

// MORTALITY PREDICTION THROUGH DNA METHYLATION BIOMARKERS

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HINTERGRUND

DNA methylation plays a role in various diseases. In addition, evidence has been accumulated that the recently established "epigenetic clock" based on age-associated DNA methylation changes is an indicator for longevity. Environmental factors as well as life style can have a crucial influence on DNA methylation. Smoking related DNA-methylation change for example can be connected to lung cancer mortality. This invention uses DNA methylation status at CpG sites to predict disease related as well as all-cause mortality independent of underlying diseases or the "epigenetic clock".

The method uses DNA methylation status of the ten CpG sites to predict mortality. The status has to be determined for at least two of the ten CpG sites compared to a reference value from the same CpG site. The deviation from the reference value can then be related to all-cause, cancer related or cardiovascular disease related mortality. The analysis can be performed on a blood sample, tissue sample or a sample of separated cells. The results may be used to recommend life style changes to the patients or support any decisions e.g. which further tests are needed.

LÖSUNG

Prediction of disease related as well as all-cause mortality independent of underlying diseases or the "epigenetic clock"



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