ICU
MANAGEMENT & PRACTICE

ICU Volume 9 - Issue 1 - Spring 2009 - Research News

Predicting Risk of Stroke From One's Genetic Blueprint

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.

CHIP researcher Marco Ramoni, PhD, an Associate Professor at Harvard Medical School, 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.

Published on : Tue, 21 Apr 2009

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