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## Abstract

Age prediction is useful to narrow down the number of potential suspects because it can provide some general characteristics for predicting appearance. Epigenetic marks consider a promising method of the age prediction model. DNA methylation has an important role in the personal information of chronological age prediction. Recent studies reported DNA methylation levels of many CpG sites in the human genome have a relationship with aging. Therefore, DNA methylation levels of specific genes provide the key information of forensic investigation. In this study, 120 blood samples were collected from healthy persons, Arabic Iraqi population age range 18-years. The genomic blood samples were subjected to bisulfate conversion and 95 amplification followed by pyrosequencing. The results included 92 samples out of 120 that detected 27 methylated CpG sites of ELOVL2, TRIM59, FHL2, KLF14, and MIR29B2CHG genes. The statistical analysis used to multivariate regression analysis to finding a correlation between the methylated CpG sites and age. The 15 CpG markers of three genes (ELOVL2, TRIM59, and FHL2) showed linear correlations with chronological age, it could age estimation with a mean error of  $\pm 6.92$  years and correction coefficient was ( $R^2= 96.8\%$ ). For the most statistical satisfaction, only nine of age-associated methylation markers of ELOVL2 gene that including strong correlation and good fitting ( $R^2= 98\%$ ) to a prediction model based on a multiregression model to assess the prediction accuracy. The nine CpG sites of ELOVL2 gene have appeared strong linear relationship with age (all P-values<0.05, 0.01). The Mean Absolute Deviation (MAD) between predicted and real chronological age was  $\pm 2.893$  years. Notably, the DNA methylation marks of ELOVL2 gene strongly suggest the prediction model of age in this work. Identification of novel single nucleotide polymorphism in the Iraq population. rs7808283 G>A associated with the loss of one CpG site of human KLF14 located at Chromosome Chr7:130734413-130734373 of Promoter gene.