GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Intracranial aneurysm risk factor genes: relationship with intracranial aneurysm risk in a Chinese Han population

L.T. Zhang[1]*, F.J. Wei[2]*, Y. Zhao[1], Z. Zhang[1], W.T. Dong[1], Z.N. Jin[1], F. Gao[1], N.N. Gao[1], X.W. Cai[1], N.X. Li[1], W. Wei[1], F.S. Xiao[1], S.Y. Yue[1], J.N. Zhang[1], S.Y. Yang[1], W.D. Li[2] and X.Y. Yang[1]

[1]Department of Neurosurgery, Tianjin Medical University General Hospital, Tianjin, China
[2]Research Center of Basic Medical Sciences, Tianjin Medical University, Tianjin, China

*These authors contributed equally to this study.
Corresponding authors: X.Y. Yang / W.D. Li
E-mail: yangxinyu@tijmu.edu.cn / liweidong98@hotmail.com6

Genet. Mol. Res. 14 (2): 6865-6878 (2015)
Received September 30, 2014
Accepted February 27, 2015
Published June 18, 2015
DOI http://dx.doi.org/10.4238/2015.June.18.30

ABSTRACT. Few studies have examined the genes related to risk factors that may contribute to intracranial aneurysms (IAs). This study in Chinese patients aimed to explore the relationship between IA and 28 gene loci, proven to be associated with risk factors for IA. We recruited 119 patients with aneurysms and 257 controls. Single factor and logistic regression models were used to analyze the association of IA and IA rupture with risk factors. Twenty-eight single nucleotide polymorphisms (SNPs) in 22 genes were genotyped for the patient and control groups. SNP genotypes and allele frequencies were analyzed by the chi-square test. Logistic regression analysis identified hypertension as a factor that increased IA risk ($P = 1.0 \times 10^{-4}$; OR, 2.500; 95%CI, 1.573-3.972); IA was associated with two SNPs in the *TSLC2A9* gene: rs7660895

(P = 0.007; OR, 1.541; 95%CI, 1.126-2.110); and in the *TOX* gene: rs11777927 (P = 0.013; OR, 1.511; 95%CI, 1.088-2.098). Subsequent removal of the influence of family relationship identified between 12 of 119 patients enhanced the significant association of these SNPs with IA (P = 0.001; OR, 1.691; 95%CI, 1.226-2.332; and P = 0.006; OR, 1.587; 95%CI, 1.137-2.213 for rs7660895 and rs11777927, respectively). Furthermore, the minor allele of rs7660895 (A) was also associated with IA rupture (P = 0.007; OR, 2.196; 95%CI, 1.230-3.921). Therefore, hypertension is an independent risk factor for IA. Importantly, the *TSLC2A9* (rs7660895) and *TOX* (rs11777927) gene polymorphisms may be associated with formation of IAs, and rs7660895 may be associated with IA rupture.

Key words: Intracranial aneurysm; Gene; SNP; Risk factor

