

"private polymorphisms" in nuclear genes. The congruence of nuclear and mitochondrial genetic data generally supports previous conclusions about the role of early tribal isolation and founder effects leading to the divergence of tribal gene pools, although there is still some debate on this point.

D. Finally, the genetic composition of ancient populations may or may not be the same as extant groups occupying the same geographic region because of population relocation, genetic drift, or other stochastic processes. For example, the ancient Stillwater Marsh population does not appear to be ancestral to any modern Amerindian population from the Great Basin region in Nevada, based on haplogroup frequency data. On the other hand, ancient Eskimo and Aleut samples have nearly the same haplogroup frequencies as their modern antecedents, and the same is true for the ancient Anasazi and Fremont cultures with modern Puebloan Indian groups. Overall, these data suggest that, once they became genetically distinct from surrounding groups, many regional populations maintained their genetic integrity over a considerable period of time.

8. Various researchers have attempted to date the antiquity of New World haplogroups A-D, as these kinds of dates provide a temporal yardstick by which to measure the length of human occupancy of the Americas. Some have used RFLP haplotype data to make these divergence or coalescence time estimates, whereas most have employed CR sequence data. In all cases, it has been assumed that the non-shared mtDNA variation evolved independently in Siberia and the Americas, since only the founding haplotypes of the various haplogroups were known to be shared between modern indigenous groups from these regions. This assumption is supported by the general starlikeness of each haplogroup in phylogenetic trees, which indicates the expansion of derivative haplotypes from a common ancestral form(s).

9. Two of the oldest mtDNA lineages in the Americans are haplogroups C and D (Table 2). Their average ages in the New World are 45,230–27,300 and 47,650–23,535 YBP, respectively, using both RFLP and CR sequence estimates. The sequence divergence estimates for Siberian haplogroups C and D are generally comparable to those for Native Americans. In this case, the lower value for Siberian haplogroup C results from using RFLP haplotypes from only three populations to make its estimate as compared to using haplotypes from

15-20 groups for the Native American estimate (Table 2). These results confirm the antiquity of haplogroups C and D in northern Asia and the Americas, and the ancient genetic links between the populations inhabiting these regions.

10. The divergence time for haplogroup A in the Americas was comparably ancient. However, the value for Siberian haplogroup A is much smaller than that for Native Americans because the Siberian estimate was based on RFLP haplotype data from essentially only two populations (the Chukchi and Siberian Eskimos), whereas that for Native Americans was based on data from 15-20 populations. A relatively low CR sequence diversity of haplogroup A mtDNAs has also been noted for North American Eskimos and Na-Dene Indians (13,000-7,000 YBP). Thus, it appears that the ancient Beringian populations which gave rise to the Chukchi, Eskimo-Aleuts, and Na-Dene Indians underwent a more recent 'bottleneck', followed by the expansion of these haplogroup A mtDNAs in the Arctic and Subarctic regions of North America.

11. Based on RFLP data, haplogroup B also had a divergence time (17,700-13,500 YBP) which was considerably shallower than those of American haplogroups A, C and D (Table 2). However, recent analyses of CR sequence variation in Native Americans have indicated that haplogroup B may be equally as diverse as haplogroups A, C and D. In addition, previous work among Asian populations has shown that haplogroup B haplotypes were present in Central-East Asia by at least 24,000-30,000 YBP (Table 2). Thus, the molecular data suggest that the four primary haplogroups in Native Americans were brought to the New World well before the last glacial maximum (~18,000 YBP).

12. Various studies have also detected mtDNAs in Native Americans that do not fall into haplogroups A-D. These were originally designated as "other" (OTHER) haplotypes. The majority of these OTHER haplotypes were attributed to non-native admixture due to their apparent affinities with European mtDNAs (Brown et al. 1992; Torroni et al. 1994d). In fact, the OTHER haplotypes detected in the Ojibwa and Navajo resembled the haplogroup X mtDNAs seen in French Canadians and other European populations. In addition, a single haplotype in the Maya appeared to belong to European haplogroup H, the most commonly observed mtDNA lineage in