STR TYPING OF HUMAN TELOGEN HAIRS- A METHOD FOR ROUTINE CASEWORK

Ingo Bastisch, A. Hellmann, U. Rohleder and H. Schmitter
Bundeskriminalamt, Wiesbaden, Germany

For a long time, it was supposed that shed hairs with telogen roots could not be analyzed by means of STR typing. The only approach was the sequence analysis of the hypervariable regions within the control region of the mtDNA. Although the chance of obtaining results is relatively good, the matching probability is low and other problems like heteroplasmies are encountered. In addition, profiles can not be searched in STR databases. Recently, a new strategy was developed (Hellmann *et al*. "STR typing of human telogen hairs- a new approach" Int. J. Legal Med. (2001) 114:269-273). This strategy included an optimized DNA extraction method and the use of modified primers leading to reduced amplicon lengths for the loci FES (76-101 bp), TH01 (57-76 bp) and TPOX (53-81 bp).

Meanwhile, further improvements of the protocols have been established. These include additional primers (with their respective amplicon lengths as measured on a 3100 Genetic Analyzer) optimized for the loci D3S1358 (81-110 bp), vWA (83-137 bp), FGA (124-175 bp), D8S1179 (70-115 bp) and Amelogenin (66 and 72 bp). Further changes in the protocol considered the low amount of nuclear DNA obtainable from telogen hairs. The extracted DNA is immobilized on a nylon membrane that can be used for sequential solid-phase amplifications of different loci. After each PCR the membrane is washed, blocked and reused in subsequent PCR.

The combination of the different steps mentioned above is essential to obtain reasonable results from telogen hair roots due to i) the physical structure of the hair (complete digestion of the hair), ii) the degradation of the DNA (modified primers with a reduced amplicon length) and iii) the low amount of genomic DNA (solid-phase PCR).