

New clues in hunt for heredity in type 2 diabetes

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Type 2 diabetes has strong hereditary tendencies and the genes we are born with cannot be changed. However, new research from Lund University in Sweden shows that we can modify the function of the genes through the epigenetic changes that take place in the course of life. Epigenetic changes are usually described as a link between heredity and environment and come about as a result of factors such as ageing, chemicals, medication, diet, exercise and drugs.

Researchers have now demonstrated that half of the known [genetic risk](#) variants for type 2 diabetes can be influenced by [epigenetic changes](#) that in turn influence the function of the insulin-producing cells.

"This means that we gain a tool to influence the function of the risk genes, improve [insulin release](#) and thereby reduce the risk of diabetes", says Charlotte Ling at Lund University Diabetes Centre, who has today published a study on epigenetic effects in connection with type 2 diabetes in the journal *Diabetologia*.

The epigenetic factor that has been studied is a chemical change on the [DNA strand](#) following a certain pattern, known as [DNA methylation](#).

"We have shown that 19 of 40 known genetic risk variants for type 2 diabetes are affected by DNA methylation, which in turn changes the function of the insulin-producing cells", says Charlotte Ling. "This is important. Many researchers have put a lot of time and resources into mapping our genome and finding genetic risk markers for diabetes and

other diseases. We know that there are genetic variants that increase the risk of type 2 diabetes, but in most cases the reasons why this happens are still not known. The next step is to find this out and after this study of the genetic risk variants, we can say that in some cases the increased risk is probably due to varying degrees of DNA methylation."

The research group has studied insulin-producing cells from 84 deceased donors. This is the first epigenetic study to be carried out on the 40 risk markers for type 2 diabetes.

The present study shows that DNA methylation of genetic risk variants for diabetes influence the insulin-producing cells in various different ways, such as the amount of insulin they contain and the amount they are able to release into the blood stream.

"The next step in our work is to test whether we can reduce the risk of [type 2 diabetes](#) by changing the degree of DNA methylation in the genetic risk variants for the disease."

More information: Dayeh, T. et al. Identification of CpG-SNPs associated with type 2 diabetes and differential DNA methylation in human pancreatic islets, *Diabetologia*, 2013 Mar 6.

link.springer.com/article/10.1007%2Fs00125-012-2815-7

Provided by Lund University

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