

Insights into the genetic diversity of indigenous Mexican populations

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Despite the development of molecular techniques to address the reconstruction of human history, there are still limitations such as the lack of systematic sampling of populations under study and the availability of samples from geographic regions which could be especially informative with respect to the processes of evolution and human dispersion. One such region is North America, which, given its ethnic and linguistic characteristics, may contribute greater information with respect to the settlement process of the New Continent, which even today is controversial.

The present project intends to address the complexity of the dynamics of the settlement of America by means of the molecular analysis of the indigenous communities that exist in present day Mexico and analyze them with publicly available sequence data from North, Central and South American native populations. For this study, blood samples were obtained from six indigenous communities: Tarahumara, Purépecha, Otomí, Mixteco, Nahuatl and Triqui, each belonging to some of the six linguistic families described in Mexico. The hypervariable region I and some biallelic markers within the coding region of the mitochondrial DNA (mtDNA) have been analysed to determine the haplotype composition of 293 individuals. We have found four Amerindian haplotypes A, B, C and D. No traces of other Amerindian haplogroups, such as X, or non-Amerindian sequences were found within our populations. Sequence diversity indices, genetic distances and haplotype composition reveal that Mexican groups are very homogeneous. Different genetic markers on the Y chromosome will be analysed in order to compare paternal and maternal lineages. The data generated will be focused on the reconstruction of the America's colonization, biological past and the phylogenetic relationships of the present day indigenous groups.