Study uncovers novel genetic variation linked to increased risk of sudden cardiac arrest

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A study by a global consortium of physician-scientists has identified a genetic variation that may predispose people to double the risk of having a sudden cardiac arrest, a disorder that gives little warning and is fatal in about 95 percent of cases. Although previous, smaller studies have identified some genes with a potential association with sudden cardiac arrest, this is the first study large enough to enable scientists to apply results to the general population. Findings are published today by the Public Library of Science (*PloS Genetics*).

"We are at the beginning of unraveling the mystery of what causes sudden cardiac arrest and how to prevent it," said senior author Sumeet S. Chugh, MD, associate director of the Cedars-Sinai Heart Institute and a specialist in cardiac electrophysiology. "If we wait until someone has a sudden cardiac arrest, it is usually too late for treatment. That is why knowing who is genetically susceptible is so important."

Unlike heart attacks (myocardial infarction), which are typically caused by clogged coronary arteries reducing blood flow to the heart muscle, sudden cardiac arrest is the result of defective electrical impulses. Patients may have little or no warning, and the disorder usually causes nearly instantaneous death. Every year, 250,000 to 300,000 people in the U.S. and up to 5 million worldwide die from sudden cardiac arrest.

Despite years of significant advances in emergency medicine and resuscitation, just five percent of those who suffer sudden cardiac arrest survive. For patients at known risk for this or other heart rhythm abnormalities, an implantable cardioverter-defibrillator (ICD) may be placed in the chest or abdomen to detect faulty electrical impulses and provide a shock to return normal rhythm. Better genetic predictors of risk may someday enable the accurate prediction of which patients are most likely to benefit from costly ICD therapy.

The discovery came from a genome-wide association study, which examines the entire set of human genes to detect possible links between genetic variations and specific conditions or diseases. In this study, researchers from the Cedars-Sinai Heart Institute, Johns Hopkins University School of Medicine, along with researchers from the National Institutes of Health, Harvard University, Wake Forest University School of Medicine, Oregon Health and Science University, Finland, Canada and the Netherlands compared the genetic makeup of 4,402 subjects who had experienced sudden cardiac arrest to the DNA of 30,000 control subjects who had no history of the disorder.

Based on a comparison of the two groups, a genetic variation in the BAZ2B gene was found to be associated with a significantly increased risk of sudden cardiac arrest.

"If you have this genetic variation in your DNA, it appears that you may have a two-fold higher likelihood of sudden cardiac arrest," said Chugh, the Pauline and Harold Price Chair in Cardiac Electrophysiology Research.

The researchers also studied the link between other genetic variations that account for EKG abnormalities and were able to pinpoint several that can also be used for improving the prediction of sudden cardiac arrest in the community.

Provided by Cedars-Sinai Medical Center