

Y-CHROMOSOME HAPLOTYPE DATABASE IN VENEZUELAN CENTRAL REGION AND ITS COMPARISON WITH OTHERS VENEZUELAN POPULATIONS

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Although haplotypes frequencies have been previously estimated in Venezuelan populations (Borjas et al, 2007) genetic homogeneity populations have to be confirmed before considering them as a Data Base for other Venezuelan populations.

The aim of this work was to characterized Y-chromosome STR haplotypes (DYS19, DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS385, DYS437, DYS438, and DYS439) in the Central Region of Venezuela (Aragua, Cojedes and Carabobo States).

One hundred and fifteen unrelated male individuals were sampled and Y-STR genotypes were determined using the PowerPlex® Y-system (Promega) and the ABI PRISM 3130 Genetic Analyzer. Allele and haplotypes frequencies, diversities, and statistical tests were performed with Arlequin version 3.1 software.

One hundred and seven different haplotypes were found. Five of them were present in more than one individual, and 101 were not found in Caracas or Maracaibo populations (Borjas et al (2007). Haplotypic Diversity in Central Region was estimated as 0.9982, which allows us to consider this set of markers as highly discriminating in our population.

When the Genetic Distance between Central Region and Caracas was estimated, no significant difference was found. Likewise, differences were not found in markers either. However, when the Central Region and Maracaibo were compared, significant differences were found in both Genetic Distance and DYS385 and DYS438 allele distributions.

A “chimerical” population was constructed joining haplotypes from the Central Region and Caracas. The Genetic distances between this “chimerical” population and both individual populations were not significant, strengthening the criteria of genetic homogeneity between them. Comparison of this “chimerical” population with Maracaibo also has shown a significant difference.