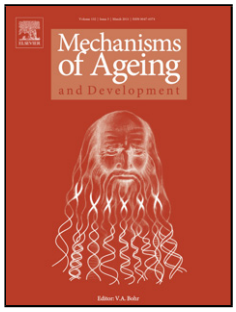

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Back to the future: epigenetic clock plasticity towards healthy aging

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Highlights

- The epigenetic clock DNA methylation signature has outperformed other biomarkers in predicting age
- Age associated DNA methylation drift is highly conserved across mammalian species
- Epigenetic clock acceleration promotes lifestyle diseases and mortality risk
- Epigenetic clock acceleration is associated with mitochondrial DNA copynumber but not with telomere length
- Lifestyle interventions are developed to extend healthy lifespan by slowing down the epigenetic clock progression

Abstract

Aging is the most important risk factor for major human lifestyle diseases, including cancer, neurological and cardiometabolic disorders. Due to the complex interplay between genetics, lifestyle and environmental factors, some individuals seem to age faster than others, whereas centenarians seem to have a slower aging process. Therefore, a biochemical biomarker reflecting the relative biological age would be helpful to predict an individual's health status and aging disease risk. Although it is already known for years that cumulative epigenetic changes occur upon aging, DNA methylation patterns were only recently used to construct an epigenetic clock predictor for biological age, which is a measure of how well your body functions compared to your chronological age. Moreover, the epigenetic DNA methylation clock signature is increasingly applied as a biomarker to estimate aging disease susceptibility and mortality risk. Finally, the epigenetic clock signature could be used as a lifestyle management tool to monitor healthy aging, to evaluate preventive interventions against chronic aging disorders and to extend healthy lifespan. Dissecting the mechanism of the epigenetic aging clock will yield valuable insights into the aging process and how it can be manipulated to improve health span.