MedicalXpress

Genome-wide survey examines recessive Alzheimer disease gene

August 26 2013

Runs of homozygosity (ROHs, regions of the genome where the copies inherited from parents are identical) may contribute to the etiology (origin) of Alzheimer disease (AD), according to a study in *JAMA Neurology* by Mahdi Ghani, Ph.D., of the University of Toronto, Ontario, Canada, and colleagues.

Caribbean Hispanics are known to have an elevated risk for AD and tend to have large families with evidence of inbreeding, according to the study background.

A Caribbean Hispanic data set of 547 unrelated cases (48.8 percent with familial AD) and 542 controls collected from a population known to have a three-fold higher risk of AD versus non-Hispanics in the same community was used in the study. The data set consisted of African Hispanic (207 cases and 192 controls) and European Hispanic (329 cases and 326 controls) participants.

In total, 17,137 autosomal regions with ROHs were identified. The mean length of the ROH per person was significantly greater in cases versus controls, and this association was stronger in familial AD. Among the European Hispanics, a consensus region at the EXOC4 locus was significantly associated with AD even after correction for multiple testing. Among the African Hispanic subset, the most significant but nominal association was observed for CTNNA3, a well-known AD gene candidate.

"We found that ROHs could significantly contribute to the etiology of AD in a population with noticeable inbreeding," the study concludes.

More information: *JAMA Neurol.* Published online August 26, 2013. DOI: 10.1001/.jamaneurol.2013.3545