

**VALIDATION OF CODIS 13 LOCI AND PENTANUCLEOTIDE (PENTA E) FOR THREE BRAZILIAN POPULATION (RIO BLACK, NON-BLACK AND BRAZILIAN CENTRAL WEST POPULATION) A STATISTIC AND COMPARATIVE STUDY**

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The objective of this study is to compile an allele and genotype frequency database of Black and Non-Black Rio de Janeiro State populations consisting of fourteen short tandem repeat loci (STR) including: CSF1PO, TPOX, TH01, vWA, D16S539, D7S820, D13S317, D5S818, FGA, D8S1179, D3S1358, D18S51, D21S11 and the Pentanucleotide Penta E. In addition, statistical analysis of Brazilian populations will be compared to North American populations.

PCR-based typing of STR loci has become a technique of growing importance in paternity and criminal investigations. The use of genetic markers such as STRs in identity testing requires collection of allele/genotype data for relevant population(s) in order to provide an estimate of the frequency of a genetic profile. Currently, STR allele frequencies and genotype distributions in Rio de Janeiro State - Brazil do not exist. This approach will provide the first STR database for use as a highly discriminatory system of genetic markers in personal identification, specifically for parentage testing, forensic identification, and medical applications.

Amplification by PCR and Fluorescence Typing of the 14 STR Loci for 728 DNA samples or 14,288 alleles were conducted at Palm Beach Sheriff's Office/Crime Laboratory/DNA Section, West Palm Beach, Florida - USA, using the *GenePrint*® STR Multiplex System PowerPlex™ 1.1 and the new STR Multiplex System PowerPlex™ 2.1 (Promega Corporation, Madison, Wisconsin). Allele data was detected using the Hitachi FMBIO® 100 and FMBIO® II (San Francisco, California). The statistical analyses were conducted at Human Genetic Center/University of Texas Health Science Center, Houston, Texas, which included analysis of allele distribution, heterozygosity, independence within a locus, comparison of loci for independence between any two loci, Independence test across all loci and genetic distance between any two database sets using "DNAType" Program.

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