American Indian Demographic History and Cultural Affiliation: A Discussion of Certain Limitations on the Use of mtDNA and Y Chromosome Testing

By

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Abstract

Mitochondrial DNA (mtDNA) and Y chromosome studies have been used increasingly over the last 20 years by anthropological geneticists and others to reconstruct the peopling of the Americas as well as to infer American Indian cultural affiliation and demographic histories. While the promise of this method is great, there are several problems inherent in some of its current uses. These limitations are discussed concerning the following six currently accepted methods: interpretation of coalescent times as times of origin; 2) the current uses of haplogroups; 3) sample sizes; 4) use of language groups to define population groups; 5) use of contemporary American Indian reservations to infer prehistoric tribal history; and 6) a combination of these to determine American Indian population history, historic migrations, and demographic history. This paper concludes that caution must be exercised in claiming too much for the method. Instead, it is recommend that it be used in conjunction with other established sources of data such as oral history, ethnography, linguistics, and archaeology when attempting to reconstruct American Indian cultural history or in determining the cultural affiliation of groups.

Key words

Genetic anthropology, haplogroups, demographics, cultural affiliation, American Indians

Introduction

Anthropological genetics is one of the more recent sub-fields in the study of American Indian cultural affiliation and demographic history, dating back some 60 years (see Matson and Schrader 1933; Matson 1938). However, in the last 20 years advances in technology have allowed anthropological geneticists to explore the origin of modern humans, the size and geographic origin of human populations, as well as the possibility of finding ethnic or even individual people's homelands. Recent articles using genetic data have claimed to link Europe/Western Asian populations with North American Indian populations as having recent common ancestry (Brown et al. 1998), identified a single wave of migration for the peopling of the New World (i.e., Bianchi et al. 1997; Easton et al. 1996; Merriwether et al. 1995) as opposed to several (i.e., Karafet et al. 1997), and concluded that some American Indian tribes recently moved into a geographic area (Kaestle 1997; Kaestle and Smith 2001) despite contrary evidence from oral history and archaeology. Some of the most publicized uses of genetic anthropology in recent years concern the question of the peopling of the Americas, and in compliance with the Native American Graves Protection and Repatriation Act (NAGPRA), as seen in such cases as the Spirit Cave Mummy and the Kennewick Man repatriation controversies. In these two examples the situation is complicated by the great antiquity of the skeletons, 9,415+/-25 years ago and 8410+/-60 years ago, respectively (Napton 1997; Chatters 2000). The potential benefits this new genetic research has to offer are vast and highly valuable. Such benefits include a better understanding of the genetic and evolutionary factors that influence populations; an understanding of maternally transmitted diseases such as blindness, epilepsy, dementias, cardiac and skeletal muscle diseases, diabetes mellitus, and movement disorders; the development of new metabolic and genetic therapies for mitochondrial diseases; and a better understanding of

the geographic origin of anatomically modern humans, to name just a few. However, caution is urged in applying the methods and results of present genetic research to the use of American Indian cultural affiliation and demographic histories. This paper examines six weaknesses inherent in current uses of genetic anthropology that attempt to resolve questions of demographic history and prehistoric cultural affiliation: 1) interpretation of coalescent times as times of origin; 2) the current uses of haplogroups; 3) sample sizes; 4) use of language groups to define population groups; 5) use of contemporary American Indian reservations to infer prehistoric tribal history; and 6) a combination of these to determine American Indian population history, historic migrations, and demographic history.

I. Coalescent Times as Times of Origin

A first problem confounding the uses of mtDNA (mitochondrial deoxyribonucleic acid) and Y chromosomes to infer American Indian demographic histories is in interpreting the coalescent times of genes as times of origin for the population. Although tracing the genealogy of mtDNA theoretically can lead to a single common ancestor, this is not evidence that the human population went through a period when only one breeding population was alive and reproducing. Tracing the coalescent times leads to one ancestor of a unilineally transmitted set of markers, but the descendents of the original mtDNA will have had haplotype frequencies that differed among themselves, resulting in a biased sample of the total historic population when using coalescent times. This is so because working back in time is does not allow one to take into account the various branches of diversity that the historic population had, but only can detect the lineal history of the specific marker being coalesced. Three primary assumptions arising

from the use of coalescent times (Hoelzer et al. 1998; Hudson 1990; Templeton 1993; Wolpoff 1999) that have been employed in understanding American Indian demographic history are:

A) gene coalescence is a regular process of mutation accumulation in neutral systems, and therefore can be timed like a regularly ticking clock with an acceptable range of error,

B) American Indian populations were isolated from each other after they originated or migrated to the Americas, and

C) the history of particular gene systems is the history of the specific populations in which they are found.

Prior to the historic period, and especially before the formation of reservations beginning in the 1850s, many American Indian groups were highly mobile autonomous entities, covering large areas of land. Similarly, many American Indians practiced a high degree of spousal exchange and intergroup marriage among other groups in order to solidify trade arrangements and political alliances. Some of these exchanges took place well over 500 miles from where the group has been historically recorded to inhabit. Examples of these trade centers are the large Native fisheries of the Northwest Coast such as The Dalles, Celilo Falls, and the Lillooet River Fishery (Schuster 1998; Stern 1998; Hayden 1992) where groups from the Northwest Coast, Plateau, Northern Plains, and Great Basin regions gathered. Other examples can be found from the archaeological record that show similar large regional centers that may have acted as gathering and/or redistribution centers such as Chaco Canyon in the US southwest (Lekson 2000) and Monte Alban, San Jose Mogote, Tlapacoya, and Tlatilco in central Mexico (Flannery and Marcus 1994). In fact, as Walker (1998:5-6) has noted for the Plateau peoples, “It is clear that Plateau peoples were and remain highly inter-active maintaining extensive intergroup

connections as well as extensive linkages with the Plains, Northwest Coast, and Great Basin groups. Connections with Subarctic groups are evident in the northern reaches of the Plateau of Canada."

One important requirement in the coalescence theory is the use of random samples of genes from the population under study. However, most studies have not used random samples, but instead have used convenience samples obtained from diabetic studies, rheumatic studies, and AIDS studies, as well as other studies (Jones, in preparation; also see below). As Donnelly and Tavare (1995: 418) point out, "In practice, genetic data are typically obtained from convenience samples rather than proper random samples. There is an obvious danger that such data may contain individuals who share relatively too much ancestry on the relevant timescales. The extent to which application of coalescent (or traditional) methods to such convenience samples may be misleading remains an open, and potentially serious, question." Furthermore, most studies rely on the idea that American Indians came over in small groups (usually thought to have occurred as part of one to three migration waves; see Dillehay 2000 to cite one recent work) across the Bering Land Bridge in prehistoric times. If this is the case, coalescence times will be shorter because smaller populations in the past are more likely to share ancestors (Donnelly and Tavare 1995: 410), and thus lead to an accelerated time of origin for American Indians and thus not truthfully demonstrating the occupational time depth American Indians have in the Americas.

Furthermore, departures from random mating due to inbreeding, assortative mating, or population stratification can lead to non-random association between genotypes and further complicate the interpretation of the data and coalescent times. One such example is the well-documented moiety and clan system among the Tlingit peoples of southern Alaska. Among the

Tlingit, marriage was always with a member of one's opposite moiety, and preferably with a member of the father's clan and house (De Laguna 1975). Therefore, the Tlingit as well as many other American Indian groups of the Northwest Coast and other regions practiced a highly selective, non-random form of mating that could influence the genetic data (see *Handbook of North American Indian* series published by the Smithsonian Institution). There is also a growing body of evidence suggesting that there could have been various forms of admixture between American Indians, Japanese, and Russians during the last 500 years (Quimby 1985; van Stone 1984; Boyd 1999), not to mention known examples of admixture during the historic period with trappers, fur traders, explorers, and other Europeans. Likewise, Karafet et al. (1997) concluded that because of the presence of the 1T haplotype (a Y chromosome combination haplotype [see next section for a discussion of haplotypes]) in both northeastern Siberia and the Americas, the possibility of historic and prehistoric back-migration is extremely likely. Similar studies have also noted the possibility of gene transfer or the "hitch-hiking theory" among American Indian and Asian populations (Bianchi et al. 1997; Bradman and Thomas 1998; Hudson 1990). Because population-coalescence times are frequently a result of the fusion of several of the ancient phylogenetic clusters and not the age of individual populations (Watson et al. 1997), faulty results may be reported. It is evident that neither American Indians nor specific American Indian groups were ever isolated populations and that the history of a contemporary group's genes are not a specific history of that American Indian population. Therefore, using gene coalescent times as possible times of origins for American Indians can lead to spurious conclusions, for there is no evidence that American Indians were ever: 1) part of a neutral system that can be timed like a regularly clicking clock, 2) were isolated from each other or from Asian populations, and 3) that the current genes systems found in a particular population fully represent the diversity

and history of that population.

II. Current Uses of Haplogroups

Although it has been noted that limitations exist when studying only one gene (Chen et al. 2000; Karafet et al. 1997; Mountain and Cavalli-Sforza 1997), most studies still rely on only one gene and its alleles because of the ease in identifying differences in a restricted location on that gene**,** especially in non-recombining genes such as mtDNA. The allele sequences that are studied are called haplotypes, which for American Indians presently fall into five recognized haplogroups (A, B, C, D, and X), and have been used in most studies concerning American Indian population genetics.

One of the current limitations with the uses of haplogroups for inferring American Indian cultural affiliation is that there is the possibility of discovering new haplotypes as more tribes are studied and techniques develop (Easton et al. 1996; Karafet et al. 1997; Schurr et al. 1990; Smith et al. 1999). By testing only for known haplotype frequencies, it is likely that other haplotypes will go undetected, resulting in spurious conclusions from simplified haplotype frequencies. Along with the possibility of new haplotypes being discovered, it is known that many prehistoric American Indian groups were not stationary and the use of within-local-population frequencies for the genetic sequences, highly affected by each population's specific recent demographic history, and thus when relying on the use of haplogroups, scientists will probably underestimate the nucleotide diversity of American Indians as a whole (Bonatto and Salzano 1997). Therefore, the differing results between CR (control region) sequences and RFLP (restriction fragment length polymorphism) data cannot be explained either by sample size or attributed to the different ways in which the haplotype frequencies were treated, but are more probably due to the

different populations or regions of the mtDNA studied. Furthermore, the only changes introduced in genes are point mutations, insertions, and deletions (with insertions and deletions being rare in comparison to point mutations). This means that each of the four possible founding lineage clusters can be thought of as containing the founding lineage haplotype plus a collection of that lineage's descendants. However, as has been noted for the Y chromosome, the original Y chromosome can eventually die out, shifting time, haplotype frequency, or relationships (Bradman and Thomas 1998) and can result in faulty data when comparing present American Indian tribal frequencies to those of ancient American Indian haplotype frequencies. As Bradman and Thomas (1998) pointed out using the insertion of the YAP (Y chromosome alu polymorphism) indel (insert) on the Y chromosome, descendents of individuals after only one generation may not carry the same Y chromosome alleles. It is possible that a descendent of the individual who first acquired the YAP indel may lose that indel, yet still remain a descendent of that individual. This is also possible with mtDNA, where a father's son or daughter will not carry the genetic information of that person's father's mother. By only looking at specific alleles, mutations, insertions, and deletions can be viewed as coming from discontinuous populations. Likewise, "the combination of a decrease in the effective population size and genetic hitch-hiking may have been the cause producing a single variety of Y-chromosomes in the earliest ancestors of extant Amerindians," (Bianchi et al. 1997: 87) which would result in faulty results in determining affiliation between American Indian groups. Similarly, because the mitochondrial genome undergoes no recombination, the 16,569-bp genome behaves evolutionarily as a single locus. As MacEachern (2000: 358) recently notes, "In particular, it appears that there may be significant variability in selection mechanisms on the genome itself and in the mitochondria and in rates of phylogenetic versus intergenerational mtDNA mutation

that are only now being appreciated (Gibbons 1998; Parsons, Muniec, and Sullivan 1997)." Therefore, inferences from any one such locus lack robustness (Pamilo and Nei 1988). As noted above, because of the potential inaccuracy in using a constant molecular clock, estimates of mutation rates are going to be imprecise (Donnelly and Tavare 1995; Hoelzer et al. 1998). Because of the high mobility of American Indian groups in the prehistoric, along with examples of intergroup marriage and non-random mating, there is ample reason to believe that the genetic history of American Indians is much more complex then the current five haplogroup frequencies lead us to believe.

III. Sample Size

Many of the discrepancies and much of the unreliability of the data employed in American Indian genetic studies lies in the sample sizes of the populations used. Variations in population size are commonly attributed to bottlenecks and the so-called founder principle in which a population encounters a severe reduction in size or a few individuals colonize a new area resulting in a small selection of gene frequencies as compared with the original population. However, an important complication that makes it impossible to determine census size of a prehistoric human group as a direct estimate of the effective population size is that human populations have overlapping generations. Rogers and Jorde (1995: 1-36) have shown that the only sense in which sequence diversity can be employed as a measure of age is as an estimation of the time during which a particular population has expanded after experiencing a severe bottleneck. This is because we are dealing with alleles (haplotypes), and not with distinct populations. In fact, the error variance increases with time and the earliest observations are the most precise. Computer simulations that suggest that the four major haplogroups found among

American Indians underwent a bottleneck followed by a large population expansion may be questioned. These simulations are based primarily on the analysis of CR sequences from haplogroup A and do not take into account haplogroups B, C, D, and X (as well as the possibility of future haplogroups being discovered). Similarly, although most studies on the problem of dating the original occupation of the Americas have used sequence diversity as a measure of age, few have investigated whether their samples met the very stringent assumptions required by this practice (Bonatto and Salzano 1997: 1417). Furthermore, Bonatto and Salzano (1997: 1417) have also noted that studies using RFLPs found that haplogroup B had a much lower diversity than the other three (A, C, D) which would lead to inaccurate computer simulations. Based on this, the current dates from mtDNA and Y chromosome studies contending that American Indians arrived in the "New World" around 35,000 years ago can be questioned (Bonatto and Salzano 1997; Brown et al. 1998). This number is actually the time during which American Indians theoretically experienced an expansion after a bottleneck. However, it is unknown if this bottleneck took place in Asia, the generally accepted origin of American Indians, or in the Americas after their arrival, nor is it known what effects migrations and subsequent bottlenecks from disease and other factors have on this time estimation. Therefore, the date of 35,000 years ago could be the time one group of American Indians entered the "New World" or when a group experienced a bottleneck in Asia and subsequently entered the Americas, or any number of other possible scenarios.

Another problem with the current sample sizes being used is the actual numbers of individuals tested to infer the genetic makeup of the entire population. Typically, sample sizes range between four and 30 individuals per tribal population; this is insufficient to detect little more than the most common haplotypes in each population. Although it is necessary to have

genetic samples from 50 males or 50 females of an individual population to accurately infer genetic demographic history, no study has done this (Wells 2000). The largest study to date on American Indians dealt with 2,198 males from 60 global populations, including 20 American Indian groups (Karafet et al. 1999; this study relied on large amounts of data gathered from previously published reports, and thus could not correct for those sample sizes). However, only the Inuit Eskimo and Navajo samples were over 50 at 62 males and 56 males respectively. All others ranged from as high as 44 to as low as two individuals. It is unrealistic to assume that one can get an accurate picture of a tribe's genetic frequencies using only two males. In fact, Weiss (1994: 834) suggests that we may not be able to distinguish loss of lineages after one migration or from separate migrations from a common source population, thus further stressing the critical need for adequate population sample sizes. A clear example of the importance of sample size is seen in Easton et al.'s (1996) study and Torroni et al.'s (1993) study on the Yanomamo. In Easton et al.'s sample they detected both haplotypes X6 and X7, but in Torroni et al.'s sample from a neighboring village they did not detect any of these two haplotypes. As Ward et al. (1993) have noted, a sample size of 25 will detect ~63 percent of the lineages in a tribe with normal diversity. In tribes with extensive diversity a sample size of 25 individuals will only detect ~40 percent of the lineages and sample sizes of 70 or above are required to detect two-thirds of the lineages. The fact that the majority of studies lack the required sample sizes necessary to detect even 63 percent of the lineages in a normally diverse tribe brings into question many of the results of these studies, especially when it has been noted that most American Indian tribes are believed to have a high level of diversity (Ward et al. 1993).

In the past, as now, choice of mates is largely dictated by geographic, socioeconomic, religious, ethnic, and other constraints. This has the effect of subdividing and stratifying the

gene pool of a population in very complex ways. Likewise, migration is also difficult to reconstruct from mtDNA and Y chromosomes. The most meaningful measure of migration from a genetic point of view is obtained by taking the generation as the time unit. Measuring the distribution between birthplaces of parent and offspring theoretically can yield a statistical measure of migration. However, this method works only for a continuous model in which the population is constant, and is not entirely satisfactory when the population is highly clustered as is believed most prehistoric American Indian populations were (Cavalli-Sforza and Bodmer 1971:433). A similar limitation in using such data to infer migrations is that exchange between non-neighboring clusters is frequent enough among American Indians to violate the rules of the simplest stepping-stone models (Cavalli-Sforza and Bodmer 1971:433).

Another aspect of human DNA confounding many of the current uses of this data to reconstruct hypothetical demographic histories is that human mtDNA variation is high. Likewise, genetic variation within populations is much greater than between populations (Walpoff 1999:551). What this means is that mtDNA evolution, and possibly the evolution of other genetic systems, is not the same as the evolution of particular populations. As Scozzori et al. (1999) have noted, groups or tribes thought to have descended from a common ancestor more than 10,000 years ago may have lost even their shared-by-descent portion of their gene pool and can no longer be detected as affiliated through genetic analysis. Likewise, population specific mutations and the gene trees inferred from these sequences are generally inconsistent with historic and prehistoric population affiliation. Page and Charleston (1990) have identified a method for visualizing and quantifying the relationship between a pair of gene and species trees that constructs a third, reconciled tree. Reconciled trees use a more critically optimal method for mapping the combined history of genes and populations. However, even this more accurate

method of depicting gene and population trees has limitations such as allele phylogenies and horizontal transfer, neither of which has been addressed in studies concerning American Indian demographic history. In fact, many of the polymorphisms observed for mtDNA probably predates population separations (Mountain and Cavalli-Sforza 1997) and would not be useful in constructing genetic, population, or reconciled trees. Mitochondrial DNA or Y chromosome lineages are not human populations. In order to estimate the significance of variation of gene frequencies between groups, it is necessary to estimate how large a sample must be in order to be representative of the group. This can only be accomplished if an accurate estimate of the real variation to be expected in the gene frequencies is possible. This estimation is valid only for genes without dominance, in which case genes can be counted. However, if people in the sample from a given tribal village or town are closely related, a single source of variation may greatly inflate the estimate of variance between populations (Cavalli-Sforza and Bodmer 1971:422). Multivariate analysis, or the use of more than one trait or gene, which is presently the most commonly employed method of analysis, poses more difficult problems in that one must determine the maximum number of genes possible for each population in order to be accurate. Unfortunately, many authors have tested only a small set of markers on one gene (univariate) for their studies (Cavalli-Sforza et al. 1994: 22), combining their data with those of others to result in several sets of markers to arrive at their multivariate analysis. Not only have limited numbers of markers been studied and subsequently combined with other studies (which was noted above), but the mutation rate for insertions and deletions on those markers is unknown.

IV. Language

Not only have sample sizes of groups or tribes being tested been inadequate, but most studies have relied on the use of controversial linguistic phyla in order to place their data into objective, quantifiable groups. However, as several papers have pointed out, not only do the correspondences between languages and populations differ (i.e., Barbujani 1997; Karafet et al. 1999; Scozzari et al. 1999; Schurr et al. 1999), but there is no agreed upon set of linguistic phyla for American Indians (Greenberg et al. 1986; Greenberg 1987; Bateman et al. 1990; O'Grady et al. 1989; Ruhlen 1987, 1994). Most studies use several linguistic phyla that are subject to serious criticism, such as Altaic s.l., Austric s.l., Indo-Pacific, Amerind (*sensu* Greenberg 1987), and Na-dene s.l., which are in turn awarded equal status as more accepted phyla from other parts of the world such as Sino-Tibetan, Indo-European, and Dravidian (Bateman et al. 1990). Furthermore, it has been noted that "given 56% correspondence between linguistic phyla and population aggregates at the coarse level of resolution, 11% correspondence at the fine level, and the poor integrity of both superphyla, the parallelism between the genetic and linguistic entities does not strike us as especially 'remarkable'" (Bateman et al. 1990:7). Likewise, "there is an important problem of time scales involved in this work, since at this point neither genetic nor linguistic research can lay claim to chronometric techniques comparable in precision to those used by archaeologists and historians" (Pluciennik 1995:44-45). Languages do not change at specific rates and therefore using contemporary linguistic phyla to extrapolate prehistoric population groups is ill-founded. For example, in 1995 there were approximately 209 native North American languages still spoken, close to only half the number that existed five hundred

years earlier (Goddard 1996). Similarly, of the Eastern Algonquian languages, only seven were spoken in 1970 out of a total of 20 from 200 years earlier (Goddard 1978).

Many of the researchers conducting genetic tests have noted the discrepancies between linguistic phyla and genetic phyla. Scozzari et al. (1999) concluded that geography is a better method for identifying affiliation then linguistics. Likewise, Poloni et al. (1997) concluded that genetic data is more accurate and useful for distinguishing between linguistic phyla than between populations in the same language family. Finally, Schurr et al. (1999) noted that populations on the Kamchatka peninsula were genetically similar based on geography but quite divergent when compared to linguistically related groups. Therefore, the use of linguistic phyla may be useful when studying the differences between language phylas (i.e., between Na-Dene and Eskimo-Aluet), but not as useful when studying groups within the same language phyla (i.e., Yakama and Nez Perce). Not taking into account the current discrepancies between American Indian language phylas can lead to several different conclusions depending on how the linguistic and genetic data are combined. For example, Karafet et al. (1997) found that Y chromosome markers did not agree with the linguistic phyla proposed by Greenberg et al. (1986) for the peopling of the Americas. However, in a later study using different Y chromosome markers Karafet et al. (1999) did agree with the linguistic phyla proposed by Greenberg et al. (1986). Other studies have arrived at similarly contradictory conclusions (see Schurr et al. 1999; Poloni et al. 1997). To use current American Indian languages as a baseline for prehistoric American Indian genetic affiliations and population groups seems presumptuous. Until linguistic specialists agree upon the classifications of American Indian languages, they should not be used as a means of inferring and objectifying prehistoric population groups.

V. Contemporary American Indian Reservations and Demographic History

As noted above, the current sample sizes of most studies fall far short of a reasonable number of individuals being tested to be considered an accurate data set of the population. However, besides the limitations arising from the small sample sizes, as well as those discussed concerning the present use of linguistic phyla, there are even greater problems lying in what the studies consider populations. Presently, studies concerning American Indian cultural affiliation and demographic history test individuals from a reservation and combine their allele frequencies to arrive at the haplotype makeup of that population. Therefore, the researchers are using contemporary American Indian reservation demographics to arrive at a population that they then infer back into prehistory. However, one of the primary problems with this method is that most contemporary American Indian reservations are not made up of a single group, but consist of several different groups of American Indians that prior to being forced onto reservations were autonomous groups. For example, Merriwether et al. (1995) use samples from Haida, Dogrib, and other contemporary American Indian reservation groups which they consider as one population group. However, the Dogrib as a whole tribe were prehistorically made up of several different bands that occupied a large area in the Northwest Territories, Canada, between the Great Slave Lake in the south to the Great Bear Lake in the north and from the lowlands on the east side of the Mackenzie River to Contwoyto, Aylmer, and Artillery Lakes. The Dogrib are known to have had regular contact with the Bearlake Indians, the Slaveys, Chipewyans, and occasionally Eskimos (Helm 1981: 291). Likewise, the Haida, along with other Northwest Coast tribes were known to have traded slaves up and down the coast. The Haida traded slaves they acquired from the Kwakiutl with the Tlingit (Blackman 1990). Other such examples can be found in the studies by Smith et al. (1999), Karafet et al. (1999), Lorenz et al. (1996), and Brown

et al. (1998) that use contemporary reservation groups as prehistoric population groups. Such contemporary groups as the Yakama and Apache are good examples. The present Yakama reservation in Washington is made up of at least five different groups that were prehistorically independent bands or groups (Schuster 1998). Similarly, there is still much disagreement among American Indian specialists as to how many different Apache groups there were prior to the arrival of Euroamericans. Currently there are seven recognized Southern Apachean speaking groups: Chiricahua, Jicarilla, Kiowa-Apache, Lipan, Mescalero, Navajo, and Western Apache. However, depending on "how much more extensive their territories are conceived to have been in the past depends upon one's view of claims that the Querechos, Vaqueros, Teyas, Janos, Jocomes, Mansos, Sumas, Cholomes, Jumanos, Cibolos, Pelones, Padoucas, and various other groups named in early Spanish and French records were Apacheans" (Opler 1983:368). Finally, over the last hundred years reservation populations have been greatly affected by outmarriage with other tribal groups and marriage with non-Indians. An example of this change can be seen in a study done by Walker (1990; see also Walker 1972) for the Confederated Tribes of the Umatilla Indian Reservation (CTUIR). This study showed that in 1990 54 different tribes were represented in the blood of CTUIR individuals (see Table 1). Furthermore, one CTUIR individual had various amounts of Cayuse, Walla Walla, Umatilla, Nez Perce, Snohomis, and non-Indian blood, while another individual had Umatilla, Cayuse, Walla Walla, Yakama, Nez Perce, Quinault, Snoqualmie, Cascade, and non-Indian blood. It is evident that the population groups current studies are using to infer American Indian cultural affiliation and demographic history are not acceptable. One cannot use contemporary allele frequencies from a few individuals of a contemporary American Indian reservation to arrive at an unequivocal haplotype for that group, either presently or prehistorically.

Table 1: Blood Types found in CTUIR Tribal Members

Tribal Affiliation	Geographic Proximity	Geographic Location
Alaskan	Distant	Arctic
Arikara	Distant	Plains
Assiniboin	Distant	Plains
Bannock	Distant	Great Basin
Blackfoot	Distant	Plains
Canadian	Distant	
Cascade	Neighboring	Plateau
Cayuse	Official Blood Line	Plateau
Cherokee	Distant	Plains
Cheyenne	Distant	Plains
Chippewa	Distant	Plains/Subarctic
Chocktaw	Distant	Southeast
Cochiti	Distant	Southwest
Coeur d'Alene	Neighboring	Plateau
Colville	Neighboring	Plateau
Cowichen	Distant	Coast
Cowlitz	Neighboring	Plateau
Cree	Distant	Plains/Subarctic
Crow	Distant	Plains
Flathead	Neighboring	Plateau
Grande Ronde	Distant	Coast
Hopi	Distant	Southwest
Klamath	Neighboring	Plateau
Klickitat	Neighboring	Plateau
Kootenai	Neighboring	Plateau
Laguna	Distant	Southwest
Lummi	Distant	Coast
Makah	Distant	Coast
Modoc	Distant	Coast
Muckleshoot	Distant	Coast
Navajo	Distant	Southwest

Nez Perce	Neighboring	Plateau
Ottawa	Distant	Northeast
Paiute	Distant	Great Basin
Palus	Neighboring	Plateau
Pawnee	Distant	Plains
Puyallup	Distant	Coast
Quinault	Distant	Coast
Sac and Fox	Distant	Plains
Seminole	Distant	Southeast
Shoshone	Distant	Great Basin
Siletz	Distant	Coast
Sioux	Distant	Plains
Snohomish	Distant	Coast
Spokane	Neighboring	Plateau
Tulalip	Distant	Coast
Walla Walla	Official Blood Line	Plateau
Warm Springs	Neighboring	Plateau
Wasco	Neighboring	Plateau
White Mountain Apache	Distant	Southwest
Winnebago	Distant	Plains
Wishram	Neighboring	Plateau
Yakama	Neighboring	Plateau

A further problem in the use of contemporary American Indian reservations can be found in the use of ancient DNA (aDNA). Several reports have used aDNA to construct ancient populations that are then compared to present American Indian reservation populations. These studies are plagued by many of the limitations already noted such as sample size, demographic histories, the possibility of mutation addition or deletion, and other factors. Kaestle (1997) attempted to compare an ancient population from western Nevada to those of contemporary tribal populations in the region through haplogroup frequencies. However, Kaestle's ancient

population spanned 5000 years in time. A genetic sample dating to 5905+/-125 years BP cannot be considered part of the same population as a genetic sample dating to 860+/-75 years BP without also automatically designating contemporary American Indians as part of that population. "Ancient DNA samples are not populations in the traditional sense of the term. The individual specimens that constitute aDNA samples may span several centuries and even geographic space. Thus they are the equivalent of sampling an individual every few generations to characterize a continuous population" (O'Rourke et al. 2000). This is especially true when these samples are then compared to contemporary American Indian reservations that each have their own, unique demographic history. Likewise, the use of aDNA models to reconstruct a population assume (or cannot accurately model) that these ancient populations were somewhat isolated, and that these populations did not practice forms of intergroup or outgroup marriage. However, as previously noted for the Northwest Coast and the Plateau regions, highly complex forms of intergroup marriage have been practiced for centuries. Complex forms of intergroup marriage have also been documented for Great Basin tribes (see D'Azevedo 1986). Not only has there been extensive intergroup marriage within regions, but also between regions as noted in Walker (1972, 1990).

Finally, it should be noted that many of the scientists conducting these studies acquire a large proportion of their blood samples or genetic material through convenience samples. Convenience samples means that the blood samples or genetic material were not collected by the investigating scientist, but instead through third parties. Many of these third parties initially acquired the blood or genetic material for other reasons, such as diabetes testing. A review of the literature has revealed that over a hundred institutions have allowed these scientists access to American Indian blood, a lot of the time without the individual who gave the blood having any

knowledge of this. Though there are many problems with this in and of itself, the point that is important in the present discussion is that the scientists have no means of verifying the actual tribal affiliation of the blood sample they are using. For example, when an individual goes in for diabetes testing, they designate themselves and their tribal affiliation, through there is no guarantee that this designation is correct, nor is there any knowledge of that individuals family genetic history. This fact could greatly mislead the scientists into concluding various tribal haplotype frequencies that may not be correct.

VI. Genetics and American Indian Cultural Affiliation

The fact that most studies have not addressed the above concerns is only part of the present problem with applying anthropological genetics to American Indian demographic history and cultural affiliation. In fact, no studies concerning American Indians have seriously taken into account the demographic history of the last 500 years when Euroamericans arrived in the "New World." Almost every contemporary American Indian tribe or group in the Americas has experienced severe epidemic diseases, depopulation, acculturation, and displacement from their native lands. These factors have caused some tribes to disappear, others have experienced population fluctuations greater than 80 percent, and some have been displaced from their home land by hundreds of miles (Boyd 1999; Dobyns 1983; Ehle 1988; Jones 2002). For example, the American Indians of California numbered upwards of 310,000 during the eighteenth century, but by the turn of the twentieth century the native population had dropped to 20,000 (Cook 1978). Similar population declines are known for the Plateau with a loss of approximately 20,000 Natives between 1805 and 1860 (Boyd 1990), the Northwest with a population decline from approximately 200,000 Natives in 1774 to 40,000 in 1874 (Boyd 1990, 2000), as well as other

regions. Furthermore, admixture with historic Europeans and Euroamericans such as fur trappers, explorers, African Americans, and earlier settlers must be accounted for; it is well known, though not well documented, that many of these non-indigenous peoples married or mixed with American Indians.

Any mtDNA or Y chromosome study that attempts to date the first appearance of a particular population in a certain geographical area as big as the Americas or as small as the Great Basin should be based on extensive sampling, not only of the population under consideration but also of potential source populations and neighboring populations. A phylogenetic analysis can then theoretically identify the putative founder sequences. This requires that the mutations distinguishing these founders must be disregarded in order to set the evolutionary clock to zero to coincide with the arrival of a particular population in the new area. Considerable scientific care must be exercised in choosing realistic demographic models to describe the process adequately. For example, current models that assume constant population size and random mating would be unrealistic in most situations for the following reasons: 1) arrival in a new area is likely to trigger subsequent population expansion for many generations; 2) for a population on the move, the demographic pressure is more relaxed, allowing population sizes to fluctuate rather freely, without statistically conforming to an expected (time-dependent) size; 3) over a period of tens of thousands of years, environmental conditions often change drastically, obviously influencing the effective population sizes; and 4) ongoing gene flow from neighboring populations will inevitably distort the estimation of nucleotide diversity, and thus the coalescence time estimate (Forster et al., 1996: 944).

Conclusion

Although mtDNA and Y chromosome studies can provide insights on America Indian origins and prehistoric relationships, they should be used with caution. Mitochondrial DNA and Y chromosome studies are in their infancy. Because of the various limitations listed above, as well as a lack of correlation between anthropological genetic data, archaeological data, ethnographic data, and oral tradition, these studies should be viewed as inchoate and requiring further investigation and support from the other fields of anthropology. Current controversies surrounding Spirit Cave Man and Kennewick Man should not be resolved only by mtDNA or Y chromosome testing. The mtDNA and Y chromosome data for American Indians, as well as many other regions throughout the world, have serious limitations. However, because of the claimed authoritative validity of these studies there is great danger that they will convince non-specialists of the validity of the hypothesized associations between American Indian groups. The non-specialists would be ill-advised to rely on the claims put forth by mtDNA and Y chromosome inferred American Indian studies because they take little account of the vast majority of ethnographic, linguistic, historical, and archaeological research. However, archaeologists, ethnologists, linguists, and historians should take note of some of the inferences currently being made by anthropological geneticists. It is believed that mtDNA and Y chromosome data offer an opportunity for discourse among our often disparate fields, allowing us to achieve a greater understanding of American Indian cultural affiliation and demographic history. However, further studies should gain tribal approval before using tribal blood, especially when claims are subsequently made denying various affiliations between that tribe's blood and other groups or ancient skeletons.

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