Genetic causes identified for disturbances in lipid metabolism

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Some of these common human gene variants are already known to be risk factors for diabetes mellitus. The pathomechanisms of diabetes have intrigued physicians and been the subject of much debate for many decades. These new research results may contribute to a better understanding of the clinical picture of diabetes and its pathogenesis - and could lead to new approaches in early diagnosis and therapy. The findings have been published in the current online issue of the renowned journal *Nature Genetics*.

The research team, made up of scientists of the Institute of Bioinformatics and Systems Biology at Helmholtz Zentrum München and of Ludwig-Maximilians-Universität München (LMU) and led by Professor Karsten Suhre, identified variants in nine different genes which could be associated with disturbances in the lipid metabolism. Together with Dr. Christian Gieger and Assistant Professor Thomas Illig of the Institute of Epidemiology at Helmholtz Zentrum München, Professor Suhre succeeded for the first time in associating variants in the well-known diabetes risk genes MTNR1B and GCKR with changes in the metabolism. "The results of our study bring us a decisive step closer in our search for markers for the early detection and therapy of serious metabolic diseases such as diabetes," Professor Suhre explained.

The variants identified in the study usually cause differences in the metabolization of important lipid building blocks of the body. Moreover, many of the identified variants are already known to be associated with elevated disease risk, for example for metabolic disorders - first and

foremost for diabetes.

As first step, the research team determined the concentrations of 163 metabolic products in blood samples of 1,800 participants of the KORA population study. Next, they investigated the metabolic profiles in a genome-wide association study for possible associations with common gene variants (SNPs). Then the scientists confirmed the identified associations by repeating their experiments in an independent study. The replication study took place in cooperation with scientists of the Sanger Centre in Hinxton and King's College in London, based on the British population study TwinsUK.

Karsten Suhre's research work belongs to the young research field of metabolomics in which scientists determine the concentrations of as many metabolic products (metabolites) as possible. In individuals with different gene variants, the affected enzymes also vary in their activity, and the concentrations of the metabolic products differ. The relationships are then categorized into distinct genetically determined metabotypes which can react differently to external environmental influences such as nutrition and other living conditions. In this way the metabolomics experts can identify risk patients for metabolic disorders earlier than they could previously. Thus, this study was able to detect genetically caused metabolic processes which play a crucial role in the pathogenesis as well as in the diagnosis and therapy of diseases such as diabetes.

More information: Illig T, Gieger C, Suhre K et al. A genome-wide perspective of genetic variation in human metabolism, Nature Genetics, online DOI: 10.1038/ng.507

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