

Identification of Body Fluid at the Crime Scene by DNA Methylation Markers for Use in Forensic Science

Authors : Shirin jalili, Hadi Shirzad, Mahasti Modarresi, Samaneh Nabavi, Somayeh Khanjani

Abstract : Identifying the source tissue of biological material found at crime scenes can be very informative in a number of cases. Despite their usefulness, current visual, catalytic, enzymatic, and immunologic tests for presumptive and confirmatory tissue identification are applicable only to a subset of samples, might suffer limitations such as low specificity, lack of sensitivity, and are substantially impacted by environmental insults. In addition their results are operator-dependent. Recently the possibility of discriminating body fluids using mRNA expression differences in tissues has been described but lack of long term stability of that Molecule and the need to normalize samples for each individual are limiting factors. The use of DNA should solve these issues because of its long term stability and specificity to each body fluid. Cells in the human body have a unique epigenome, which includes differences in DNA methylation in the promoter of genes. DNA methylation, which occurs at the 5'-position of the cytosine in CpG dinucleotides, has great potential for forensic identification of body fluids, because tissue-specific patterns of DNA methylation have been demonstrated, and DNA is less prone to degradation than proteins or RNA. Previous studies have reported several body fluid-specific DNA methylation markers. The presence or absence of a methyl group on the 5' carbon of the cytosine pyridine ring in CpG dinucleotide regions called 'CpG islands' dictates whether the gene is expressed or silenced in the particular body fluid. We described methylation patterns at tissue specific differentially methylated regions (tDMRs) to be stable and specific, making them excellent markers for tissue identification. The results demonstrate that methylation-based tissue identification is more than a proof-of-concept. The methodology holds promise as another viable forensic DNA analysis tool for characterization of biological materials.

Keywords : DNA methylation, forensic science, epigenome, tDMRs

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