Epigenetic age-predictions

Aging is associated with highly reproducible DNA-methylation changes at specific sites in the genome (so called CpG sites). These modifications occur particularly in developmental genes. Using a broad range of DNA-methylation profiles we elaborated an Epigenetic-Aging-Signature for blood samples based on three relevant CpG sites. DNA-methylation levels at these three loci can be combined into a mathematical model to predict the donor age with a mean absolute deviation from chronological age of only 5 years (Figure 1). This deviation can at least partly be attributed to life-style parameters, gender, and disease. Therefore, the Epigenetic-Aging-Signature is indicative for the biological age of blood.

Comparison with other assays

In comparison to other methods, such as telomere length measurements or racemization of aspartic acid, the precision and accuracy of epigenetic age predictions are higher. The method is applicable for fresh and cryopreserved samples. Only small blood volumes or DNA amounts are required. As DNA is relatively stable, it can be shipped at room temperature. In contrast to methylation array based methods, the Epigenetic-Aging-Signature facilitates fast, robust, and cost effective analysis. Pricing is particularly dependent on required sample preparation and sample numbers.

How does it work?

DNA-methylation profiles of three CpG sites located in the genes aspartoacylase (*ASPA*), integrin alpha 2b (*ITGA2B*), and phosphodiesterase 4C (*PDE4C*) are analyzed by pyrosequencing. The DNA-methylation levels are then integrated into the linear regression model for prediction of biological age. In comparison to the "real" chronological age it is then possible to identify parameters that affect epigenetic aging.
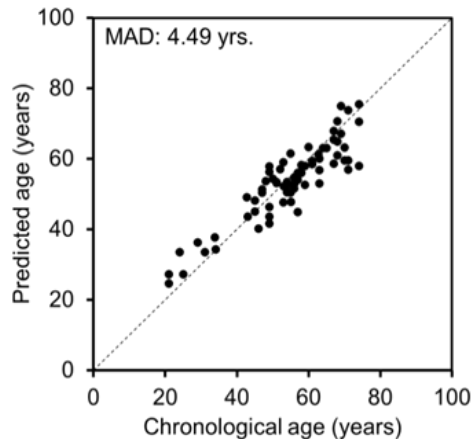

Figure 1: Age-estimation of blood samples. Blood samples were analyzed by pyrosequencing of the three specific CpG sites of the Epigenetic-Aging-Signature. The prediction model facilitates age-estimation with a mean absolute deviation (MAD) from chronological age of about 5 years.

Our service for you:

- You provide either 1 mL of freshly/frozen blood or 500 ng of genomic DNA (isolated from blood). There is no need to separate specific subsets of blood cells.

- We perform DNA isolation (optionally) and bisulfite conversion of genomic DNA

- We analyze the DNA-methylation at three relevant CpG sites by pyrosequencing

- We predict the biological age of your sample

- Results - including pyrograms, raw data, and graphical presentation - are provided by Email

Publication:

- Weidner CI., Lin Q., et al., *Genome Biology* **15**, R24 (2014)

- Patent application: 2012; EP12185698.3

Further Information

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