GENETIC STRUCTURE AND EVOLUTIONARY HISTORY OF 14 AMERINDIAN TRIBES OF THE AMAZONIAN AND ORINOQUIAN REGIONS OF COLOMBIA BASED ON SEVEN LOCI Y-CHROMOSOME STR HAPLOTYPES. A COMPARISON WITH THE LINGUISTIC AFFILIATION

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We have determined the genetic structure and evolutionary history in 157 individuals from 14 Amerindian tribes of Colombia belonging to four linguistic families: Arawak (Curripaco and Piapoco tribes), Macú-Puinave (Puinave and Nukak tribes), Guahibo (Guahibo and Guayabero tribes) and Tucano (Cubeo, Desano, Piratapuyo, Tatuyo, Tucano and Wanano tribes) based on 7 loci Y-chromosome STR haplotypes (DYS19, DYS389-I, DYS389-II, DYS390, DYS391, DYS392 and DYS393). A total of 59 haplotypes were identified with a haplotype diversity of 0.9553. The most frequent haplotype was H29: 13,12,30,24,10,15,13 (14%); followed by H17: 13,12, 30,23,10,15,13 (8.92%); H45:13,13,30, 24,10,14,13 (8.3%); and H10:13,14,32,24,10,15,13 (5.73%). A comparison of the Amerindian haplotype with the Caucasian Mestizo and Afro-Colombian populations showed that only 2.75% of the Amerindian haplotypes were shared with these ethnic groups.

The AMOVA showed that 36% of the genetic differences were due to differences between groups ($\Phi st= 0.3672$, $p<0.00000$), a result likely due to genetic drift. In addition 25% of the genetic variation was due to differences in linguistic affiliation. We have correlated the genetic data with the geographic and linguistic classification using similarity dendrograms, Mantel test, and Multidimensional Scaling analysis. The results indicate that the Amerindian tribes have evolved in the genetic, linguistic and geographic aspects in a highly correlated fashion.

A median network analysis for the entire continent was carried out in order to determine the ancestral haplotype as well as the most recent common ancestor (time of entry into America) for the Amerindian population. This analysis included a total of 465 individuals from 35 Amerindian, Na-Dene and Skimo-Aleutian populations described in the literature. The ancestral haplotype found was H45: 13, 13, 30, 24,10,14,13 and the time of entry into the continent was 22300 ybp (15695-28905 ybp) corroborating previous findings based on archeological data and mtDNA analysis. Thus, Y-STR haplotypes represent a powerful tool for anthropological studies in order to reconstruct the evolutionary history of human populations.