

DIFFERENTIATING MONOZYGOTIC TWINS WITH DNA METHYLATION TECHNOLOGY

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Prosecuting cases with physical evidence from monozygotic twins (MZ) is a challenge because DNA cannot be used to identify an individual beyond a reasonable doubt since conventional DNA markers only provide the same genetic profile for both twins. Many real cases remain unsolved because the primary suspect has a MZ twin. As the rate of twin births are on the rise, the incidence of forensic evidence samples originating from a MZ twin will likely also increase and result in further unsolved cases due to a lack of cost effective and accurate forensic analysis methods for differentiating MZ twins. Fortunately, new advances in genomic technologies, specifically epigenetics, provide the forensics community a potential tool to be applied in MZ twin identification. While some research has indicated that twin differentiation can be conducted with epigenetics, newly available high capacity methylation arrays (> 850,000 CpG sites) have yet to be tested across a wide range of tissue sources. In this study, CpG sites were longitudinally analyzed with the Infinium MethylationEPIC Kit (Illumina) from multiple tissue sources (blood, saliva and semen), different times of the twin pairs' lives and from different twin pairs with varying age range. Methylation data were analyzed to remove CpG sites that changed as dependent with time, gender, genetic background, and tissue type, but were consistently of varying levels between twin pairs. The final datasets were evaluated with several statistical models to identify methylation marker panels that could reliably differentiate each contributor from the MZ pairs. This discovery project will help the criminal justice community move forward with intelligently designed methylation analysis methods for assessing physical evidence.