Prediction of mortality through DNA methylation biomarkers (P-1333)

Key facts

- A “ready to use” kit
- Just 10 CpG sites to predict the chances of mortality
- Method is independent of underlying diseases or biological health

Abstract

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 Technology

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.

Applications and Commercial Opportunity

A “ready to use” kit to perform the methods for patients or consumers interested in their genetic health.
Testing methods for practitioners to support decision for further diagnostic tests or close monitoring.

Development Stage

The method has been validated through a 14 year long study and an independent cohort.

Inventors

The investigators are: Yan Zhang, Hermann Brenner

Intellectual Property

A patent application has been filed.

Further Information

No other public information is currently available, but further information is available under a signed Confidential Disclosure Agreement (CDA).

For further information, including a CDA, please contact:

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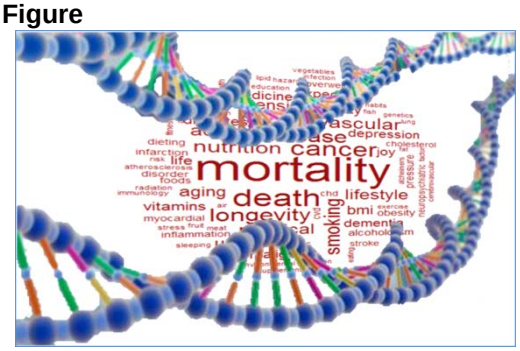
Figure



References

Yan Zhang, et al. DNA methylation signatures in peripheral blood strongly predict all-cause mortality. Nature Communications, 2017; 8: 14617 DOI: 10.1038/ncomms14617