

# Researchers show genetic variants and environmental exposures have influence on health

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Scientists at the Wayne State University School of Medicine's Center for Molecular Medicine and Genetics have shown for the first time the extent by which interactions between environmental exposures and genetic variation across individuals have a significant impact on human traits and diseases like diabetes, heart disease and obesity, strengthening the case for precision medicine initiatives.

The discovery is particularly important when considering communities with different ancestries sharing the same risk environment—the case for many urban communities, including Detroit, the researchers said. Generally, people may share the same genetic risk factors but their chances to develop a disease are increased by specific [environmental exposures](#). Human environments are difficult to measure, especially when trying to study these complex interactions. For example, the researchers explained, it is hard to quantify the amount of stress in a person's life or the caffeine or vitamin content in their diets.

"Both genes and environmental conditions are major influences on our health and who we are. For example, stress is a risk factor for cardiovascular disease; however, the actual risk to have a heart attack depends not only on the amount of stress in a person's life but also on the specific DNA sequences—genetic variants—that he or she inherited from their parents," said researcher Francesca Luca, Ph.D., who led the study with co-principal investigator Roger Pique-Regi, Ph.D. "The

interplay between genetic variants and environments during human evolutionary history provided the driving force that shaped our genome. Today, genetic adaptations that helped us in the past to better store energy in fat, for example, can make us more likely to develop a disease like diabetes or obesity."

Luca and Pique-Regi are assistant professors of [molecular medicine](#) and genetics, and of obstetrics and gynecology, and have spent three years working on the project with a dedicated team of collaborators that included several WSU students and postdoctoral fellows, including recent graduate Gregory Moyerbrailean, Ph.D.; graduate student Cynthia Kalita; postdoctoral fellow Allison Richards, Ph.D.; and third-year medical student Daniel Kurtz.

Studying the interaction between genetic variants and environment is an incredibly complex problem to tackle at the organismal level. The WSU-based team explored, at the molecular level, gene expression changes across 250 different cellular environments, including caffeine, vitamins, metal ions, hormones, contaminants and common drugs.

"Our cellular system simplifies the complexity of the environment, and allows us to develop robust statistical tests to identify 215 genes with an activity modulated by genetic variants that interact with our controlled environmental perturbations," Luca said. "Surprisingly, 50 percent of these interactions are in genes important for human traits and diseases. For example, one of these interactions in the GIPR gene suggests that caffeine intake in the presence of a genetic protective factor may decrease the risk to develop obesity. Similarly, low selenium intake, in the presence of a [genetic risk factor](#) in the LAMP3 gene, may further increase the risk for Parkinson's disease."

This is the first time that large-scale genomic experiments have shown that an individual's personal environment and genetic makeup can

directly affect and influence their health.

The results of the project are presented in the open-access *Genome Research* article "High-throughput allele-specific expression across 250 [environmental conditions](#)," published last month.

In addition to the *Genome Research* publication, the researchers presented two talks on their work at October's American Society of Human Genetics in Vancouver.

The research team is now investigating the precise molecular mechanisms of the interactions, exploring additional environmental exposures—including the human microbiome—and performing similar studies in a large number of individuals of African American origin to explore a larger number of genetic variants.

**More information:** Gregory A Moyerbrailean et al. High-throughput allele-specific expression across 250 environmental conditions, *Genome Research* (2016). [DOI: 10.1101/gr.209759.116](https://doi.org/10.1101/gr.209759.116)

Provided by Wayne State University

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