Dental age estimation: evaluation of DNA methylation age predictions

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ABSTRACT

It is known that the ageing process leads to modification of the human tissues and organs. In teeth specific morphological changes were used to estimate age (Gustafsion, 1947). On molecular level changes in the methylation patterns of a set of associated DNA methylation makers (ASPA, PDE4C, ELOVL2 and EDARADD) obtained from teeth enabled to predict age (Bekaert 2015).

The study aim was to establish and evaluate anage prediction method based on DNA methylation and to compare its age outcomes with the results of commonly used dental age estimation methods.

A sample of 75 (41 M / 34 F) fully developed extracted monoradicular teeth was collected in Dental Services Malaysian Armed Forces Dental Clinic (DSMAF). The age of the related subjects ranged between 15.6 and 76.8 year, with a mean age of 41.5 year. The following non-destructive dental age estimation methods were applied: Miles et al. (1963), Bang et al. (1970), Lamendin et al. (1992), Kvaal et al (1994). Therefore, the following parameters were measured: the loss of periodontal attachment, the transparent root dentin, occlusal attrition and the amount of apical root resorption. As dental DNA sources the pulp, cementum and dentin were collected. DNA methylation of the markers (ASPA, PDE4C, ELOVL2 and EDARADD) was quantified in each source and correlated with age. Age prediction models were established and validated. Age prediction performances of the dental and DNA based predictions were compared using appropriate statistics. The study hypothesis is that the age predictions based on DNA methylation markers is providing better age prediction results than the non-destructive dental age estimation methods.

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