

Study finds gene does not increase risk for Type 2 diabetes in all Hispanic/Latino background groups equally

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A recent study found that people of Mexican background are more likely to be at risk for Type 2 diabetes than other Hispanic/Latino background

groups. The study, which was led by Bertha Hidalgo, Ph.D., a professor of epidemiology at the University of Alabama at Birmingham School of Public Health, examined variants—alterations to the DNA sequence—of the SLC16A11 gene in six different Hispanic and Latino background groups: Mexican, South American, Central American, Dominican, Puerto Rican and Cuban. The study was published in *Scientific Reports*.

The researchers analyzed data from the Hispanic Community Health Study/Study of Latinos (HCHS/SOL), which is a multicenter, community-based cohort study of Hispanic/Latino populations in the United States. The cohort collected data from approximately 16,000 people.

"Traditionally, large studies of Hispanic/Latinos have grouped several subgroups into a single category, ignoring the ancestral diversity that exists within this heterogeneous population," Hidalgo said. "The data from the Hispanic Community Health Study/Study of Latinos allows us to better understand the similarities and differences within and across these different subgroups."

Previous studies have shown that variants of the SLC16A11 gene put people of Mexican descent at [higher risk](#) for developing Type 2 diabetes. However, this is the first study to look at the [genetic risk](#) in the other five subgroups.

While researchers confirmed the increased risk for the Mexican background group, they found there was not an increased risk in the South and Central American, Dominican, Puerto Rican, and Cuban background groups of HCHS/SOL.

"These findings confirm the heterogeneity of the population; however, additional work will be needed to better understand the lack of replication of SLC16A11 variants in the non-Mexican background

groups of HCHS/SOL," Hidalgo explained. "The current literature suggests that SLC16A11 may be a therapeutic target for Type 2 diabetes, and our study adds evidence to further explore that hypothesis."

Confirming the findings from previous studies and discovering that the gene may not lead to an increased risk of developing Type 2 diabetes in the five other subgroups in the HCHS/SOL study means more work needs to be done to explain the risk factors of involved in developing Type 2 diabetes in other populations.

"The findings from this paper suggest we may have to take a more careful look at the role of the gene and what this means in terms of its generalizability as a therapeutic target for Type 2 diabetes," Hidalgo said. "Variants of the gene were identified and replicated in the Mexican background group of HCHS/SOL. We now need to do additional work to better understand the risk of Type 2 diabetes in other non-Mexican background groups."

Hidalgo plans to continue to research to identify risk factors for Type 2 [diabetes](#) in diverse populations, including Hispanic/Latinos.

More information: Bertha A. Hidalgo et al. Associations between SLC16A11 variants and diabetes in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL), *Scientific Reports* (2019). [DOI: 10.1038/s41598-018-35707-7](https://doi.org/10.1038/s41598-018-35707-7)

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