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Tracking age-correlated DNA methylation markers in the young

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Highlights

- Candidate age-correlated CpG sites explored in public datasets of 398 young subjects (3-17 yrs).
- 3 most correlated genes selected and tested in 209 new DNAs (2-18 yrs) + 7 previous adult-informative age markers.
- CpGs in KCNAB3 have strongest correlation of methylation status with pre-adult age ranges.
- Quantile regression prediction model extended with 6 most young-informative CpGs has ±0.94 yr median absolute error.

Abstract

DNA methylation is the most extensively studied epigenetic signature, with a large number of studies reporting age-correlated CpG sites in overlapping genes. However, most of these studies lack sample coverage of individuals under 18 years old and therefore little is known about the progression of DNA methylation patterns in children and adolescents. In the present study we aimed to select candidate age-correlated DNA methylation markers based on public datasets from Illumina BeadChip arrays and previous publications, then to explore the resulting markers in 180 blood samples from donors aged between 2 to 18 years old using the EpiTYPER® DNA methylation analysis system. Results from our analyses identified six genes highly correlated with age in the young, in particular the gene *KCNAB3*, which indicates its potential as a highly informative and specific age biomarker for childhood and adolescence. We outline a preliminary age prediction model based on quantile regression that uses data from the six CpG sites most strongly correlated with age ranges extended to include children and adolescents.

Keywords: DNA methylation; children; adolescents; individual age; Illumina; EpiTYPER®; age estimation