THE USE OF METHYLATION MARKERS FOR AGE ESTIMATION OF AN UNKNOWN BASED ON BIOLOGICAL TRACES

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Biological samples/traces collected at the scene of crime have potential to be used to predict the age of an individual from whom the samples originated. In no-suspect cases and cases where there is no DNA profile match against a database, such information could be critical for providing additional intelligence for criminal investigations.
One of the most promising methods for determining age from a biological sample is analysis of methylation status of CpG sites within the DNA using bisulfite conversion and subsequent pyrosequencing.

Here we describe analysis of DNA methylation at five CpG sites located in ELOVL2, C1orf132, TRIM59, KLF14 and FHL2 using the PyroMark Q24 instrument from QIAGEN. Analysis of these markers was found to facilitate human chronological age prediction with ±3.9 year accuracy. Correct predictions at ±5 year level were observed in 78.3% of subjects aged 2–59 years but only 50% at age 60–75 years, indicating that selected DNA methylation markers are less efficient in older individuals. This could be a reflection of the longer lifespan, medical history, life style or environment differences that lead to different levels of selected marker methylation and increased error of age estimation in our model.

The algorithm developed using these five methylation markers with optimized Pyrosequencing assays provides a valuable tool for forensic age prediction.