



# Type 2 Diabetes Genetic Exploration by Next-generation sequencing in multi-Ethnic Samples (T2D-GENES)

consortiapedia.fastercures.org/consortia/t2d-genes/

## Research Areas



### Biomarker Research

Diagnostic, Genomic Biomarker



### Basic Research

## At a Glance

- Status: **Active Consortium**
- Year Launched: **2012**
- Initiating Organization: **National Institutes of Health**
- Initiator Type: **Government**
- Location: **International**

## Abstract

Type 2 Diabetes Genetic Exploration by Next-generation sequencing in multi-Ethnic Samples (T2D-GENES) is a National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK)–funded research consortium that seeks to identify genetic variants for Type 2 diabetes (T2D) through multiethnic sequencing studies.

## Mission

T2D-GENES is currently undertaking two sequencing studies and one genome-wide association study (GWAS)–based fine-mapping study.

Project 1 seeks to assess (a) whether less common variants play a role in T2D risk and (b) similarities and differences in the distribution of T2D risk variants across ancestry groups. Project 1 is carrying out deep exome sequencing of 10,000 individuals, 5,000 with T2D and 5,000 controls, equally divided among five ancestry groups: Europeans, East Asians, South Asians, American Hispanics, and African Americans. Sequencing is under way at the Broad Institute using the Agilent v2 capture reagent on



HiSeq machines.

Project 2 focuses on the role of rare and private variants on T2D risk and is based on deep whole genome sequencing of approximately 600 members of 20 Mexican American pedigrees. Pedigree members are extensively phenotyped and have been genotyped with Illumina GWAS chips. By applying an algorithm for efficient choice of individuals to sequence and highly-accurate pedigree-based imputation methods T2D-GENES will have the equivalent of approximately 1,100 sequenced individuals. Because of large family size, even private variants are likely to be present multiple times, allowing for an assessment of the impact of such variants currently impractical in case-control or population studies. Sequence data on all but approximately 40 individuals has been delivered by Complete Genomics (CGI); the remainder is expected soon.

Project 3 seeks to determine whether multiethnic GWAS meta-analysis might assist in fine-mapping T2D association signals by strengthening evidence for T2D association and narrowing the association interval. Project 3 has focused initially on analysis of five T2D loci chosen as likely candidates for success of this approach.

## Financing

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NIH funded consortium

## Links/Social Media Feed

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Homepage

<http://t2d-genes.sph.umich.edu/>

Other website

<http://www.type2diabetesgenetics.org/informational/t2dgenes>

## Sponsors & Partners

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