

Study identifies gene expression patterns associated with fatty liver disease

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A fatty liver disease known as NASH—non-alcoholic steatohepatitis—is the nation's major cause of chronic liver disease, and is projected to become the most common indicator for liver transplants.

The number of Americans with NASH has soared in recent decades to more than 6 million. NASH is strongly associated with patients who are

obese and those with type 2 diabetes. Yet, despite the growing number of patients, there are no effective treatments for this disease, which most often progresses to liver inflammation, [fibrosis](#), cirrhosis and death.

In an effort towards discovering a drug target, scientists at the Translational Genomics Research Institute (TGen), an affiliate of City of Hope, for the first time have identified significant [gene expression patterns](#) associated with obesity-related NASH inflammation and fibrosis.

The study, which was done in collaboration with the Geisinger Obesity Institute and Temple University, was published June 5 in the Journal of the Endocrine Society.

"These patients are in desperate need of effective new treatments," said Dr. Johanna DiStefano, Professor and Head of TGen's Diabetes and Fibrotic Disease Unit, and the study's senior author. "Our study results suggest that there may be a genomic framework around which new treatments might be based."

The researchers sequenced mRNA to profile the liver samples of obese patients from 24 healthy individuals, 53 with inflammation, and 65 with some degree of fibrosis or cirrhosis. They discovered 176 genes specific to fibrosis, revealing three associated cellular pathways, and 16 genes previously associated with [liver fibrosis](#) and cirrhosis.

"The results obtained in this study demonstrate that advanced NASH fibrosis is characterized by a distinct set of molecular changes that are shared with other causes of cirrhosis," said Dr. DiStefano. "Future investigations, including validation in independent cohorts and functional characterization of dysregulated genes and pathways, will be important to extend these findings."

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More information: Glenn S Gerhard et al. Transcriptomic profiling of obesity-related nonalcoholic steatohepatitis reveals a core set of fibrosis-specific genes, *Journal of the Endocrine Society* (2018). [DOI: 10.1210/js.2018-00122](https://doi.org/10.1210/js.2018-00122)

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