Why centenarians consistently present a younger epigenetic age than their chronological age

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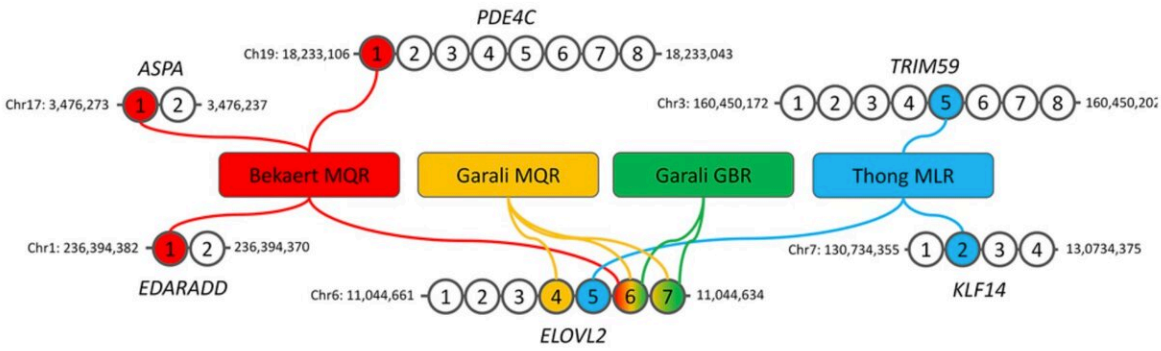

Description of the four DNA methylation-based epigenetic clocks used in our study. Credit: 2022 Daunay et al.

Aging is a progressive time-dependent biological process affecting individuals differentially. Some may present exceptional longevity. One of the hallmarks of aging is epigenetic alterations, which comprise the epigenetic drift and clock at DNA methylation level.

In a new study published in *Aging*, researchers Antoine Daunay, Lise M. Hardy, Yosra Bouyacoub, Mourad Sahbatou, Mathilde Touvier, Hélène

Blanché, Jean-François Deleuze, and Alexandre How-Kit from Foundation Jean Dausset—CEPH, Laboratory of Excellence GenMed, Sorbonne Paris Nord University, University of Paris (CRESS), and Institut François Jacob investigated the DNA methylation-based age (DNAmage) of long-lived French individuals in the CEPH Aging Cohort using four epigenetic clocks.

"In the present study, we estimated the DNA methylation-based age (DNAmage) using four epigenetic clocks based on a small number of CpGs in French centenarians and semi-supercentenarians (CSSC, n=214) as well as nonagenarians' and centenarians' offspring (NCO, n=143) compared to individuals from the French general population (CG, n=149)," report the researchers.

DNA methylation analysis of the nine CpGs included in the epigenetic clocks showed high correlation with chronological age (-0.66>R>0.54) and also the presence of an epigenetic drift for four CpGs that was only visible in CSSC. DNAmage analysis showed that CSSC and to a lesser extend NCO present a younger DNAmage than their chronological age (15-28.5 years for CSSC, 4.4-11.5 years for NCO and 4.2-8.2 years for CG), which were strongly significant in CSSC compared to CG (p-values