Ischemic Stroke and Six Genetic Variants in CRP, EPHX2, FGA, and NOTCH3 Genes: A Meta-Analysis

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Background Ischemic stroke (IS) is a leading cause of death and disability worldwide. As genetic heritability for IS is estimated at about 35%-40%, the identification of genetic variants associated with IS risk is of great importance. The main objective of this study was to carry out a meta-analysis for polymorphisms in CRP, EPHX2, FGA, and NOTCH3 genes and the risk for IS. Methods
Literature search for 6 candidate polymorphisms and IS was conducted using HuGE Navigator,
PubMed, and Google Scholar databases. Meta-Analyst program was used to calculate pooled odds ratios (ORs) with a random effects model. Results Twenty-five published studies for 6 candidate polymorphisms were included: CRP-rs1800947 (5 studies), CRP-rs1205 (3 studies),
EPHX2-rs751141 (5 studies), FGA-rs6050 (6 studies), NOTCH3-rs3815188 (3 studies), and
NOTCH3-rs1043994 (3 studies), for a total number of 7,825 IS cases and 56,532 control subjects.
We did not find significant pooled ORs (P values?>?.05) for any of the genetic variants evaluated in this work. Conclusions Our meta-analysis results did not show significant associations between these 6 polymorphisms in 4 candidate genes and IS, despite the functional role of some of these single nucleotide polymorphisms (e.g., rs6050 in FGA gene). Future studies are needed to identify additional main genetic risk factors for IS in different populations. © 2016 National Stroke

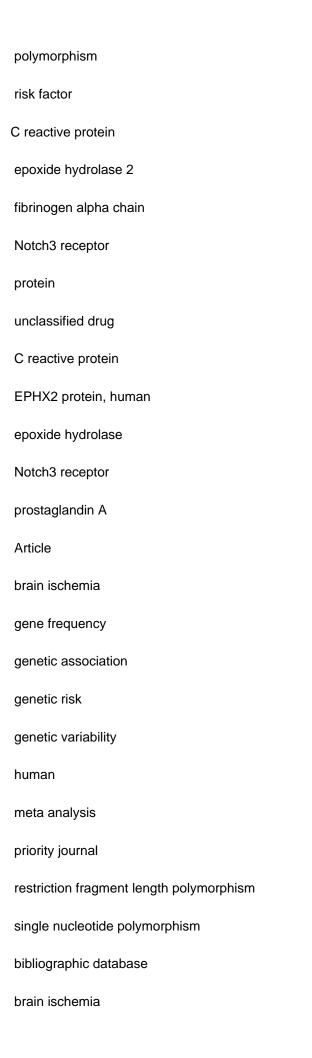
Association

Candidate gene

genetic factors

ischemic stroke

meta-analysis



complication
genetic predisposition
genetic variation
genetics
statistics and numerical data
Stroke
Brain Ischemia
C-Reactive Protein
Databases, Bibliographic
Epoxide Hydrolases
Genetic Predisposition to Disease
Genetic Variation
Humans
Prostaglandins A
Receptor, Notch3
Stroke