OPEN ACCESS



# The Association between VEGF Gene Polymorphisms and Stroke: an updated systematic review and meta-analysis

Bingdong Xu,Rui Zhan,Hongcheng Mai,Zhengdong Wu,Peizhi Zhu,Yubin Liang,Yusheng Zhang

#### **Abstract**

**Citation:** Bingdong Xu,Rui Zhan,Hongcheng Mai,Zhengdong Wu,Peizhi Zhu,Yubin Liang,Yusheng Zhang The Association between VEGF Gene Polymorphisms and Stroke: an updated systematic review and meta-analysis. **protocols.io** 

dx.doi.org/10.17504/protocols.io.pgmdju6

Published: 14 Apr 2018

### **Protocol**

Methods
A systematic literature search of PubMed, Embase, Wed of Science, The Cochrane Library, Elsevier, China National Knowledge Infrastructure, China Biology Medicine disc, WanFang Data, VIP Database for Chinese Technical Periodicals, Sciencepaper Online were conducted by two study investigators independently. The latest data for searching articles was November 1st, 2017. Key words used in the research were: "VEGF" or "vascular endothelial growth factor" or "vasculotropin", "single nucleotide polymorphism" or "SNP" or "polymorphism" or "mutation" or "genetics" or "variant", and "stroke" or "cerebral infarction" or "cerebrovascular disorders".

## Step 1.

Inclusion and exclusion criteria Studies eligible for inclusion in this meta-analysis needed to meet the following criteria: (1) independently published case-control studies focused on associations between VEGF polymorphism and risk of stroke; (2) these studies provided genotype or allelic distributions; (3) genotype or allelic distributions in the control group was in accordance with the Hardy-Weinberg equilibrium (HWE). The exclusion criteria for the meta-analysis were: (1) animal studies; (2) there were a large difference in the general data of the subjects, such as age, gender, and there may be a significant bias in the literature. When individual authors published several articles from the same patient population, only the most recent or complete articles were taken into account in the analysis.

#### **Step 2 - Enter case name.**

Data extraction All qualified information was drawn from all the eligible publications. The following data were collected from each study: the first author's name, the date of publication, country, ethnicity, sample size, the genotyping method.

**Step 3 - Enter case name.**