

GENETIC ANALYSIS BASED ON EIGHT LOCI Y-CHROMOSOME STR HAPLOTYPES IN A SAMPLE OF CAUCASIAN-MESTIZO AND AFRICAN DESCENT MALE INDIVIDUALS OF COLOMBIA

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Eight loci Y-Chromosome STR minimal haplotypes were analyzed in 134 unrelated African descent individuals collected in four different towns of the Choco department and 137 unrelated Caucasian Mestizo individuals from the east-central Andean region of Colombia in order to establish haplotype frequencies to be used in forensic casework and to evaluate their genetic relationship in order to correlate previous findings with autosomic markers. No evidence of population sub-structuring for the African descent population was found (Φ_{st} value 2.6%, p 0.054). Only six out of 232 haplotypes were shared between these two ethnic groups (2.59%). Three out of these six haplotypes were the most frequent haplotypes found in Colombian Caucasian Mestizos implying a genetic flow from Caucasian into African descent individuals. Genetic distance analysis showed clustering between the Caucasian Mestizo population with other Caucasian populations found in the Iberian Peninsula (Andalucía, Galicia, Portugal) and other European populations, results that are in agreement with historical data since the Colombian Caucasian population are descendants of Spanish conquerors that arrived more than 500 years ago in these lands. On the other hand the African descent populations clustered with other African descent populations reported in the literature such as the Afro-American populations and the Afro-Caribbean population from Surinam.

The haplotype diversity for the African descent population was 0.9955 and 0.9971 for the Caucasian mestizo population. However, a lower power of discrimination for the African descent population (0.8082) than that obtained for the Caucasian mestizo (0.8905) was observed. The results for the Afro-Colombian population of the Choco department could be due in part to a limited gene pool that has remained unchanged for the last 350 years with little admixture with other ethnic groups, limiting the effective size of Y-chromosome haplotypes in this population.