

A genetic approach to clinical addiction symptoms

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Jinbo Bi, associate professor of computer science and engineering, discusses her research. Credit: Sean Flynn/UConn Photo

When it comes to diagnosing substance abuse, health care professionals are mainly limited to relying on patient honesty. But a new study aims to

find the genetic causes of addiction, which could lead to a more nuanced way of treating complex medical and social problems.

The study, led by Jinbo Bi, associate professor of computer science and engineering, recently received a \$1.12 million grant from the National Institutes of Health (NIH). Bi and her fellow researchers aim to develop new statistical tools and techniques to better classify the many variations of [substance dependence](#). The hope is that a better understanding of the role genes play in these disorders will lead to more effective treatment.

Researchers have made great progress in using genetic information to diagnose and treat other diseases in patients. Genome sequencing, for instance, is leading to customized treatment for certain cancers.

Substance addiction, with its multiple causes, has been a tougher nut to crack for genetics researchers. Currently doctors rely on the symptoms listed in the Diagnostic and Statistical Manual (DSM) of Mental Disorders. The current edition provides several criteria, based mostly on behavior. Examples include whether a patient worries about stopping, or spends a lot of time trying to obtain drugs or alcohol.

While previous studies have looked at the genes associated with the diagnoses of [substance abuse](#), Bi's study will take a more specific approach by looking at the genes associated with the clinical symptoms that lead to abuse.

For instance, two people diagnosed with [alcohol dependence](#) can have different symptoms. Perhaps only one has trouble sleeping, or one cites a diminished social life while the other goes to so many parties that it's affecting work. Bi says the study will look at whether genetic variances can account for these differences.

To integrate multiple clinical symptoms with multiple genetic variants,

however, requires more sophisticated algorithms than what researchers have now. Developing new ones is the first task in the four-year study.

The study will make use of a database of more than 11,000 subjects who were identically assessed in genetic studies of cocaine, opioid, and alcohol dependence, the largest sample of its kind.

With such a robust sample, the researchers expect to put a much finer point on diagnosing different addictions. For instance, the criteria provided in the DSM doesn't discern between different types of [cocaine dependence](#). Preliminary studies by Bi's team, though, show that a variant in what's known as the CLOCK gene could be the difference between addicts who inject the drug and those who consume it in other ways. And the more that is known about which genes are associated with specific subtypes of [drug dependence](#), the closer it brings researchers to developing more effective treatments. The fact that the CLOCK gene regulates our circadian rhythms, for instance, could be significant.

"Maybe then we can design something to control the circadian rhythm," Bi says. "If we know a specific property of a particular sub-population of the patients, then we can design something to target it."

Provided by University of Connecticut

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