

## Genetic risks for type 2 diabetes span multiple ethnicities

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A recent large and comprehensive analysis of 50,000 genetic variants across 2,000 genes linked to cardiovascular and metabolic function has identified four genes associated with type 2 diabetes (T2D) and six independent disease-associated variants at previously known loci. The findings, which provide valuable insight into the genetic risk for T2D across multiple ethnicities, add to the growing list of genetic variants that affect the risk of developing T2D and could pave the way for identification of valuable drug targets. The research will be published by Cell Press on February 9th in The *American Journal of Human Genetics*, the official journal of the American Society of Human Genetics.

Multiple environmental and genetic factors are linked with T2D, which is the most common form of diabetes. "Together, known T2D genetic variants explain only about 10% of the genetic variance, indicating that additional genetic factors are likely to contribute to disease risk," explains senior co-author Dr. Brendan J. Keating, from The Children's Hospital of Philadelphia. "Further, previous studies have been based almost exclusively on individuals of <u>European ancestry</u>, and genetic contributors to T2D are less well understood in non-European populations. An important first step towards understanding genetic risk across populations is to establish whether known T2D-associated genes span ethnicities or are population specific."

Dr. Keating, senior co-author Dr. Richa Saxena, from Massachusetts General Hospital and Harvard Medical School, and a large international cohort of colleagues undertook an ambitious genetic screening study to



gain a better understanding of genetic variants associated with T2D. Their analysis, the largest T2D genomics study conducted to date, included 39 multiethnic T2D association studies representing more than 17,000 cases of T2D and 70,000 controls and was designed to assess the impact of genetic variants across multiple ethnicities.

"As a result of our large-scale genetic analysis, we uncovered previously unknown European and multiethnic genetic variants and confirmed that, together, known <u>genetic risk</u> factors influence T2D risk in multiethnic populations, including African-Americans, Hispanics, and Asians," concludes Dr. Saxena. "Several additional signals were of borderline significance. Overall, our results demonstrate that this type of large multiethnic genome-wide screening study should lead to identification of additional T2D genetic variants relevant to multiple ethnic groups. Further, identification of additional genes associated with T2D may guide strategies for developing new therapeutics."

**More information:** Saxena et al.: "Large-Scale Gene-Centric Meta-Analysis across 39 studies Identifies Type 2 Diabetes Loci." *American Journal of Human Genetics*, March 9, 2012 print issue. doi:10.1016/j.ajhg.2011.12.022

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