Predicting risk of stroke from one's genetic blueprint

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A new statistical model could be used to predict an individual's lifetime risk of stroke, finds a study from the Children's Hospital Informatics Program (CHIP). Using genetic information from 569 hospital patients, the researchers showed that their predictive model could estimate an individual's overall risk of cardioembolic stroke -- the most common form of stroke -- with 86 percent accuracy. The findings are reported in the March issue of *Stroke*.

"For complex diseases like stroke, it's not just a single mutation that will kill you," explains CHIP researcher Marco Ramoni, PhD, the study's senior author, who is also an Associate Professor at Harvard Medical School. "More likely it is an interaction of many factors."

Ramoni, in collaboration with Karen Furie, MD, the director of the stroke unit at Massachusetts General Hospital (MGH), and Rachel Ramoni, DMD, ScD, of the Harvard School of Dental Medicine, identified 569 patients that had presented to MGH's emergency department and outpatient neurology clinics between 2002 and 2005 with symptoms of suspected stroke. They collected genetic information from the 146 patients with confirmed cardioembolic stroke, and 423 controls who were followed and found not to have stroke, and looked for 1,313 genetic variants (called single nucleotide polymorphisms or SNPs) known to correlate with stroke. The SNPs that each patient had were then entered into the model -- known as a Bayesian network — which not only identified the genetic variants that correlated with stroke, but also determined how these factors interplayed and the strength of these

interactions.

"The model looks for factors, combines them and finds out which are the best predictive factors," explains Ramoni. "It's never one factor at a time, it's always more than one factor. What this technology allows you to do is to generate a network of factors that contribute to stroke."

The researchers found that the model was able to predict an individual's risk of cardioembolic stroke with an accuracy of 86 percent. Ultimately, Ramoni envisions doctors using it as a diagnostic tool: a patient's genetic information would simply be entered into the model, which would correlate and analyze the data and output an overall probability of stroke, based on the stroke-related SNPs in the patient's genome. "It sounds like magic," says Ramoni. "But it's just a piece of technology. It gives hope that we will be able to predict early on whether someone is at risk of getting stroke, and allow you to convince them to make life changes."

"The next step is to get more SNPs," Ramoni adds. "These analyses looked at only 1,313 out of 3.3 million known SNPs. Even a million SNPs would cover the vast majority of the genome. We would get much better predictions."

Ramoni also says that by identifying all the genetic variants that modulate the risk of stroke, it could provide insight into its mechanisms and provide targets for future drugs. He is currently refining the model and believes that this technology could be used to predict inherited risk of many other conditions.

Source: Children's Hospital Boston