VKORC1 Haplotypes Are Associated With Arterial Vascular Diseases (Stroke, Coronary Heart Disease, and Aortic Dissection)

Yibo Wang, BS; Weili Zhang, PhD; Yuhui Zhang, MD; Yuejin Yang, MD, PhD; Lизhong Sun, MD; Shengshou Hu, MD; Jilin Chen, MD; Channa Zhang; Yi Zheng, MD; Yisong Zhen, PhD; Kai Sun, PhD; Chunyan Fu, MD; Tao Yang, BS; Jianwei Wang, BS; Jing Sun, BS; Haiying Wu, MD; Wayne C. Glasgow, PhD; Rutai Hui, MD, PhD

Background—The haplotypes in the gene vitamin K epoxide reductase complex subunit 1 (VKORC1) have been found to affect warfarin dose response through effects on the formation of reduced-form vitamin K, a cofactor for γ-carboxylation of vitamin K–dependent proteins, which is involved in the coagulation cascade and has a potential impact on atherosclerosis. We hypothesized that VKORC1–dependent effects on the coagulation cascade and atherosclerosis would contribute to susceptibility for vascular diseases.

Methods and Results—To test the hypothesis, we studied the association of polymorphisms of VKORC1 with stroke (1811 patients), coronary heart disease (740 patients), and aortic dissection (253 patients) compared with matched controls (n = 1811, 740, and 416, respectively). Five common noncoding single-nucleotide polymorphisms of VKORC1 were identified in a natural haplotype block with strong linkage disequilibrium (D' > 0.9, r² > 0.9), then single-nucleotide polymorphism (SNP) +2255 in the block was selected for the association study. We found that the presence of the C allele of the +2255 locus conferred almost twice the risk of vascular disease (odds ratio [OR] 1.95, 95% confidence interval [CI] 0.58 to 2.41, P < 0.001 for stroke; OR 1.72, 95% CI 1.24 to 2.38, P < 0.01 for coronary heart disease; and OR 1.90, 95% CI 1.04 to 3.48, P < 0.05 for aortic dissection). We also observed that subjects with the CC and CT genotypes had lower levels of undercarboxylated osteocalcin (a regulator for the bone), probably vascular calcification, and lower levels of protein induced in vitamin K absence or antagonism II (PIVKA-II, a des-γ-carboxy prothrombin) than those with TT genotypes.

Conclusions—The haplotype of VKORC1 may serve as a novel genetic marker for the risk of stroke, coronary heart disease, and aortic dissection. (Circulation. 2006;113:1615-1621.)

Key Words: vitamin K epoxide reductase ■ haplotypes ■ stroke ■ coronary disease ■ aortic dissection

Stroke and coronary heart disease (CHD) are the leading causes of morbidity and mortality in China.1 Each year, more than 2.5 million Chinese have strokes, 1 million have heart attacks, and 2 million die of stroke- and CHD-related causes. Furthermore, 7 million patients have survived a stroke and are disabled (http://www.moh.gov.cn). Elucidation of the pathogenesis of these diseases and identification of subjects at risk for these events are major challenges to medical society. A high degree of comorbidity and common risk factors have been observed among myocardial infarction (MI), stroke, and aortic dissection. Most of these cases result from atherosclerotic disease that is characterized by lesions in large and medium-sized elastic and muscular arteries.2-4

Platelet adhesion and mural thrombosis are ubiquitous in the initiation and generation of lesions of atherosclerosis in animals and in humans.5,6 Plaque adhesion and thrombosis formation result from activation of the coagulation cascade, initiated by atherosclerotic plaque erosion or rupture contributing to propagation of thrombosis.7-9

Vitamin K–dependent proteins play very important roles in activation of the coagulation cascade and in maintaining blood flow and integrity of the vasculature.10-13 The biological activity of all known vitamin K–dependent proteins is

Received August 1, 2005; revision received January 18, 2006; accepted January 20, 2006.
From Sino-German Laboratory for Molecular Medicine (Y.W., W.Z., C.Z., Y. Zheng, Y. Zhen, K.S., C.F., T.Y., J.W., J.S., R.H.), Hypertension Division (Y. Zhang, H.W., R.H.), Department of Cardiology (Y.Y., J.C., R.H.), and Department of Cardiovascular Surgery (L.S., S.H.), Fuwai Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College and National Genome Center (Beijing); and Division of Basic Medical Sciences (W.C.G.), Mercer University School of Medicine, Macon, Ga.
Reprint requests to Rutai Hui, MD, PhD, Cardiovascular Institute & Fuwai Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, 167 Beilishilu, Beijing 100037, People’s Republic of China. E-mail huirutai@sglab.org
© 2006 American Heart Association, Inc.
Circulation is available at http://www.circulationaha.org DOI: 10.1161/CIRCULATIONAHA.105.580167
highly dependent on correct γ-carboxylation. Vitamin K hydroquinone, a cofactor for γ-carboxylation, is converted to vitamin K epoxide, which in turn is recycled to vitamin K hydroquinone by vitamin K epoxide reductase. Undercarboxylation of vitamin K–dependent proteins in patients with a specific mutation in the γ-carboxylase results in bleeding disorders. Common polymorphisms in the gene vitamin K epoxide reductase complex subunit 1 (VKORC1) affect warfarin dose response and blood clotting through effects on the formation of the reduced form of vitamin K, which subsequently alters carboxylation of vitamin K–dependent hemostatic and nonhemostatic proteins. Numerous studies indicate that vitamin K–dependent proteins have additional activities that extend their roles beyond hemostatic and bone metabolism, perhaps in vascular calcification and atherosclerotic complications. Price et al showed that inhibition of VKORC1 by warfarin results in undercarboxylation of matrix Gla protein (MGP) and subsequent medial calcification of the arterial vessel wall. Gene-deletion studies in mice have shown that MGP is an inhibitor of calcification.

Arterial calcification has been correlated with an increased probability of dissection and a higher incidence of future ischemic episodes in patients undergoing angioplasty. Intimal calcification of atherosclerotic plaques correlates with plaque burden and high risk of cardiovascular events. Medial calcification has been shown to be associated with diabetes mellitus and end-stage renal disease and as a prognostic marker for cardiovascular mortality in patients requiring hemodialysis. Despite the fact that VKORC1 mediates vitamin K–dependent γ-carboxylation, which is involved in calcification, it remains unknown whether this could translate into higher risk for arterial disease. We hypothesized that VKORC1–dependent effects on the coagulation cascade and vascular calcification would contribute to susceptibility to vascular diseases. To test the hypothesis, we investigated the association of VKORC1 polymorphisms with stroke, CHD, or aortic dissection.

Methods
The study was approved by both the ethics committee of Fuwai Hospital and the local ethics committee of the collaborative hospitals. All subjects who participated in the study were written informed consent and reported themselves to be of Han nationality.

Stroke Cohort
The primary study population has previously been used to investigate risk factors of stroke. Briefly, case and control subjects were recruited from 7 clinical centers located in 7 provinces from the same demographic area and at the same time from November 2000 to November 2001. Only 3 subtypes of stroke—cerebral atherosclerosis, lacunar infarction, and intracerebral hemorrhage—were included. Diagnosis of stroke was based on strict neurological examination, computed tomography, or MRI according to the International Classification of Diseases, 9th revision. Controls were selected from inpatients (21.5%) with minor illness from the departments of ophthalmology, gastroenterology, otolaryngology, and orthopedics and from community-based inhabitants (78.5%) free of neurological diseases, following the same exclusion criteria as case subjects. In each local community, both men and women 35 to 74 years of age in the range of selection were grouped by age (5-year range for each group), and the control subject was randomly selected from the corresponding group.

CHD and Aortic Dissection Cohorts
Patients for the 2 studies were consecutive patients admitted to Fuwai Hospital from December 2001 to December 2002. The second population comprised 740 unrelated patients with CHD aged from 30 to 75 years and 740 control subjects. Inclusion criteria were ≥70% narrowing of the lumina of at least 1 major coronary artery. A detailed history of angina or MI was obtained. Of the patients, 57.8% had MI judged by typical ECG change (Minnesota Code 1.1 or 1.2 in ECG) and by changes in serum enzymes (troponin T, troponin I, creatine kinase-MB, aspartate aminotransferase, and glutamic pyruvic transaminase). The 740 control subjects were selected from hospital inpatients whose major coronary arteries had no more than 20% stenosis and who did not have any vascular disease.

The third study sample comprised 253 unrelated cases with aortic dissection who were 20 to 75 years old and 416 control subjects. Aortic dissection was diagnosed on the basis of symptoms, signs, ECG, cardiac enzymes, coronary angiography, magnetic resonance angiography, and/or aortic angiography. Seventy percent of the patients underwent aortography, aortic surgery, and pathological examination. One hundred sixty-three patients were excluded because of known causes of disease, including aortic disease caused by coarctation of aorta, congenital aortic valve disease, inflammation arteritis, and trauma during cardiovascular procedure or glucocorticoid treatment. The diagnosis of Marfan syndrome (11.5% in these patients with aortic dissection) was based on revised clinical criteria of the Gent nosology. None of the control subjects had a history or symptoms of cardiovascular disease.

Biological Variable Determination and Clinical Data Collection
Blood samples were collected after a 12-hour overnight fast before cardiovascular procedures. In subjects with an acute event, the drawing of blood was delayed for at least 6 weeks. The plasma and cell buffett coat were kept at −70°C. Genomic DNA was extracted, and biological variables were determined within 3 months. A complete clinical history was obtained from all subjects. In addition to neurological history and family history of hypertension, CHD, and diabetes mellitus (DM), the following vascular risk factors were also recorded: history of vascular disease, cigarette smoking, alcohol consumption, body mass index, systolic blood pressure (SBP), diastolic blood pressure (DBP), blood glucose, HDL cholesterol (HDL-C), non–HDL-C lipids, total plasma cholesterol (TC), and triglycerides (TG). Plasma biochemical parameters were assessed by an automatic analyzer (Hitachi 7060, Hitachi, Tokyo, Japan). Non-HDL-C was calculated by the Friedewald formula. Hypertension was defined as a mean of 3 independent measures of blood pressure ≥140/90 mm Hg or the use of antihypertensive drugs. DM was diagnosed when the subject had a fasting glucose level >7.8 mmol/L, >11.1 mmol/L at 2 hours after oral glucose challenge, or both. All lipids were determined in a Centers for Disease Control and Prevention (CDC)–qualified laboratory in Fujwai hospital.

Screening for Single-Nucleotide Polymorphisms
The entire gene region of VKORC1 and the 2-kilobase (kb) 5′ upstream promoter region and 2-kb 3′ downstream region were screened by sequencing (ABI Prism 377, Perkin-Elmer Applied Biosystems, Foster City, Calif) in 50 stroke patients and 50 control subjects. No polymorphism was found in the entire coding sequence. The alleles with frequencies <0.05 were excluded; 5 common noncoding polymorphisms were identified in the VKORC1 gene, including −1639A/G (rs9923231) in the promoter region, +1173T/C (rs9934438) in the first intron, +1542C/G (rs8050894) and +2255T/C (rs2359612) in the second intron, and +3730G/A (rs7294) in the 3′ downstream region (defined by the nucleotide position from the translational start site). These single-nucleotide polymorphisms (SNPs) are located at positions 3673, 6484, 6853, 7566, and 9041 of the VKORC1 reference sequence (GenBank
accession number AY587020). We calculated linkage disequilibrium (LD) between pairs of SNPs using the standard definition of D' and r² and found all 5 SNPs were in strong LD, with D'>0.9 and r²>0.9, which indicates that any 1 of the 5 SNPs could reflect the natural haplotype block of VKORC1. SNP +2255 was selected for genotyping in all studied subjects because its frequency was slightly higher than the other 4 SNPs, and there is a natural digestion site of NcoI in the SNP +2255 fragment.

**Genotyping of SNP +2255**
The polymorphism +2255 was analyzed by amplification of a 198-bp sequence with the use of the following primers: 5'-TCTGAAACATGGTCAGCCAGGACC-3' and 5'-GAACAGAGAAGAAGGAGTAGTGGAGA-3'. The resultant polymerase chain reaction products were digested with NcoI (New England Biolabs, Beverly, Mass), which yielded 2 DNA fragments of 26 and 172 bp for the T allele on 4% agarose gel and only 1 band for the C allele. Reproducibility of genotyping was confirmed by bidirectional sequencing in 500 samples, and the reproducibility was 100%.

**Testing of Genetic Stratification of the Populations**
The possible unequal genetic admixture or population subdivision in the control and patient populations could have resulted in a spurious association between a marker and disease. We additionally typed 7 unlinked microsatellite markers: TNNT2 (1q32; D15S262), MYL3 (3p21.3-p21.2; D3S3560), NEXLIN (1p31.1; D15S2876), MYH7 (14q12; D14S990), TPM1 (15q22.1; D15S993), PKR2 (7q35-q36; D7S483), and TNND1 (19q13.4; D19S927). The allele frequencies at those markers were tested for association with phenotypes. The primer sequences were obtained from the Human Genome Database (http://www.gdb.org/), and the primers were synthesized and fluorescently labeled commercially. Genotype results were analyzed with GeneScan and Genotyper software (Applied Biosystems), with those markers tested for association with phenotypes. The possible unequal genetic admixture or population subdivision in the control and patient populations could have resulted in a spurious association between a marker and disease. We additionally typed 7 unlinked microsatellite markers: TNNT2 (1q32; D15S262), MYL3 (3p21.3-p21.2; D3S3560), NEXLIN (1p31.1; D15S2876), MYH7 (14q12; D14S990), TPM1 (15q22.1; D15S993), PKR2 (7q35-q36; D7S483), and TNND1 (19q13.4; D19S927). The allele frequencies at those markers were tested for association with phenotypes. The primer sequences were obtained from the Human Genome Database (http://www.gdb.org/), and the primers were synthesized and fluorescently labeled commercially. Genotype results were analyzed with GeneScan and Genotyper software (Applied Biosystems), with those markers tested for association with phenotypes.

**Statistical Analysis**
The distribution of quantitative variables was tested for normality by use of a 1-sample Kolmogorov-Smirnov test. Because the TG level was highly skewed, we compared the difference between cases and controls with a Mann-Whitney nonparametric test. Quantitative variables, including age, body mass index, SBP and DBP, glucose, HDL-C, non-HDL-C, and TC, were compared with the 1-way ANOVA test. A χ² test was used to test for qualitative variables, genotype/allele frequencies, and Hardy-Weinberg equilibrium of the polymorphisms. Association of SNP +2255 with vascular disease was analyzed by multivariable logistic regression adjusted by age, sex, body mass index, blood pressure, smoking, alcohol consumption, glucose, HDL-C, non-HDL-C, TC, and TG. The association was expressed as an odds ratio. The Student t test and Spearman correlation were used to assess the difference and correlation between serum levels of undercarboxylated osteocalcin and PIVKA-II in 3 genotypes of SNP +2255. A 2-tailed probability value of ≤0.05 was considered significant. Analyses were performed with SPSS 11.0 (SPSS Inc, Chicago, Ill) for Windows (Microsoft Corp, Redmond, Wash). The χ² measurement was used to determine LD with the software EMILD (http://request.mdacc.tmc.edu/quicksoftware/Pubware.htm). The D' and r² were used to indicate the strength of LD.

The authors had full access to the data and take full responsibility for its integrity. All authors have read and agree to the manuscript as written.

**Results**

**Characteristics of the Subjects**
Clinical characteristics of the subjects in the present study are shown in Table 1. In the stroke study, of the 4000 subjects initially recruited for that study, 189 cases and 189 controls were excluded because of lack of definite diagnosis, insufficient DNA, or failure of genotyping. Significantly higher levels of SBP and DBP and a higher incidence of cigarette smoking and hypertension were found in cases than in controls (all P<0.01). In the CHD study, 740 cases and 740 controls were enrolled; higher frequencies of DM, hypertension, and cigarette smoking were found in cases than in controls (all P<0.01). In the aortic dissection study, 253 cases and 416 controls were recruited. Significantly higher levels of SBP and HDL-C, lower levels of non-HDL-C, TC, and TG, and a lower drinking frequency were found in patients than in controls (all P<0.05).

**The C Allele of +2255 Was Associated With Stroke, CHD, and Aortic Dissection**
The distribution of VKORC1 genotypes of +2255 is shown in Tables 2, 3, and 4, respectively, and fulfilled expectations of Hardy-Weinberg equilibrium in both cases and controls. The estimated risk of vascular disease for subjects with the CT genotype (1 copy of the risk allele C) was significantly higher than for those with the TT genotype (no copy of the risk allele C) but was comparable to those with the CC genotype, which indicates a dominant effect of the at-risk allele C. We used the dominant model to analyze the association of the SNP with vascular disease. The frequency of the CC+CT genotype was significantly higher in patients than in controls (stroke 19.7% versus controls 11.7%, P<0.001; CHD 16.9% versus controls 11.2%, P<0.01; aortic dissection 17.0% versus controls 9.9%, P<0.05). The association remained after adjustment for age, sex, and other conventional risk factors with multiple logistic regression analysis; the OR was 1.95 (95% CI 1.58 to 2.41) for stroke (P<0.001), 1.72 (95% CI 1.24 to 2.38) for CHD (P<0.01), and 1.90 (95% CI 1.04 to 3.48) for aortic dissection (P<0.05). In subtypes of stroke patients, the frequencies of CC+CT were 18.4% for thrombosis (OR 1.75, 95% CI 1.34 to 2.29, P<0.001), 23.2% for lacunar stroke (OR 2.33, 95% CI 1.09 to 2.16, P<0.05), and 18.2% for hemorrhage (OR 1.53, 95% CI 1.76 to 3.06, P<0.001). The presence of the C allele of the +2255 locus conferred an almost 2-fold increase in vascular disease risk within these studied populations. Because the C allele of +2255 can reflect the G-C-G-C-A (3673-6484-6853-7566-9041) haplotype of VKORC1 gene, one can reasonably expect that the
G-C-G-C-A haplotype of VKORC1 is also associated with a high risk of stroke, CHD, and aortic dissection.

**No Evidence of Strong Population Stratification**
Among the 7 highly polymorphic markers that we genotyped, no significant allele-frequency differences were detected between controls and patients within each clinic center and among these centers, which indicates that there was no obvious evidence for genetic stratification in the cohort. The serum levels of undercarboxylated osteocalcin and PIVKA-II were lower in the subjects carrying the C allele of the VKORC1 locus. The levels of both undercarboxylated osteocalcin and PIVKA-II antigen were lower in carriers of the C allele than in T allele carriers (Figure). The Spearman coefficient for the existing correlation was $r = -0.219$ for undercarboxylated osteocalcin and $-0.567$ for PIVKA-II with genotype, respectively. The differences were also significant in undercarboxylated osteocalcin and in PIVKA-II between TT and CC carriers ($P=0.021$ and $P<0.001$, respectively), which suggests that the C allele contributes to a higher functional efficiency of the VKORC1 complex.

**Discussion**
The present study is the first clinical investigation of the significance of the polymorphisms of VKORC1 in vascular disease, including stroke, CHD, and aortic dissection. We found that the variants of VKORC1 are associated with almost double the risk of stroke, CHD, and aortic dissection. Next, we examined whether the disease-associated allele was related to specific vascular risk factors, such as hypertension, diabetes, age, and sex. No significant association was observed between the +2255 allele and these risk factors, which suggests that the contribution of SNP +2255 to the risk of vascular disease is independent of those conventional vascular risk factors. We examined the population stratification effect by genotyping 7 unlinked highly polymorphic microsatellite markers in the case subjects and in control subjects, and no association was found between these markers and vascular disease.

Stroke, CHD, and aortic dissection are all vascular diseases. The pathologies of these diseases are quite different. Atherothrombotic stroke mainly results from large-artery atherosclerosis, whereas intracerebral hemorrhages may be due to vascular disease.

**TABLE 2. Association of SNP+2255 in VKORC1 Gene With Stroke**

<table>
<thead>
<tr>
<th>Genotype, n (%)</th>
<th>Controls (n=1811)</th>
<th>TT</th>
<th>Total (n=1811)</th>
<th>Thrombosis (n=798)</th>
<th>Lacunar stroke (n=514)</th>
<th>Hemorrhage (n=499)</th>
<th>Crude OR (95% CI)</th>
<th>Adjusted OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CT+CC</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>11.7</td>
<td>1.00</td>
</tr>
<tr>
<td>Groups</td>
<td>CC</td>
<td>CT</td>
<td>TT</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Controls (n=1811)</td>
<td>9 (0.5)</td>
<td>203 (11.2)</td>
<td>1599 (88.3)</td>
<td>19.7</td>
<td>1.85 (1.54–2.23)</td>
<td>1.95 (1.58–2.41)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cases (n=1811)</td>
<td>20 (1.1)</td>
<td>337 (18.6)</td>
<td>1454 (80.3)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thrombosis (n=798)</td>
<td>5 (0.6)</td>
<td>142 (17.8)</td>
<td>651 (81.6)</td>
<td>18.4</td>
<td>1.70 (1.35–2.14)</td>
<td>1.75 (1.34–2.29)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lacunar stroke (n=514)</td>
<td>6 (1.2)</td>
<td>113 (22.0)</td>
<td>395 (76.8)</td>
<td>23.2</td>
<td>2.27 (1.77–2.92)</td>
<td>2.33 (1.76–3.06)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hemorrhage (n=499)</td>
<td>9 (1.8)</td>
<td>82 (16.4)</td>
<td>408 (81.8)</td>
<td>18.2</td>
<td>1.68 (1.29–2.20)</td>
<td>1.53 (1.09–2.16)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

ORs and 95% CIs were calculated with the use of multivariate logistic regression analyses. Adjusted ORs were stratified by age, sex, body mass index, blood pressure, cigarette smoking, alcohol consumption, glucose, HDL-C, non-HDL-C, TC, and TG.

$\chi^2$ Test vs control, $^*P<0.05$, $^\dagger P<0.001$. 

BMI indicates body mass index. Clinical characteristics of age, BMI, SBP, DBP, glucose, HDL-C, non-HDL-C, and TC values are given as mean (SD); TG values as median (range); and other values as number of individuals (%).
Vitamin K–dependent nonhemostatic proteins may impact the control of the vitamin K cycle. Polymorphisms of \( \text{VKORC1} \) have been shown to affect the expression and activity of these proteins, likely leading to increased morbidity and mortality of arterial disease. Vitamin K plays a role in the carboxylation of hemostatic and nonhemostatic proteins by controlling the vitamin K cycle. Polymorphisms of \( \text{VKORC1} \) have been shown to affect the expression and activity of \( \text{VKORC1} \) and thus warfarin dose response and blood clotting.

The \( \text{VKORC1} \) variation could serve as a common genetic risk factor for all vascular diseases. It involves mediation of \( \gamma \)-carboxylation of hemostatic and nonhemostatic proteins by control of the vitamin K cycle. Polymorphisms of \( \text{VKORC1} \) have been shown to affect the expression and activity of \( \text{VKORC1} \) and thus warfarin dose response and blood clotting. Vitamin K–dependent nonhemostatic proteins mediate calcification. Vessel calcification decreases vessel elasticity and increases shear stress and is associated with increased morbidity and mortality of arterial disease. Rieder et al\(^{24} \) reported that mRNA levels in the group with the G-C-G-C-A (3673-6484-6853-7566-9041) haplotype were \( \approx 3 \) times as high as those in the wild-type group. Yuan et al\(^{23} \) reported that the \( \text{VKORC1} \) promoter with the G allele yielded a 44% increase of activity compared with the A allele of -1639. Consistent with these results, we found that subjects with the TT genotype of +2255 had higher levels of undercarboxylated vitamin K–dependent proteins, osteocalcin and PIVKA-II. We proposed that the \( \text{VKORC1} \) haplotype G-C-G-C-A (3673-6484-6853-7566-9041) would increase the promoter activity and higher expression of \( \text{VKORC1} \) mRNA and protein. This would result in increased \( \gamma \)-carboxylation, as indicated by the decreased levels of the undercarboxylated vitamin K–dependent proteins osteocalcin and PIVKA-II and a potential need for increased warfarin dosage.

The biological activity of all known vitamin K–dependent proteins is highly dependent on correct \( \gamma \)-carboxylation, which affects not only procoagulatory (factor II, VII, IX, and X) but also anticoagulatory (protein C, S, and Z) clotting factors and osteocalcin in the same way as MGP.\(^{39} \) The greater functional activity of the C allele may also lead to higher levels of MGP and less vascular calcification. Therefore, the observed association may not be related to the effect on the \( \gamma \)-carboxylation of the vitamin K–dependent proteins but may be caused by another yet-unknown function of \( \text{VKORC1} \).

One possibility is that \( \text{VKORC1} \) haplotypes are only markers for LD, and some genes in the linkage region independent of or in conjunction with \( \text{VKORC1} \) confer susceptibility to arterial disease. At least 6 other genes are found in the natural haplotype block over the 68,000 bases around \( \text{VKORC1} \).\(^{40} \) \( \text{ZNF668} \) (zinc finger protein), \( \text{ZNF646}, \text{BCKDK} \) (branched chain ketoacid dehydrogenase kinase), \( \text{MYST1} \) (histone acetyltransferase1), \( \text{PRSS8} \) (protease serine

### Table 3: Association of SNP +2255 in \( \text{VKORC1} \) Gene With CHD

<table>
<thead>
<tr>
<th>Genotype, n (%)</th>
<th>Controls (n=740)</th>
<th>Cases (n=740)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>CC</td>
<td>CT</td>
</tr>
<tr>
<td></td>
<td>2 (0.3)</td>
<td>81 (10.9)</td>
</tr>
<tr>
<td>Frequency, %</td>
<td>11.2</td>
<td>16.9</td>
</tr>
<tr>
<td>Crude OR</td>
<td>1.00</td>
<td>1.61 (1.19–2.17)*</td>
</tr>
<tr>
<td>Adjusted OR</td>
<td>1.00</td>
<td>1.72 (1.24–2.38)*</td>
</tr>
</tbody>
</table>

### Table 4: Association of SNP +2255 in \( \text{VKORC1} \) Gene With Aortic Dissection

<table>
<thead>
<tr>
<th>Genotype, n (%)</th>
<th>Controls (n=416)</th>
<th>Cases (n=253)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>CC</td>
<td>CT</td>
</tr>
<tr>
<td></td>
<td>0 (0.0)</td>
<td>41 (9.9)</td>
</tr>
<tr>
<td>Frequency, %</td>
<td>9.9</td>
<td>17.0</td>
</tr>
<tr>
<td>Crude OR</td>
<td>1.00</td>
<td>1.87 (1.18–2.97)†</td>
</tr>
<tr>
<td>Adjusted OR</td>
<td>1.00</td>
<td>1.90 (1.04–3.48)*</td>
</tr>
</tbody>
</table>

ORs and 95% CIs were computed with the use of multivariate logistic regression analyses. Adjusted ORs were stratified by age, sex, body mass index, blood pressure, cigarette smoking, alcohol consumption, glucose, HDL-C, non-HDL-C, TC, and TG. \( \chi^2 \) Test vs control, *\( P<0.05 \), †\( P<0.01 \).
Undercarboxylated osteocalcin and PIVKA-II antigen serum levels in carriers of different genotypes of the VKORC1 gene SNP +2255. Levels of the 2 proteins are presented as means; T bars represent SDs. VKORC1 antigen serum levels were significantly correlated with SNP +2255 (P<0.001). Five samples in the CC group, 18 in the CT group, and 26 in the TT group were analyzed. *P<0.05, **P<0.001 for the comparison between genotype TT and CC groups.

8), and PRSS36. No evidence through a search of the PubMed database shows that these genes have any definite biological function. Previously, we found that VKORC1 is involved in angiogenesis; others have shown that polymorphisms of VKORC1 are associated with differences in dose requirements in warfarin sensitivity among patients of different ancestries. In the present report, lower levels of undercarboxylated osteocalcin and PIVKA-II antigen were associated with the C-allele of SNP +2255 of the VKORC1, which supports the idea that the association between the haplotype of the VKORC1 block and vascular disease is attributable to VKORC1.

Furthermore, vascular calcification is more complex in humans than in rodents. In women, progression of atherosclerotic calcification is associated with increased bone loss during menopause. In patients with mutations in the MGP gene, arterial calcification is not a common feature. These have been proposed as feedback mechanisms to attempt calcium clearance. Thus far, the pathophysiology behind this exciting finding is not clear and needs to be addressed by further studies.

In conclusion, the prevalence of the haplotype G-C-G-C-A of VKORC1 was significantly more frequent in patients with vascular disease than in controls. The haplotype may serve as a novel genetic marker for the risk of stroke, CHD, and aortic dissection.

**Acknowledgments**

We thank Dr Thomas Eling (NIH/NIHES) for his text editing. The study was supported by the Ministry of Science and Technology of China with grant 2002BA711A05 and National 973 Basic Research Project (973 G2000056901) to Dr Rutai. The authors also acknowledge the International HapMap Consortium for the data of LD around VKORC1.

**Disclosures**

None.

**References**

Vitamin K–dependent proteins play a critical role in the coagulation cascade and may potentially impact atherosclerosis. Epidemiological data indicate that coronary atherosclerosis is an important cause of morbidity and mortality worldwide. To minimize the devastating consequence of vascular disease, we must reliably distinguish those individuals who will experience an event from those who will not. The haplotypes in VKORC1 and GGCG polymorphisms associated with warfarin dose. Pharmacogenomics J. 2005;5:262–270.


### CLINICAL PERSPECTIVE

Epidemiological data indicate that coronary atherosclerosis is an important cause of morbidity and mortality worldwide. To minimize the devastating consequence of vascular disease, we must reliably distinguish those individuals who will experience an event from those who will not. The haplotypes in VKORC1 affect warfarin dose response through effects on the formation of the reduced form of vitamin K, a cofactor for γ-carboxylation of vitamin K–dependent proteins. Vitamin K–dependent proteins play a critical role in the coagulation cascade and may potentially impact atherosclerosis. We tested the association of the single-nucleotide polymorphisms of the VKORC1 gene and arterial vascular diseases including coronary heart disease, stroke, and aortic dissection. We observed that VKORC1 variation is significantly associated with each of these diseases. Although the pathophysiology behind the present findings is not entirely clear, confirmation of these observations in additional studies is warranted. Additional research is necessary to elucidate the potential role of VKORC1 and its downstream products in the pathogenesis of vascular disease.
VKORC1 Haplotypes Are Associated With Arterial Vascular Diseases (Stroke, Coronary Heart Disease, and Aortic Dissection)
Yibo Wang, Weili Zhang, Yuhui Zhang, Yuejin Yang, Lizhong Sun, Shengshou Hu, Jilin Chen, Channa Zhang, Yi Zheng, Yisong Zhen, Kai Sun, Chunyan Fu, Tao Yang, Jianwei Wang, Jing Sun, Haiying Wu, Wayne C. Glasgow and Rutai Hui

Circulation. 2006;113:1615-1621; originally published online March 20, 2006; doi: 10.1161/CIRCULATIONAHA.105.580167
Circulation is published by the American Heart Association, 7272 Greenville Avenue, Dallas, TX 75231
Copyright © 2006 American Heart Association, Inc. All rights reserved.
Print ISSN: 0009-7322. Online ISSN: 1524-4539

The online version of this article, along with updated information and services, is located on the World Wide Web at:
http://circ.ahajournals.org/content/113/12/1615

Permissions: Requests for permissions to reproduce figures, tables, or portions of articles originally published in Circulation can be obtained via RightsLink, a service of the Copyright Clearance Center, not the Editorial Office. Once the online version of the published article for which permission is being requested is located, click Request Permissions in the middle column of the Web page under Services. Further information about this process is available in the Permissions and Rights Question and Answer document.

Reprints: Information about reprints can be found online at:
http://www.lww.com/reprints

Subscriptions: Information about subscribing to Circulation is online at:
http://circ.ahajournals.org//subscriptions/