

New method measures the risk of type 2 diabetes in blood

March 31 2016



Charlotte Ling. Credit: Gunnar Menander

Researchers at Lund University in Sweden have found a new type of biomarker that can predict the risk of type 2 diabetes, by detecting epigenetic changes in specific genes through a simple blood test. The

results are published today in *Nature Communications*.

"This could motivate a person at risk to change their lifestyle", says Karl Bacos, researcher in epigenetics at Lund University.

Predicting the onset of diabetes is already possible by measuring the blood glucose level average, HbA1C, over time. However, the predictive potential of this method is modest and new methods are needed.

The discoveries made by the research group at Lund University have now made it possible to measure the presence of so-called DNA methylations in four specific genes, and thereby predict who is at risk of developing type 2 diabetes, long before the disease occurs. Methylations are chemical changes that control gene activity, that is, whether they are active or not.

"The hope is that this will be developed into a better way to predict the disease", says Karl Bacos, first author of the study.

The researchers started by studying insulin-producing beta cells from deceased persons. They found that the DNA methylations in the four genes in question increased, depending on the donor's age. This in turn affected the activity of the genes.

When these changes were copied in cultured beta cells, they proved to have a positive effect on [insulin secretion](#).

"We could then see the same DNA methylation changes in the blood which was really cool", says Karl Bacos.

The blood samples from the participants of two separate research projects - one Danish and one Finnish - were then studied and compared with blood samples taken from the same participants ten years later. The

Finnish participants, who had exhibited higher levels of DNA methylation in their first sample, had a lower risk of type 2 diabetes ten years later. In the Danish participants, higher DNA methylation in their first sample was associated with higher insulin secretion ten years later. All of the Danish participants were healthy on both occasions, whereas approximately one-third of the Finnish participants had developed type 2 diabetes.

"Increased insulin secretion actually protects against type 2 diabetes. It could be the body's way of protecting itself when other tissue becomes resistant to insulin, which often happens as we get older", says professor and research project manager Charlotte Ling.

The studies were based on a relatively small number of [participants](#), and a selection of genes. The researchers therefore now want to continue with finding markers with a stronger predictive potential by implementing so-called epigenetic whole-genome sequencing when analysing a person's entire genetic make-up and all the DNA methylations that come with it, in a larger population group.

The research group has previously shown that age, diet and exercise affect the so-called epigenetic risk of type 2 diabetes.

"You cannot change your genes and the risks that they entail, but epigenetics means that you can affect the DNA methylations, and thereby gene activity, through lifestyle choices", says Charlotte Ling.

More information: Karl Bacos et al. Blood-based biomarkers of age-associated epigenetic changes in human islets associate with insulin secretion and diabetes, *Nature Communications* (2016). [DOI: 10.1038/ncomms11089](https://doi.org/10.1038/ncomms11089)

Provided by Lund University

Citation: New method measures the risk of type 2 diabetes in blood (2016, March 31) retrieved 26 April 2024 from <https://medicalxpress.com/news/2016-03-method-diabetes-blood.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.