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CpG MODELS FOR AGE PREDICTION IN CRIMINAL INVESTIGATIONS: CONSIDERATIONS FOR FUTURE TRANSITIONING TO FORENSIC PRACTICES - A NARRATIVE LITERATURE REVIEW

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ABSTRACT
For age estimation effectively assist criminal investigations, precision is required that, currently, still lack adjustments in many aspects addressed in this review.

Keywords: Age-prediction, methylation.

Introduction
Estimating an individual's age from DNA found in forensic evidence provides the prediction of externally visible characteristics, which reduces the number of potential suspects in criminal investigations. DNA methylation has great potential for forensic individual age prediction and several DNA methylation-based Age Prediction Models (APMs) have been proposed so far, mainly in blood. However, the lack of standardization in the results obtained among the various publications still prevents this methodology from being applicable to forensic practice.

Objective
This review aimed to summarize the already proposed APMs based on age-related CpG (AR-CpG) markers in blood samples, highlighting considerations and recommendations for the future transition to forensic practices.

Methodology
A literature search was carried out between July 2014 and July 2022, using electronic databases.

Results and Discussion
28 publications were selected, covering 34 different APMs proposed for blood samples, ranging from 2-16 CpG markers, distributed in single- or multi-loci models and with prediction measure results around 5-10 years from the actual age. Each APM is subject to several factors: (1) the AR-CpGs selection; (2) tissue specificity; (2) possible population effects impacting methylation, such as ancestrality and those resulting from environmental stimuli and lifestyle habits; (3) age-related factors, such as characteristic methylation oscillations in different age groups or senile diseases that directly impact the methylation patterns; (4) the applicability of models in samples from deceased individuals; (5) interlaboratory variations such as experimental conditions or statistical calculations used that may differently affect methylation measurements or age prediction itself. In view of this, we recommend that, in addition to assessing the real need for investment in multi-tissue models, some of these factors be standardized in research for APMs to be considered effective, such as establishing which and how many populations should be tested; the size and age range of the tested groups; the study of how senile illness or death affects methylation; and the standardization of experimental and statistical criteria.

Conclusion
Standardizations are urgently required to allow the application of age estimation in forensic practice.

References
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