EVALUATION OF A METHYLATION ASSAY FOR AGE PREDICTION IN FORENSICS

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Age prediction of the unknown donor from biological materials deposited at crime scenes can provide valuable information to assist the law enforcement agencies in narrowing down the list of possible perpetrators. The correlation of the DNA methylation status of age-related CpG sites with age is currently one of the well documented and most pertinent age-predictive methods. In this study, five DNA methylation markers (*ELOVL2, C1orf132, TRIM59, KLF14* and *FHL2*) previously reported by Renata Zbieć-Piekarska *et al*. were investigated with the local Singapore Chinese, Malay and Indian population samples to establish their correlation with age.

Genomic DNA isolated from blood samples collected from 145 individuals aged between 3 to 80 years were bisulfite converted, amplified and subjected to pyrosequencing. Examination of the 32 CpG sites from the five methylation markers revealed that they were highly correlated with age, with correlation coefficients ranging from 0.72 to 0.95. The three most informative CpG sites from *ELOVL2*, *TRIM59* and *KLF14* were identified through stepwise regression analysis and were used to build an age prediction model, using multiple linear regression, with the 145 training samples. This age prediction model explained 95.5% of the age-correlated variation observed. The mean absolute deviation and the standard error of estimate were 3.29 and 4.46 years, respectively. The accuracy of the training model was consequently assessed with an independent set of samples.