

Mitochondrial DNA diversity in indigenous populations from Central Mexico and its implications for the peopling of Mesoamerica

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Introduction: During the 13th and 14th centuries CE, the Aztecs (Mexico) relocated to and expanded in the Valley of Mexico (VM). Through intermarriage with neighboring peoples to establish political and military alliances, the Aztecs became a dominant power in Mesoamerica and, in the process, created an ethnically and linguistically diverse population. At the time of contact with Spanish explorers in the 16th century, the VM was the most densely populated region of Mesoamerica. Today, the region supports more than half a million indigenous people, including the linguistically distinct Otomi and Nahua, its two largest native groups.

Methods: To assess the genetic history of the Valley of Mexico, we analyzed mitochondrial DNA (mtDNA diversity) in Otomi and Chichimeca (Oto-Manguan), Nahua (Uto-Aztecan), and Tepehua (Totonocan) populations. In total, we analyzed genetic variation in 550 individuals from twenty-three communities in the states of Guanajuato, Hidalgo, Morelos and Queretaro. MtDNA diversity was characterized through control region sequencing of more than 800 DNA base pairs (bp), as well as through coding-region SNP genotyping. In addition, more complete coding region diversity was assessed in 25 samples using the GenoChip microarray.

Results: Genetic analysis of the Otomi, Chichimeca, Nahua and Tepehua samples revealed a high frequency (>98%) and great diversity of the four major Native American haplogroups (A2, B2, C1 and D1), along with the presence of D4h3 among the Otomi. The GenoChip generated high resolution SNP genotypes for the selected samples, and revealed new A2 mitogenomes in the study populations. In addition, control region sequence data were used to estimate genetic differentiation in and gene flow amongst these ethnic groups, and assess genetic diversity within the different language families represented by them.

Conclusions: Our findings show high haplotypic diversity as well as a large number of founding lineages from each of the major Amerindian mtDNA haplogroups. This pattern suggests that VM may have served as a hub for population growth, as well as a launching point for subsequent migration, both to the north and south, for millennia.

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