetic predispositions to nutritional

preferences and tolerances perpetuates in populations today. These cuisines and paradigmatic dishes reflect ancestral diets; they represent what food sources and nutrients were available and what foods were most suited to the metabolisms of individuals within ethnic groups. As Nabhan (2004:1) suggests, “there are dynamic connections between our culinary predilections, our genes, the diet of our ancestors, and the places that our ancestral cultures called home for extended periods of time.”

While genetic patterns in populations can provide information about founding groups and the lifestyles of ancestral populations, archaeogenetics can also examine the complex factors underlying some of the leading causes of death in the world, including diabetes, cardiovascular disease, and complications from obesity (Acuna-Alonozo 2006:2881; Kaati 2010:158). The tools of archaeogenetics and genome analyses can enhance the identification of genes that increase susceptibility to disease, as well as ways that a susceptibility gene may perpetuate in descendent generations. After all, if a gene variant persists in an ethnic group, it is likely that the variant either confers some benefit or persists via neutral drift. Archaeogenetics and nutrition genomics provide a great setting in which to better explore such elements of nutrition-based disorders (Kaati 2010:65; Ridley 1999:263; Viertler et al. 2010:55).

Obtaining Ancient DNA: Methods and Challenges

Damage and Contamination

The first successful extraction and sequencing of ancient human DNA occurred in 1985 (Pääbo 1985), prior, even, to the amplification techniques that have proven vital to the study of ancient DNA. The field of archaeogenetics is still developing, but with careful practice, refined techniques, and rapidly improving technology, it can begin to reveal very valuable information

regarding ancestral genomes. The study of ancient DNA remains characterized by many challenges, however. The first and most significant of these being the state of preservation of the ancient DNA. Sequences obtained from ancient DNA are very limited in length due to high levels of damage and subsequent fragility. Its presence in an adequate amount for analysis is contingent upon the age of the specimen, the environment of the archaeological site, and the level of diagenesis (Brown & Brown 2011:123-128). To gauge whether the archaeological sample likely has appreciable quantities of ancient DNA, several proxies can be employed. First, the state of mineralization: the bone matrix serves to protect the DNA from extensive damage to a certain extent, but if the bone is severely demineralized, then DNA is likely too damaged to be successfully extracted and sequenced (Brown and Brown 2011: 126, Kaestle & Horsburgh 2002). Furthermore, the level of amino acid racemization is increasingly used as a determining measure in specimen selection (Mulligan 2006:366).

If the sample appears likely to produce ancient DNA, the next challenge lies in DNA extraction. It seems logical that ancient DNA would be obtained in the greatest quantities from the interior of long bones and teeth, which are characterized by a large amount of cancellous bone and spongy tissues encased in a protective outer matrix. Yet, surprisingly, other skeletal remains, such as ribs and vertebrae, have also proven to be sources of successful ancient DNA extraction (Kaestle & Horsburgh 2002:106; Kemp et al. 2005:27). Other sources include coprolites, which serve as possible sources for mitochondrial DNA, and—if preserved—hair, a potential source of both nuclear and mitochondrial DNA (Brown & Brown 2011:144; Tito et al. 2008:2). To distinguish, nuclear DNA contains the majority of genomic DNA, but is present in only two copies in the cell. Mitochondrial DNA, on the other hand, is present in the thousands. Therefore, it is very likely that amplifiable mitochondrial DNA can be obtained from an

archaeological specimen that lacks nuclear DNA suited for successful extraction and sequencing (Brown & Brown 2011:177; Kaestle & Horsburgh 2002:94). Mitochondrial DNA is very important to archaeogenetics, due in large part to its greater quantity, but also to its use in studying ancestry, population histories, and the etiologies of nutritional disorders (Kahn et al. 1996:518).

Once the source of potential ancient DNA has been identified, attempts to extract the DNA can proceed. A small sample of bone is removed from the specimen (typically 0.5-2g, taken from an inner surface), soaked in a chelating agent then either introduced into an organic phase (phenol:chloroform) or to silica powder, to which the DNA can bind in the presence of guanidium thiocyanate. These procedures function to isolate the DNA from calcium ions, RNA, and proteins (Brown & Brown 2011:25; Kaestle & Horsburgh 2002:94; Kemp et al. 2005:31). For coprolite analysis, slightly larger quantities can be extracted from the inner matrix; 2-5g is has proven sufficient for ancient DNA extraction and analysis (Tito et al. 2008:4).

Contaminating macromolecules and environmental contaminants are not the only concern, however. Ancient DNA is also frequently contaminated with modern DNA, thereby posing a huge problem to archaeogenetic analysis. To best prevent introduction of such contamination in analysis, an ancient DNA lab must be totally sterile, all lab equipment must be treated with UV radiation or extremely high temperatures, and all lab workers must wear complete protective suits. Yet despite these precautions, specimens are likely affected by contaminants previously introduced during archaeological excavation, curation, and analysis (Brown & Brown 2011:138). In this case, artifacts can also be treated to remove surface contaminants, given the assumption that most handling introduces contamination to the surface only. Such methods include soaking the sample in 3% sodium hypochlorite and/or exposing it to

UV radiation (Brown & Brown 2011:140). However, studies have shown that despite meticulous protocols, it is near impossible to completely rid a sample of modern DNA contamination. Therefore, ancient DNA analysts should focus on preventing further contamination, yes, but also on improving methods for identifying and accommodating contamination (Willerslev and Cooper 2005: 9). This can be accomplished by using controls with no starting DNA to check for the presence of contaminating DNA, and by cloning amplified DNA to analyze the quality and number of resultant sequences. Additional methods include tagging ancient DNA samples with unique multiplex identifier tags, and testing the reproducibility of the results by repeating the experiment in two separate lab facilities (Brown & Brown 2011; Tito et al. 2008:2; Willerslev & Cooper 2005:6).

Despite small quantities, sequencing of ancient DNA can occur through the “exquisite sensitivity of the polymerase chain reaction,” without which ancient DNA analysis would not be possible (Brown & Brown 2011:7). PCR has had profound effects on the field of genetics, and, in regards to archaeogenetics, PCR holds the particularly important ability to amplify the extremely short, damaged DNA fragments that are characteristic of ancient DNA extractions. The improving technology and increased availability of computer programs for genetic analysis further advance ancient DNA analyses. Such programs can find overlap between short sequences to obtain longer contigs, can analyze distance matrices to determine evolutionary relationships, and can compare the obtained sequences to existing databases to compare ancient and modern genomes and to identify disease genes in ancient DNA (Brown & Brown 2011:34-35; Nabhan 2004:5). The results of many of the initial ancient DNA studies have since been proven fallacious due to the presence of exogenous DNA contamination. Thus, it is extremely important to eliminate error from current ancient DNA studies through multiple checks,

reproducible results, and thorough analysis prior to publication. It is understandable that such a young field experienced some difficulties at its start, but with improved understanding, technology, and methodology, further studies should be extremely thorough.

Ethics

Not only is skepticism regarding ancient DNA research prevalent due to its initial struggles and erroneous results, but the field is also plagued with uncertainty and debates regarding proper ethical considerations. In genetic studies of modern populations, a system of informed consent, strictly regulated by federal and institutional legislature, must be employed before any genetic testing and research can proceed (Kaestle & Horsburgh 2002:106). Herein lies the challenge with ancient Native American remains: from whom do you obtain consent? Obtaining consent from the probable descendants of the deceased is complicated by the difficulties of assigning ancient remains to modern population groups. It is further complicated by the refusal of some modern cultural groups to recognize common ancestry due to rifts or legends that render modern Native American groups enemies, despite their recent common ancestor (Kaestle & Smith 2005:255; O'Rourke et al. 2005:232). For proposed research to be approved social and scientific significance must be demonstrated on a level that will offset the destructive nature of DNA extraction (Kaestle and Horsburgh 2002:95). Adequately indicating this to all involved parties could take a great deal of time, as the research proposal could likely become tied up in litigation, a battle between NAGPRA and the Archaeological Resources Protection Act. This could prove disadvantageous to archaeogenetics, as successful DNA extractions are best obtained when the sample is taken within the field. However, even though delayed research consent could decrease the quality and potential of the sample, obtaining

consent is a necessary evil. Although there are no fully defined standards, it remains the researcher's ethical responsibility to obtain consent from all involved parties, maintaining detailed documentation of all discussions, negotiations, and stipulations (Kaestle & Smith 2005:247, O'Rourke et al. 2005:238).

Archaeogenetics as Part of a Multidisciplinary Approach

In order to express the importance of a particular study, a researcher must emphasize how archaeogenetic information is an integral element of a larger, multidisciplinary study of a population or ethnic group. As with all anthropological studies, research collaboration and interdisciplinary analyses are of vast importance in drawing reliable conclusions. In the context of studying nutrition genomics, ancient DNA analyses provide a valuable supplement to information provided from osteology, population genetics, paleoethnobotany, cultural anthropology, history, and many other disciplines. Paleoethnobotany and historical records can be used to create dietary reconstructions from archaeological remains, population genetics can deduce the relatedness of different ethnic groups and identify genes that respond to dietary compounds, and osteology has the potential to identify disease markers manifested in skeletal remains. Archaeogenetics has the potential to tie all of this information together, providing explanations for the origins and causes of mutations and, given social and environmental conditions in prehistory, the possible pressures influencing positive selection and persistence of these gene variants. With improving techniques in archaeogenetics, we now have a better ability to identify how and why an individual's genome predisposes them to certain diseases, disorders, and dietary preferences (Brown & Brown 2011:6; Kaati 2010:80; Lieberman 2003:353; Viertler 2010:52)

Conclusions

In tandem with environmental and dietary reconstructions, we can begin to discern how the conditions of our ancestors shaped our genes and thus affect the way we react to one of the most significant aspects of our lives—what we eat. Ethnic cuisines reflect the nutritional availability and requirements of ancestral populations, which calls into question the degree to which food choices are an aspect of taste and free-will or a manifestation of our genes and programmed nutritional preferences. Archaeogenetics, compared to genomic sequence databases of modern populations, can be used to identify the genes most affected by different dietary compounds. In the case of Native Americans, dietary compounds that exert significant effects include lactose, glucose, alcohol, and fatty acids. Identifying genes that are affected by these compounds can shed light on how long nutritional disorders have been present in a lineage and the on pressures that caused them to arise and perpetuate. Using archaeogenetics, we could perhaps examine trends between the reactions of certain haplotypes and blood groups to proteins and dietary compounds in certain foods, better discerning the genetic basis and selective pressures of the heritable food allergies that affect 200 million people worldwide (Nabhan 2004:11).

The favism condition provides a perfect example of how a food allergy can benefit an individual. Favism is diagnosed as a serious allergy to fava beans and their pollen and is prevalent among ethnic groups from regions where malaria poses a significant threat. Consuming small amounts of the bean, or even inhaling its pollen, can cause an allergic reaction of enough significance to prevent the survival and spread of the malarial parasite. Interestingly, the time of peak harvest of fava beans correlates with the time of highest risk for contracting

malaria (Nabhan 2004: 67). Clearly, food has a drastic, integral role in the functioning of our bodies, influencing adaptations that increase an individual's resistance to adverse conditions. The complex interactions that underlie these adaptations are between genes, the environment, and dietary chemicals and have major potential to advance the fields of nutrition and public health. Better understanding our genetic programming can provide information on how to best nourish our bodies, providing a "prescription for intelligent food" that enables the design of a personalized diet on an individual level (Hart 2003:23). During the initial stages of attempts to provide aid for Native American groups, the United States government did not know enough of nutrition genomics to understand how much the calorie- and simple sugar-rich aid provisions would decrease the health conditions of the groups. Perhaps knowing more of nutrition genomics, more of "intelligent food," could enhance public health and better attune future aid to the dietary needs of recipient populations.

Furthermore, archaeogenetics and nutrition genomics have the potential to greatly benefit the medical field by identifying susceptibility genes for metabolic- and nutritionally-based disorders. This proves to be very important considering that "single-gene disorders such as galactosemia, celiac disease, familial hypercholesterolemia, lactose intolerance, and PKU can largely be controlled by specific dietary interventions and thus may be considered the 'classic' cases of gene-diet interactions." (Castle et al. 2007:25). Physicians and medical researchers are making great strides in the field of nutrition as alternative medicine: diets reduced in simple sugars (often gluten-free diets) have been shown to decrease the severity of symptoms in autism patients, and polyphenols derived from berries have shown to ease pain in individuals suffering from arthritis. We are just beginning to understand the effects that nutrients and dietary compounds have on our genes. Going to the source—to the ancient DNA of our ancestors—

could advance the field of nutrition genomics and the health of specific ethnic groups even further.

Archaeogenetics can help us focus on smaller-scale questions, enabling comparative studies among different ancestral lineages and haplogroups. Studying the genes of our ancestors can give insight into evolutionary processes, current human conditions, and the past social structures. The different ways that food defines our cultures, affects our bodies, and shapes our lives holds major implications for the study of the human race. Nutrition genomics, with genetic evidence, have “the potential to take on significant weight in social, political, and legal arenas” (Kaestle & Horsburgh 2002:107) not only in Native American populations, but worldwide.

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