Team finds 14 new biomarkers for type 2 diabetes

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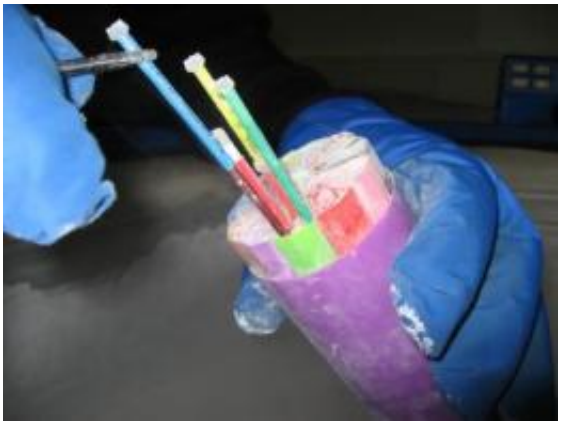

A research team led by Anna Floegel of the German Institute of Human Nutrition and Tobias Pischon of the Max Delbrueck Center for Molecular Medicine has identified 14 novel biomarkers for type 2 diabetes. Credit: Birgit Große/Copyright: DIfE

A research team led by Anna Floegel of the German Institute of Human Nutrition (DIfE) and Tobias Pischon of the Max Delbrueck Center for Molecular Medicine (MDC) has identified 14 novel biomarkers for type 2 diabetes. They can serve as basis for developing new methods of treatment and prevention of this metabolic disease. The biomarkers can also be used to determine diabetes risk at a very early point in time. At the same time the markers enable insight into the complex mechanisms of this disease, which still have not been completely elucidated.

The researchers studied the blood of study participants from three different studies with respect to their metabolites (metabolomics). The study was based on data and blood samples of the prospective EPIC-Potsdam study with more than 27,500 study participants, the Tuebingen family study and the KORA study. The study was conducted in collaboration with the German Center for Diabetes Research (DZD) and funded by the Federal Ministry of Education and Research (BMBF).

Metabolomics is still a young research field and serves the understanding of biological systems. It studies the dynamic network of metabolites of an organism and thus provides insight into ongoing biochemical processes. Metabolites have quite diverse functions. For instance, they play a role in cellular communication and regulation, transport energy or are building material for the cells. Changes in metabolite concentrations may therefore directly reflect alterations in metabolism and thereby, shed light on the pathogenesis or presence of disease.

The aim of the current study was to identify metabolites in blood which provide insight into the pathomechanisms of type 2 diabetes and in addition can be used as biomarkers to determine the disease risk. To this end, the researchers studied a total of 4,000 blood samples. About 3,000 of these samples came from the EPIC-Potsdam study, nearly 900 samples from the KORA study in Augsburg and 76 from the study in Tuebingen. At the time the blood sample was taken, none of the study participants suffered from type 2 diabetes: However, during the average follow-up time of seven years, 800 Potsdam study participants and 91 Augsburg participants were diagnosed with type 2 diabetes. The 76 participants in the Tuebingen study were already classified at the beginning of the study as individuals at high risk for type 2 diabetes. At the time the blood sample was taken, however, they were still healthy.

163 metabolites analyzed per blood sample Jerzy Adamski and his team at the Institute of Experimental Genetics of Helmholtz Zentrum

Muenchen analyzed the concentrations of 163 metabolites per blood sample. Fourteen of these metabolites exhibited a strong association with the development of type 2 diabetes.

"In addition to simple sugars, the 14 identified metabolites include various protein components and choline-containing phospholipids which play a role in the structure of cell membranes and in the transport of blood lipids," said Anna Floegel, lead author of the study. "Our findings particularly indicate a previously unknown role of phospholipids in type 2 diabetes development. This is a first clue which should definitely be pursued."

"At the same time the metabolites can also be used as biomarkers to precisely determine the risk of diabetes at a very early stage, since the study is based on prospective data, that is data that were collected before the onset of the disease," said Tobias Pischon, who led the study. "The results of the new metabolomic analysis thus provide a good basis for developing new treatment and prevention methods."

More information: Identification of Serum Metabolites Associated with Risk of Type 2 Diabetes Using a Targeted Metabolomic Approach, *Diabetes*, A. Floegel et al., 2012; DOI 10.2337/db12-0495

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