Pre-Hispanic and Contemporary Maya Migrations


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Introduction. The Maya civilization developed in Mesoamerica persisted approximately three thousand years and was one of the most advanced of its time. Mayas had the only known full writing system, as well as highly-developed mathematical and astronomical systems. Moreover, they developed sophisticated architecture and arts. This civilization was localized in the Southeast part of Mexico, in the Yucatan Peninsula, in Yucatan and Quintana Roo states, and parts of Tabasco and Chiapas states. In Central America, Mayas lived in Guatemala, Belize, Western Honduras, and El Salvador. Maya civilization reached its peak of power and influence in the Preclassic period, from 2000 Before the Current Era (BCE)-250 Current Era (CE). This research investigates the genetic variation of ancient populations of the Pre-Hispanic Mayas from archaeological sites in the states of Yucatan, Chiapas, Quintana Roo, and Tabasco, and their relationship with the contemporary communities in this region. This research utilizes mtDNA of bone remains found in excavations of archaeological sites of the region.

Methods. Mitochondrial DNA (mtDNA) sequences were obtained by amplification of total DNA extracted from the powdered bone remains using specific primers for the hypervariable region I (HVS-I). Sequences of the Pre-Hispanic individuals and contemporary populations were compared to assess interactions and gene flow between populations in the different archaeological sites and with contemporary Mesoamerican Maya and populations from Asia, Beringia, and South America.

Results revealed 1) Interactions and gene flow between Maya populations in the different archaeological sites; 2) Maya and Ciboneys sharing haplotype H10 belonged to haplogroup C1 and haplotype H4 of haplogroup D. This indicates a shared genetic ancestry, which further suggests regional interaction between populations in the Circum-Caribbean region than previously found; 3) haplotype sharing between the Pre-Hispanic Maya and the indigenous populations from Asia, the Aleutian islands, and North, Central and South America provides evidence for gene flow from the ancestral Amerindian population of the Pre-Hispanic Maya to Central and South America.

Conclusions. Gene flow occurred within the Maya area, with a directional flow to South America in the Preclassic and Classic eras of the Mesoamerican chronology, and our analysis support historical documentation which showed that the ancestors of Maya civilization entered the Yucatan Peninsula after the first movement of people from Northern Asia into the Americas, with later migration of the Maya south to Central America and the Caribbean towards the northern region of South America are supported.

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