IDENTIFICATION OF HUMAN SKELETON REMAINS BY STR-MULTIPLEX ANALYSIS

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Human identification and forensic criminal casework may involve DNA profiling of skeleton remains. However, it may be difficult to analyze these samples by STRs multiplex methods, Problems, as the contamination and the degradation of the samples are very usual during the process of typing bone samples. In addition many inhibitors may affect the multiplex PCR reaction. The DNA was extracted using proteinase K, SDS and phenol-isoamyl alcohol-chloroform and washed and concentrated using Centrex™-30 micro concentrator devices and finally, in all cases purified using QIAquick™ columns (Qiagen). A critical point when working with old bone samples is the final purification with QIAquick™. To avoid contamination very strict technical precautions were taken during all steps of the process.

The aim of this study is to evaluate the efficiency of the two multiplex PCR kits: AmpF*l*STR® Profiler™ and AmpF*l*STR® SGM Plus in forensic casework. The SGM Plus kit is composed of Amelogenin and ten STR markers: D3S1358, vWA, D16S539, D2S1338, D8S1179, D21S11, D18S51, D19S433, TH01 and FGA. The Profiler™ kit is composed of Amelogenin and nine STR markers: D3S1358, vWA, FGA, TH01, TPOX, CSF1PO, D5S818, D13S317 and D7S820.

DNA amplification was performed according to the manufacturer's protocol. The amplified samples were analyzed on an ABI PRISM® 310 Genetic analyzer. Quality of results was judged by considering a number of factors – condition of baseline, peak height across loci, presence of non-specific bands, stutter-bands etc. The bio statistical evaluation was performed by DNA-View (C. Brenner, USA).
In about 40% of our analyzed bone samples there were one or more drop out loci. Usually, there is a good correlation between dropping out percent and length of the molecule but that is not always the case. Most of our forensic cases were between 0 and 10 years old, but in two cases nuclear STR loci successfully could be analyzed from 21 and 35 years old skeleton remains. In conclusion, STR multiplex analysis using AmpF*l*STR® SGM Plus and AmpF*l*STR® Profiler™ is sufficient to identify old human remains.