

ANALYSIS OF MITOCHONDRIAL SEQUENCES OF HVI AND HVII CONTROL REGIONS FROM INDIVIDUALS LIVING IN BOGOTÁ, COLOMBIA

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We analyzed the control region sequences (HVI and HVII) of mitochondrial DNA from 50 individuals not related, living in Bogotá. We found a total of 47 different sequences from these, two sequences have a common type for two and three different individuals analyzed respectively. We found a total of 87 different nucleotidic positions (nps), 56 in the HVI regions and 31 in the HVII region.

Most of the variation of the sequences were due to substitutions (82 different sites), transition (77 different sites), transversions (5 different sites), deletions (7 different sites) and insertions (2 different sites). The insertions were evident only in the polycytosine stretch in both hypervariable regions (HVI and HVII). Within the 47 sequences analyzed we found a variation average of 10.5 \pm 4.8 nucleotides, 6.8 nucleotides for the HVI region and 3.7 nucleotides for the HVII region. The nucleotide diversity obtained for the two regions was 1.4%. The genetic diversity calculated was 96.7% and 91.65% for the HVI and HVII region respectively. The genetic diversity for the two regions was 99.67%. The match probability was 2.3%.