

Differences in gene expressions that tracked to progression of Type I diabetes identified

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A team of researchers from multiple countries in Europe and the U.S. has discovered differences in gene expression in children who later develop Type 1 diabetes. In their paper published in the journal *Science Translational Medicine*, the group describes their search for transcriptome patterns in blood samples collected from 400 children believed to be at high risk for developing Type 1 diabetes.

Type 1 diabetes, which usually affects children, occurs when the [immune system](#) attacks islet beta cells in the pancreas. The cells are killed and the child becomes unable to produce insulin. Type 1 diabetes is a lifelong condition that is treated via frequent blood testing and regular injections of insulin. Prior research has shown that Type 1 diabetes is likely a progressive disease, with the immune system increasingly targeting islet beta cells. Unfortunately, it is still not possible to predict whether a patient will develop Type 1 diabetes prior to onset. Doctors would like to have some lead time because it would help with preventing

health effects. It is possible to identify children who are most at risk of developing the disease, however, through [genetic testing](#). In this new effort, the researchers looked for changes in [gene expression](#) in children who were identified as likely to develop the disease and who later did.

The work involved obtaining and testing blood samples from children participating in the Environmental Determinants of Diabetes in the Young study. All of the children were considered to be at high risk for developing Type 1 diabetes. The researchers looked only at [blood samples](#) from those children who went on to actually get the disease. In all, they analyzed 2,013 samples given by 400 of the children in the study, looking specifically for transcriptome patterns. They discovered differences in gene expressions in the children that went on to develop Type 1 diabetes, including autoimmunity natural killer gene signatures. They suggest the expression changes they identified could someday be used to predict Type 1 [diabetes](#) in [children](#) prior to destruction of islet beta cells.

More information: Louis-Pascal Xhonneux et al. Transcriptional networks in at-risk individuals identify signatures of type 1 diabetes progression, *Science Translational Medicine* (2021). [DOI: 10.1126/scitranslmed.abd5666](#)

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