

Genetic risk scores help predict type 2 diabetes in people of south Asian origin

May 19 2022



Researchers from Queen Mary University find that genetic risk scores help predict type 2 diabetes in people of south Asian origin. Credit: Genes & Health Research Team, Queen Mary University (CC-BY 4.0, <https://creativecommons.org/licenses/by/4.0/>)

Combining a genetic risk score with a clinical risk score improved the

prediction of type 2 diabetes in British Pakistani and British Bangladeshi individuals, especially in the young, according to a new study publishing May 19 in the open access journal *PLOS Medicine* by Sarah Finan of Queen Mary University of London, U.K., and colleagues.

The common genetic changes associated with type 2 [diabetes](#) have been extensively studied in people of European ancestry. However, it is not known whether all previous findings can be applied to people of south Asian ancestry, who are disproportionately affected yet also underrepresented in genetic studies. The new study used genomic and routine health data from Genes & Health, a large population study of British Pakistanis and British Bangladeshis, including 7,599 with a diagnosis of type 2 diabetes.

The researchers found significant genetic differences in type 2 [diabetes risk](#) compared to what had been seen in previous studies on European populations. Out of 338 genetic loci identified in European populations, just 76 (22.5%) were transferable to the study population of British Pakistanis and British Bangladeshis. The team then constructed a type 2 diabetes [polygenic risk score](#) for the population in the study. When combined with QDiabetes, a routinely-used clinical risk score, the tool improved the prediction of type 2 diabetes (OR per SD of 1.57, 95% CI 1.50-1.65). The tool was particularly effective in assessing risk in British Pakistani and British Bangladeshi people under the age of 40 (net reclassification index 5.6%, 95% CI 3.6—7.6%), and also in predicting the development of type 2 diabetes after [gestational diabetes](#). Finally, the polygenic risk score was able to elucidate disease subgroups which are linked to differences in the risk of future diabetes complications.

"Our work highlights the importance of greater representation of diverse ancestry groups in [genetic studies](#) of type 2 diabetes," the authors say.

"Our polygenic risk score has multiple potential uses, but importantly, it helped identify young, otherwise healthy, individuals who were in fact

living at high risk of type 2 diabetes, 1 in 20 of whom might have been mistakenly labeled as low risk by current clinical risk tools. Our work also shows the potential use of polygenic risk scores in characterizing distinct disease subgroups at diagnosis which have different rates of progression to diabetes complications."

Finer adds, "We hope to see polygenic risk scores being adopted in [clinical care](#) in the future, after careful evaluation to understand their potential to improve health outcomes cost-effectively, and with diverse populations who are at greatest need."

More information: *PLoS Medicine* (2022). [DOI: 10.1371/journal.pmed.1003981](https://doi.org/10.1371/journal.pmed.1003981)

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Citation: Genetic risk scores help predict type 2 diabetes in people of south Asian origin (2022, May 19) retrieved 23 June 2024 from <https://medicalxpress.com/news/2022-05-genetic-scores-diabetes-people-south.html>

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