

FORENSIC SCIENCES DEVELOPMENT WITH MOLECULAR IDENTITY OF 16 STRS ZONES FOR THE FIRST TIME IN IRAN

Tavallaei Mahmood Ph.D. a , Saremi Mohammad Ali a b, Sajedifar Mohammad Mahdi b, Zeinali Sirous Ph.D. b

a Imam Hussein University, Faculty of Science, Tehran, Iran

b Kawsar Human Genetic Research Center, Tehran, Iran

Abstract

Repetitive sequences of DNA throughout the human genome occur in about 10% of total genome and it naturally leads to generation of certain polymorphisms. This sequence is used as an important genetic maker in investigation of gene mapping, diagnosis of diseases and identity recognition.

The STR (Short Tandem Repeat) sequences include those short sequences consisted of 2-6 bp repetitive units and they are identifiable and reproducible by PCR.

STRs are widely extensive utilized in forensic medicine laboratories over the world. It is due to this point that this method requires low amount of DNA (about 0.5-1 ngr) and even degraded DNA will be sufficient for working, including blood, bone, tissue specimens, etc. We have used Genetic Analyzer device to determine STR profiling of 400 DNA samples from Iranian population of different ethnic origin. For this we have used 16 Powerplex Identifiler PCR Amplification Kit. We have used this system for Forensic, Criminal, Investigation, Paternity of Identification applications.

Following running of the above system which is based on Capillary Array and Fluorescent Labeled Primers, the frequency of different alleles over different Iranian populations, determination of paternal relationship (father-child), diagnosis and determination of identity of criminals and identification of anonymous individuals as a consequence of natural catastrophes like flood, earthquake as well as unnatural events like war.

Using this system human identification, in Iran, can be done with high precision and speed and to be able to Forensic Sciences Development in Iran.

Keyword : Forensic Sciences, STR , Profiling , Human Identification , DNA Sequence.