DNA Typing from Hair Shaft: A Case Report

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The hair root that is rich in cells has been traditionally believed the sole source of DNA. This study evaluates the possibility of DNA extraction from the medulla contained in hair shaft, because the medulla's cells are only partially horny and so they have nuclei that contain DNA. The success of DNA extraction comes from the quantity of medulla contained in the shaft.

In this report, for testing the validation of DNA typing from hair shaft, we have compared DNA profiling from blood samples of 30 unrelated healthy donors with the one from hairs without roots belonging to the same blood donors. The length of hair shaft was on average 4 cm.

DNA was extracted from 10 hairs immediately after they were taken from donor: the other 20 hairs were placed inside paper bags at room temperature as usually happens in Italy with forensic specimens kept at Judicial Offices. 10 hairs of them were analyzed after 6 months, and the other 10 after 12 months. DNA was typed from 30 blood samples just after the drawing. For DNA typing, 8 short tandem repeat loci (ABI PRISM STR Primer Set TH01, vWA31, F13A1, FES/FPS, TPOX, CSF1PO, D21S11, FGA) were analyzed. Sex was determined by amplification of a segment of the X-Y homologous gene Amelogenin. Amplification was performed using GeneAmp PCR System 9600 and 2400 (Perkin-Elmer). Amplified products were analyzed by capillary electrophoresis on the ABI Prism 310 Genetic Analyzer (PE-Applied Biosystems) employing ABI software (DATA Collection, GeneScan Analysis, Genotyper Fragment Analysis).

For each donor analyzed we have compared DNA profiling from blood with the one from hair and so we have found a full concordance between them. During this experiment, after many tests, we found the number of PCR cycles for DNA amplification from hair shaft which provided the best ratio between signal and noise. We observed, also, that some loci failed to amplify as the degradation gets on: CSF1PO and D21S11 are the first to drop out.

We report one of our caseworks in which we have applied the method above with good outcome. In 1995 in a Calabrian city a boy, after a grips, was killed inside a bar. In his right hand were found 12 hair shafts. During the autopsy were taken 3 locks of hair with roots from the cadaver's head. Two years later, after a first inconclusive legal advice performed in another laboratory, the Public Prosecutor commissioned us to do a new legal advice on the same evidence.

DNA typing showed that the hair shafts found in the crime scene were not from the dead boy. After about 5 months by comparing DNA profiling from a cigarette found in the scene of another homicide which happened at a distance of about 100 km from the first one, with DNA profiling in a file of previously examined caseworks in the SIMEF laboratories, it was shown a match between DNA from the cigarette and the hair shafts found in the boy's right hand.

It was supposed that cigarette and hairs were from the same killer that nowadays is still unknown. The discriminating power (DP) of the STR loci analyzed was calculated by a special software (S.H.S.-Baril) using the frequencies of the Reggio Calabria and its district population. DP for the DNA profiling of the boy's hairs was 2,19/1.000.000.000, instead for the hairs belonging from the unknown man it was 3,90/100.000.000.

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