DNA methylation markers of age(ing) and other things in non-model organisms

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Abstract

An accurate inference of the chronological and biological age of individuals is fundamental to population ecology and our understanding of ageing itself, its evolution and the biological processes that affect or even cause ageing. In humans, epigenetic clocks based on the DNA methylation (DNAm) at selected CpG sites correlate highly with chronological age. Discrepancies between the inferred epigenetic and known chronological age predict morbidity and mortality, and therefore epigenetic clocks are thought to reflect biological age. Recently, a growing number epigenetic clocks in non-model organisms have been developed towards a diverse array of purposes in commercial, conservation and ageing research. Here we review those studies and conduct the first meta-analysis to assess the effects of different aspects of experimental protocol on the accuracy of epigenetic clocks for non-model species. Our analysis reveals higher coefficients of determination (R^2) of chronological age for epigenetic clocks based on the HorvathMammalMethylChip4, compared to other DNAm quantification approaches. No dependence of (R^2) was detected for the number of CpG sites in a clock; the sample size; the number or kind of tissue(s) used; the class of animals; or whether captive or wild animals were sampled to infer the epigenetic clocks. We further conclude that epigenetic clocks can predict chronological age with relatively high accuracy, suggesting great potential for the field of ecological epigenetics. We therefore encourage further research on the topic of ecological epigenetics in relation to ageing and, perhaps more importantly, discuss the potential of employing DNAm to assess key traits other than age.

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