

ANALYSIS OF CODIS AND Y-STR LOCI IN DIFFERENT PAKISTANI ETHNIC GROUPS

Muhammad Hussain¹, Abdul Hameed², Abid Azhar¹

¹*Institute of Biotechnology and Genetic Engineering (KIBGE), Karachi*

²*Institute of Biotechnology and Genetic Engineering (IBGE), Islamabad*

The human genome is full of repeated DNA sequences. These repeated sequences come in various sizes and are classified according to the length of the core repeat units. DNA regions with short repeat units (usually 2-6 bp in length) are called Short Tandem Repeats (STR). STRs have proven to have several benefits that make them especially suitable for human identification.

For human identification purposes, it is important to have DNA markers that exhibit the highest possible variation in order to discriminate between samples. An individual inherits one copy of an STR from each parent, which may or may not have similar repeat sizes. The number of repeats in STR markers can be highly variable among individuals, which make these STRs effective for human identification purposes.

It is often challenging to obtain PCR amplification products from forensic samples because either the DNA in those samples is degraded, or mixed, such as in a sexual assault cases. The smaller size of STR alleles makes STR markers better candidates for use in forensic applications, in which degraded DNA is common. PCR amplification of degraded DNA samples can be better accomplished with smaller target product sizes. STR alleles also have lower mutation rates, which makes the data more stable and predictable.

Because of these characteristics, STRs with higher power of discrimination are chosen for human identification in forensic cases on a regular basis. They are used to identify victim, perpetrator, missing persons, and others.

In 1997, the Federal Bureau of Investigation (FBI) of the United States launched a nationwide forensic science effort to establish core STR loci for inclusion within the national database known as CODIS (Combined DNA Index System). The 13 CODIS loci are CSF1PO, FGA, TH01, TPOX, vWA, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51 and D21S11. These loci are nationally and internationally recognized as the standard for human identification. Information on uniparental lineage markers from the Y chromosome also continues to accumulate in the literature. These lineage markers are also widely used for human evolutionary studies and the emerging field of genetic genealogy. The availability of commercial kits for Y-STR amplification has enabled more widespread usage of these important male specific markers in forensic DNA laboratories.

Therefore, this study was aimed to generate data for CODIS and Y-STR loci for various Pakistani ethnic groups. The data obtained from this study will help us in human identification and comparison, both nationally and internationally. The study that helps in finding the ethnic background has become particularly crucial after the increased number of suicidal attacks in the recent past.