QUANTITATIVE PCR ASSAYS FOR THE ESTIMATION OF THE DNA DEGRADATION IN BONE SAMPLES

Tetsushi Kitayama, Hiroaki Nakahara, Koji Fujii, Natsuko Mizuno, Kazumasa Sekiguchi, Kentaro Kasai
National Research Institute of Police Science, Japan

To perform STR analysis from degraded DNA is a special challenge for forensic biologists. DNA fragments are subject to degradation by nuclease, oxidation and/or hydrolysis. Degraded DNA fragment can be quantitated by quantitative PCR assay. Quantitative PCR assay is very useful tool for determining the adequate amount of DNA input into the PCR reaction in STR analysis.

For the purpose of assessing the quality and quantity of DNA, we had previously developed quantitative PCR assays determining degree of DNA degradation using primers targeting various sized amplicons in D17Z1 on chromosome 17. The nuclear target for quantification is human specific alpha satellite DNA present in 500-1000 copies. Owing to the high copy numbers of the PCR targets, these assays are highly sensitive. We had already tested quantitative PCR assays for artificially damaged (enzymatic degradation and oxidative reaction) DNA samples.

In this study, we performed quantitative PCR assays for casework samples (e.g., bone). STR analyses using Identifiler and/or MiniFiler kit was performed from each casework samples. The quantitative PCR assays using the primers generating the various sizes of amplicons from the same region of genomic DNA could be used to estimate the degree of DNA degradation based on the degradation ratio and, thus, would be helpful for selecting the adequate STR kit to obtain profiles successfully. Moreover, it could be expected to save time, labor and limited amount of DNA extracted from casework samples.