

The evolution of the 16051G mtDNA lineage in American human populations

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Latin American populations provide an excellent model to analyze microevolutionary processes. The Native Americans conform the base of the present populations, and before mixing, they have suffered different processes as migration and genetic drift. Some of these process can be seen analyzing mitochondrial DNA (mtDNA).

Mt DNA (mtDNA) of Native American populations is defined by the presence of the four major (founding) haplogroups A, B, C, and D, each of them with several variants originated in Northeast Asia and Beringia. Recently, it was determined that haplogroup C is divided the founding components C1b, C1c y C1d, widely distributed in the Americas. We detected a lineage of haplogroup C1d specific for Uruguay in prehistoric (late Holocene) remains, as well as in a sample of living Uruguayan individuals. Additionally, two early Holocene individuals from site Arroyo Seco 2, in the Province of Buenos Aires, Argentina carry mtDNA sequences that correspond to haplogroup C1d. Based on the possible connection between the Argentinean and Uruguayan prehistoric populations we analyzed the variation, dispersal and age of haplogroup C1d.

Based on these analyses, we obtained an age of of 11450 years before present (ybp) for the origin of haplogroup C1d, with a 95% confidence interval of 7034.6 – 16841 ybp. The interval concurs with some of the most recent estimations of the age of peopling of the Americas, being nevertheless in discrepancy with other calculations that place the peopling of the continent at 19000 ybp. The presence of variants of haplogroup C1d in prehistoric remains of Argentina and Uruguay opens an independent line of evidence in the investigation of early contacts between populations suggested by archaeological data.