

Buccal-Cell-Signature



Non-invasive harvesting of DNA

DNA can be harvested non-invasively from cells at the inside of a person's cheek using buccal swabs – but these specimens resemble heterogeneous mixtures of buccal epithelial cells and leukocytes. The percentages of leukocytes vary between 5% - 60% in buccal swabs and 16% - 95% in mouthwash samples (saliva); the rest largely consists of buccal epithelial cells.

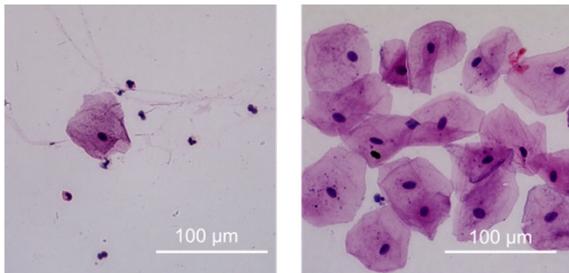


Figure 1: Heterogeneous composition of cell types. Representative mouth swab smears with predominant leukocytes (left) or epithelial cells (right).

The cellular composition is relevant

The cellular composition needs to be considered for various applications – particularly for epigenetic analysis since the epigenetic makeup differs significantly between buccal epithelial cells and leukocytes. For example, epigenetic age predictions based on buccal swabs become more precise with this additional information.

How does it work?

Using multiple genome-wide datasets we have identified two genomic regions that are specifically methylated either in buccal epithelial cells or in leukocytes (associated with the genes *CD6* and *SERPINB5*). We developed pyrosequencing assays for two CpG sites located in these regions. These measurements are combined in the “Buccal-Cell-Signature” to facilitate robust estimates of the cellular composition.

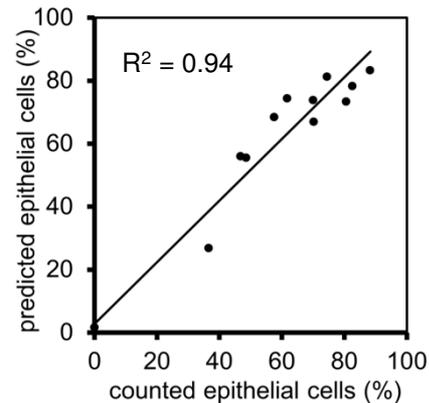


Figure 2: Estimation of buccal epithelial cells. The percentage of buccal epithelial cells versus leukocytes was determined by cell counting in 11 stained mouth swab smears and estimated by the Buccal-Cell-Signature

The Buccal-Cell-Signature can be combined with the Epigenetic-Aging-Signature to improve the precision of age-predictions in buccal swabs.

Our service for you:

- We either send you swabs by mail, which you can send back by mail after harvesting of the sample. Alternatively, you provide already isolated genomic DNA from buccal swabs or mouth washes
- We perform DNA isolation (optionally) and bisulfite conversion of genomic DNA
- We analyze the DNA methylation at the two relevant CpG sites by pyrosequencing
- We predict the cellular composition of your sample
- Results - including pyrograms, raw data, and graphical presentation - are provided by E-mail

Publication:

- Eipel M., et al., *Aging US* 2016;8(5):1-15
- Patent application: DE 10 2016 109 291.6

Further Information

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