Male-Specific Association between a \(\gamma\)-Secretase Polymorphism and Premature Coronary Atherosclerosis

Karen M. J. van Loo\(^1\), Tim Dejaegere\(^2,3\), Martine van Zweeden\(^1\), Jessica E. van Schijndel\(^1\), Cisca Wijmenga\(^4,5\), Mieke D. Trip\(^6\), Gerard J. M. Martens\(^1*\)

1 Department of Molecular Animal Physiology, Radboud University Nijmegen, Donders Institute for Brain, Cognition and Behaviour and Nijmegen Centre for Molecular Life Sciences (NCMLS), Nijmegen, The Netherlands, 2Department of Molecular and Developmental Genetics, VIB, Leuven, Belgium, 3Center for Human Genetics, KULeuven, Leuven, Belgium, 4The Complex Genetics Section, Department of Biomedical Genetics, University Medical Center Utrecht, Utrecht, The Netherlands, 5Department of Genetics, University Medical Center Groningen and University of Groningen, Groningen, The Netherlands, 6Department of Cardiology, Academic Medical Center, Amsterdam, The Netherlands

Abstract

**Background:** Atherosclerosis is a common multifactorial disease resulting from an interaction between susceptibility genes and environmental factors. The causative genes that contribute to atherosclerosis are elusive. Based on recent findings with a Wistar rat model, we speculated that the \(\gamma\)-secretase pathway may be associated with atherosclerosis.

**Methodology/Principal Findings:** We have tested for association of premature coronary atherosclerosis with a non-synonymous single-nucleotide polymorphism (SNP) in the \(\gamma\)-secretase component APH1B (Phe217Leu; rs1047552), a SNP previously linked to Alzheimer’s disease. Analysis of a Dutch Caucasian cohort (780 cases; 1414 controls) showed a higher prevalence of the risk allele in the patients (odds ratio (OR) = 1.35), albeit not statistically different from the control population. Intriguingly, after gender stratification, the difference was significant in males (OR = 1.63; p = 0.033), but not in females (OR = 0.50; p = 0.20). Since Phe217Leu-mutated APH1B showed reduced \(\gamma\)-secretase activity in mouse embryonic fibroblasts, the genetic variation is likely functional.

**Conclusion/Significance:** We conclude that, in a male-specific manner, disturbed \(\gamma\)-secretase signalling may play a role in the susceptibility for premature coronary atherosclerosis.

Introduction

Atherosclerosis is the basis of coronary artery disease and thought to be a multifactorial disease caused by susceptibility genes that act in concert with environmental factors. A number of susceptibility genes have been identified (e.g. apolipoprotein E (APOE) [1], low density lipoprotein receptor [2] and methylenetetrahydrofolate reductase [3]), but the signalling pathways responsible for vascular cell pathology are elusive. Interestingly, Wistar rats that display a high susceptibility for the dopamine receptor agonist apomorphine, the so-called apomorphine-susceptible (APO-SUS) rats [4,5], show an impaired vasorelaxation to adrenergic stimuli when compared with their phenotypic counterparts APO-UNSUS rats [6,7]. Impaired vasorelaxation is associated with an increased risk for the development of hypertension and vascular diseases such as atherosclerosis [8]. We recently identified a gene-dosage imbalance of the \(\gamma\)-secretase component Aph1b as the molecular-genetic basis of the difference between the APO-SUS and -UNSUS rats [9]. The \(\gamma\)-secretase enzyme complex cleaves many type I transmembrane proteins, including the amyloid-\(\beta\) (\(A\beta\)) precursor protein APP (known to be involved in neuronal amyloid plaque formation in Alzheimer’s disease [AD], NOTCH1-4, neuregulin, low-density lipoprotein receptor related protein (LRP1, 2 and 8) and N-cadherin [10,11].

In view of the above findings, we hypothesize that the \(\gamma\)-secretase pathway may be linked to atherosclerosis. Increasing evidence suggests a link between altered vascular homeostasis, as seen in atherosclerosis, and the neurodegenerative disease AD. Apart from a partially overlapping epidemiology and an altered cholesterol homeostasis, atherosclerosis and AD have also been found to share genetic risk factors, including APOE and LRP1 [1,12–14]. Since the rare non-synonymous single-nucleotide polymorphism (SNP) Phe217Leu (rs1047552; T\(\rightarrow\)G) in the human APH1B gene has recently been found to be associated with AD [15], we have now tested whether this SNP is also associated with premature coronary atherosclerosis.

Results

Male-specific association of APH1B Phe217Leu with premature coronary atherosclerosis

Since a gene-dosage imbalance of the Aph1b gene was the molecular-genetic basis of the APO-SUS/-UNSUS rat model [9] and the model was characterized by a disturbed endothelium-
dependent vascular reactivity [6,7], we tested the hypothesis that a genetic variation in the APH1B gene may contribute to atherosclerosis susceptibility in humans. In a Dutch case-control cohort consisting of 780 patients with premature coronary atherosclerosis and 1414 controls, we found a higher prevalence of the APH1B Phe217Leu risk allele (G-allele) in the patients, albeit not statistically different ($\chi^2 = 2.09$, df = 1, p = 0.15; OR = 1.35; CI = 0.90–2.01). Intriguingly, after gender stratification, the difference was significant in the male population ($\chi^2 = 4.52$, df = 1, p = 0.033; OR = 1.63; CI = 1.04–2.50), whereas females were not significantly different ($\chi^2 = 1.62$, df = 1, p = 0.20; OR = 0.50; CI = 0.17–1.48) (Table 1). Power analysis showed that for the detection in the female subpopulation of a risk effect similar to that observed in the male subpopulation, the power was insufficient (92% power for the total population; 81% power for the male subpopulation and 38% power for the female subpopulation, assuming a relative risk of 1.63, a disease allele frequency of 3.3% and a disease prevalence of 5%). All genotype distributions tested (cases and controls) fulfilled the Hardy-Weinberg criteria (data not shown).

Association of APH1B Leu217 with fibrinogen levels in premature coronary atherosclerosis

We then compared the association of the APH1B Leu217 allele with clinical parameters in the atherosclerosis patients, including the presence of risk factors (e.g. smoking behavior and occurrence of hypertension and diabetes mellitus), and the blood levels of lipid compounds (e.g. cholesterol, triglycerides, and low- and high-density lipoprotein cholesterol) (for a detailed overview of the parameters tested, see Table 2). These parameters were not related to the APH1B Phe217Leu variation (Table 2), except for a significant association (p = 0.028) with the fibrinogen levels in patients containing or lacking the APH1B Leu217 allele. Patients without the Leu217 allele displayed fibrinogen levels of 322.8±80.55 gr/l (n = 327, plus SD), whereas patients with the Leu217 allele had levels of 375.0±82.08 gr/l (n = 12, plus SD) (Table 2); due to low female patient numbers, gender stratification for fibrinogen levels was not possible. After Bonferroni adjustment for multiple comparisons, however, no statistically significant association of the fibrinogen levels with the Leu217 allele was detected (Bonferroni’s adjustment requires a significance level of p≤0.00156).

Evolutionary conservation of amino acid residue Phe217 within the APH1 family

The degree of conservation of an amino acid within a protein family is usually indicative of its importance for protein functioning. A multiple sequence alignment of members of the APH1 family (Figure 1) showed that the Phe217 residue is conserved from plant, invertebrates, lower vertebrates, rodents and primates to man. The various APH1 proteins all contain at residue 217 either a phenylalanine (F) or the conservative change to tyrosine (Y). The Support Vector Machine (SVM) score (http://www.SNPs3D.org) [16] of –1.12 for Phe217Leu indicates a likely impact of this substitution on APH1B protein function.

Functional analysis of the APH1B Phe217Leu polymorphism

We wondered whether the presence of a leucine instead of the conserved residue Phe217 of the APH1B protein would be of functional importance. Aph1abc−/− mouse embryonic fibroblasts were stably transfected with human APH1B Phe217 or Leu217. γ-Secretase activity was measured by quantifying the levels of different γ-secretase substrates in cell culture extracts. We observed a 1.6-fold reduction (p<0.05, n = 8) of γ-secretase activity towards one of its substrates, syndecan-3 [17], indicating a subtle influence on γ-secretase cleavage activity. The cleavages of two other substrates, N-cadherin and APP, were slightly but not significantly changed (Figure 2). Thus, in a substrate-dependent manner the Phe217Leu substitution affected γ-secretase cleavage activity.

Discussion

In this study we show that the non-synonymous Phe217Leu polymorphism in the human APH1B gene is a male-specific risk factor for premature coronary atherosclerosis. The reduced γ-secretase cleavage activity of Leu217 APH1B, albeit in a substrate-specific manner, suggests a functional relevance of this polymorphism. Functional consequences of reduced gene dosage of Aph1b were also observed in the APO-SUS/–UNSUS rat model [9], an animal model with complex features, including an impaired vasorelaxation response to adrenergic stimuli [6,7], which increases the risk for the development of hypertension and vascular diseases. The gene-dosage imbalance of the Aph1b gene

Table 1. Genotype and allele frequencies for the APH1B Phe217Leu variation in a Dutch case-control study on premature coronary atherosclerosis.

<table>
<thead>
<tr>
<th>N</th>
<th>Genotype Frequencies (%)</th>
<th>Allele Frequencies (%)</th>
<th>p</th>
<th>OR</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>TT</td>
<td>TG</td>
<td>GG</td>
<td>T</td>
</tr>
<tr>
<td>total</td>
<td>controls</td>
<td>1414 96.0  4.0 0</td>
<td>98.0 2.0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>patients</td>
<td>780 94.6  5.4 0</td>
<td>97.3 2.7</td>
<td>0.15 1.35</td>
</tr>
<tr>
<td>males</td>
<td>controls</td>
<td>938 95.9  4.1 0</td>
<td>98.0 2.0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>patients</td>
<td>582 93.5  6.5 0</td>
<td>96.7 3.3</td>
<td>0.033* 1.63</td>
</tr>
<tr>
<td>females</td>
<td>controls</td>
<td>476 96.0  4.0 0</td>
<td>98.0 2.0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>patients</td>
<td>198 98.0  2.0 0</td>
<td>99.0 1.0</td>
<td>0.20 0.50</td>
</tr>
</tbody>
</table>

Standard Chi-square tests were applied to evaluate the association with premature coronary atherosclerosis. OR = odds ratio; *p < 0.05.

doi:10.1371/journal.pone.0003662.t001
(three gene copies in APO-UNSUS rats and one or two gene copies in APO-SUS rats) segregated with differences in \( \gamma \)-secretase cleavage activity and a number of other phenotypic characteristics [9]. We therefore speculate that a subtle effect on \( \text{APH1B} \) expression or function (copy number variation in rat or Phe217Leu variation in human, respectively) may affect \( \gamma \)-secretase activity and signalling downstream of gamma-secretase cleavage and, consequently, give rise to vascular complications.

Interestingly, the \( \text{APH1B} \) Phe217Leu polymorphism was recently found to be also associated with AD [15]. AD pathogenesis is frequently characterized by a peripheral vascular disturbance and is often linked to other cholesterol/lipoprotein diseases, including atherosclerosis [18]. In addition, cerebral atherosclerosis has been found to be a strong contributory factor to sporadic AD pathogenesis [19]. The \( \text{APH1B} \) Phe217Leu variation may thus play a dual role by affecting atherosclerosis as well as AD pathogenesis, suggesting that the two diseases have converged and that the \( \gamma \)-secretase signalling pathway is a susceptibility pathway for vascular complications.

In line with the above supposition, a number of the \( \gamma \)-secretase substrates have been implicated in vascular pathogenesis. \( \text{LRP} \), which belongs to a gene family involved in mediating cellular uptake of cholesterol-rich lipoproteins (the \( \text{LDLR} \) gene family), is highly expressed in atherosclerotic lesions [20,21] and has been shown to represent a susceptibility gene for atherosclerosis [13]. The AD-associated \( \gamma \)-secretase

**Table 2. Clinical and biochemical characteristics of the premature coronary atherosclerosis patients with and without the \( \text{APH1B} \) 217Leu allele.**

<table>
<thead>
<tr>
<th></th>
<th>without ( \text{APH1B} ) Leu217</th>
<th>with ( \text{APH1B} ) Leu217</th>
<th>( p )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>43.3 ± 5.3</td>
<td>42.9 ± 5.3</td>
<td>0.60</td>
</tr>
<tr>
<td>BMI (kg/m2)</td>
<td>26.9 ± 4.2</td>
<td>26.8 ± 3.1</td>
<td>0.88</td>
</tr>
<tr>
<td>Age first manifestation of vascular event (years)</td>
<td>41.6 ± 5.9</td>
<td>40.9 ± 6.1</td>
<td>0.47</td>
</tr>
<tr>
<td>Systolic blood pressure (mmHg)</td>
<td>129.1 ± 17.2</td>
<td>127.0 ± 18.5</td>
<td>0.45</td>
</tr>
<tr>
<td>Diastolic blood pressure (mmHg)</td>
<td>79.5 ± 10.5</td>
<td>81.2 ± 12.6</td>
<td>0.32</td>
</tr>
<tr>
<td>Total cholesterol prior to medication (mmol/l)</td>
<td>6.3 ± 1.9</td>
<td>6.6 ± 1.4</td>
<td>0.50</td>
</tr>
<tr>
<td>LDL-cholesterol prior to medication (mmol/l)</td>
<td>3.9 ± 1.3</td>
<td>4.4 ± 1.3</td>
<td>0.20</td>
</tr>
<tr>
<td>HDL-cholesterol prior to medication (mmol/l)</td>
<td>1.1 ± 0.4</td>
<td>1.0 ± 0.2</td>
<td>0.43</td>
</tr>
<tr>
<td>Triglycerids prior to medication (mmol/l)</td>
<td>1.8 ± 1.2</td>
<td>1.9 ± 0.7</td>
<td>0.77</td>
</tr>
<tr>
<td>Total cholesterol with medication (mmol/l)</td>
<td>5.0 ± 1.5</td>
<td>4.9 ± 1.7</td>
<td>0.88</td>
</tr>
<tr>
<td>LDL-cholesterol with medication (mmol/l)</td>
<td>3.0 ± 1.2</td>
<td>3.1 ± 1.8</td>
<td>0.78</td>
</tr>
<tr>
<td>HDL-cholesterol with medication (mmol/l)</td>
<td>1.1 ± 0.3</td>
<td>1.1 ± 0.4</td>
<td>0.41</td>
</tr>
<tr>
<td>Triglycerids with medication (mmol/l)</td>
<td>2.1 ± 4.0</td>
<td>1.8 ± 1.6</td>
<td>0.68</td>
</tr>
<tr>
<td>Apo A1 lipoprotein (mmol/l)</td>
<td>1.3 ± 0.3</td>
<td>1.2 ± 0.2</td>
<td>0.12</td>
</tr>
<tr>
<td>Apo B100 lipoprotein (mmol/l)</td>
<td>1.1 ± 0.6</td>
<td>1.0 ± 0.4</td>
<td>0.40</td>
</tr>
<tr>
<td>Lipoprotein (a) (mg/l)</td>
<td>215.2 ± 309.4</td>
<td>240.7 ± 377.1</td>
<td>0.66</td>
</tr>
<tr>
<td>Blood sedimentation rate (BSE) (mm/h)</td>
<td>10.4 ± 11.3</td>
<td>9.4 ± 5.2</td>
<td>0.74</td>
</tr>
<tr>
<td>Fibrinogen (g/l)</td>
<td>322.8 ± 80.5</td>
<td>375.0 ± 82.1</td>
<td>0.028 *</td>
</tr>
</tbody>
</table>

Values are given as mean levels ± SD or as percentages. \( N \), number of individuals tested; BMI, body mass index; LDL, low density lipoprotein; HDL, high density lipoprotein; Apo, apolipoprotein. *\( p<0.05. \)

**DOI:** 10.1371/journal.pone.0003662.t002
substrate APP may be involved in vascular pathogenesis as well, since it metabolises cholesterol [22], physically interacts with LRP1 [23], and gives rise to the amyloid plaque constituents Ab40 and -42. Besides these well-studied substrates, the γ-secretase substrates NOTCH3, colony-stimulating factor 1 (CSF1), CD44, neuregulin and ERBB4 may also be involved in the vascular complications in patients with the APH1B Phe217Leu variation. Mutations in NOTCH3 may cause cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL), a syndrome characterized by systemic vascular smooth muscle cell (VSMC) degeneration [24]. CSF1 can contribute to atherosclerosis development via fatty streak formation and progression to complex fibrous lesions [25], and CD44 may enhance atherosclerosis pathogenesis via reactive oxygen species [26], whereas neuregulin and ERBB4 are necessary for vascular growth and development [27–29].

Our results show that, remarkably, only male individuals with atherosclerosis seem to be associated with the APH1B Phe217Leu variation. This might indicate a role for hormones or the involvement of a Y-chromosome-linked modulation. Such a gender-specific association has been observed for other SNPs as well, like a male-specific association of the APOE2 and APOE4 alleles with cardiovascular disease [30]. Thus, susceptibility to many common diseases may well be the result of complex interactions involving gender, genes and environmental factors. Following Bonferroni correction for multiple testing, no significant associations between the APH1B polymorphism and plasma lipoprotein parameters or other risk factors were observed in the atherosclerosis patients. More detailed studies will be necessary to establish the biochemical mechanisms underlying atherosclerosis in patients carrying the Phe217Leu polymorphism.

In the present study, association was only tested for premature coronary atherosclerosis, a disease with a substantial heritability [31]. To investigate whether the Phe217Leu SNP constitutes a susceptibility factor for other vascular complications, it would be of interest to also test for association in elderly atherosclerotic patients and in patients with other vascular defects (e.g. myocardial infarction). No significant association of the APH1B chromosomal region with coronary artery disease, myocardial infarction or other related diseases has been found in recent genome-wide association studies (GWAS) [32–35]. Thus, apart from the functional Phe217Leu polymorphism, the contribution of any additional genetic variant in the APH1B gene to the phenotype is expected to be small. Unfortunately, no results for the APH1B Phe217Leu polymorphism are available from the GWAS since this polymorphism was not represented on the arrays used in these studies. In addition, based on the data from the International HapMap-CEU project none of the SNPs tested in the GWAS is in high perfect proxy (r²≥0.8) to the Phe217Leu polymorphism. Therefore, the GWAS data do not provide any additional information concerning the functional APH1B Phe217Leu SNP.

In conclusion, our results suggest that the γ-secretase pathway is a candidate pathway for premature coronary atherosclerosis and warrant further studies on genetic variations in this pathway in various diseases with vascular complications.

Materials and Methods

Subjects

We selected consecutive Dutch premature coronary atherosclerosis patients (n = 780), age 43.3±5.3; 582 males, age 43.6±5.3 and 198 females, age 42.5±5.5) who qualified for inclusion after a myocardial infarction, surgical or percutaneous coronary revascularization, or a coronary angiogram with evidence of at least a 70% stenosis in a major epicardial artery (Atherosclerosis Outpatient Clinic of the Academic Medical Center of the University of Amsterdam). The study was approved by the Medical Ethical Committee of the Academic Medical Center (Amsterdam, The Netherlands) and all patients gave written informed consent. The control subjects (n = 1414, age 51.8±11.9;
APH1B genotyping

Following the isolation of genomic DNA, APH1B (MIM #607630) P2c217Leu genotyping was performed via allele-specific PCR using primers specific for SNP rs1047552 (outer/general primers: forward: 5'-TGGCCCCGTTAGGGTACCAGCTGA-3' and reverse: 5'-AGTGGGTTATCACTGTGCGCA-3'). Inner/spicific primers: forward specific for the "T-allele": 5'-AA-TAAAACCTGGGTCTACATTTT-3' and reverse specific for the "G-allele": 5'-GCCCATGAGCACCAGATTAC-3').

Generation of Aph1abc-/- mouse embryonic fibroblast (MEF) lines

Conditionally targeted (Aphla and Aphlc) or classically targeted (Aphlb) mice were described before [36]. Animals carrying a null allele were obtained after breeding with transgenic mice expressing a Pgk driven Cre-recombinase. Mouse embryos were dissected at E8.5 from Aph1abc-/- crosses and genotype was determined by PCR analysis on yolk sacs. Mouse embryonic fibroblast (MEF) cultures were derived from dissociated Aph1abc-/- mouse embryos [37].

Generation of stable cell lines

The P2c217 to Leu217 mutation was made using the QuickChange II site-directed mutagenesis kit (Stratagene), using human wild-type APH1B cloned into pcDNA3.1 Zeo+ (Invitrogen) as template. The primers used to introduce the mutation were: 5'-CCTGGGGCTGATGATCTGCT3' (forward); 5'-GAGCACCCAGATTATCTCAATGCTGAGCC-3' (reverse). P2c217 and Leu217 hAPH1B were recloned into pMSCVpuro* and cotransfected into HEK293 cells with helper plasmid pIK Ecopac for packaging into retroviruses. Retroviruses were harvested and snap frozen aliquots were stored at -80°C until use. MEF Aph1abc-/- cells were transduced with retrovirus for 24 hrs followed by puromycin selection in DMEM/F12 supplemented with 10% FCS until stable lines were obtained.

Measurement of gamma-secretase activity towards different substrates

Stably transfected MEFs were seeded and grown to confluency. Cells were rinsed twice with ice-cold PBS and lysed in 1% Triton, and postnuclear fractions were isolated by centrifugation at 10,000 g for 15 min at 4°C. Proteins were quantified using a standard Bradford assay (Pierce) and 10–15 µg protein/lane was loaded on Bio-Rad SDS-PAGE gels (Invitrogen) and transferred to nitrocellulose membranes for Western blot detection for the indicated proteins. Gamma-secretase activity towards each substrate was expressed as the level of substrate C-terminal fragment (the direct gamma-secretase substrate) relative to levels of full-length protein. For densitometric quantification, the films were scanned using an Image Scanner (Amersham Pharmacia) and analyzed using ImageMaster.

Antibodies

APP was detected with C-terminal pAb B63.1 and syndecan 3 with C-terminal mAb 2E9. An antibody against the N-cadherin C-terminal (clone 32, BD Biosciences) was purchased.

Statistical analysis

Genotype frequencies were tested for the Hardy-Weinberg equilibrium. Differences between cases and controls were analysed by standard contingency table analysis using two-tailed $\chi^2$ test probabilities. Odds ratios (95% confidence intervals (CI)) were calculated as an index of the association of the APH1B genotypes with premature atherosclerosis. Continuous and categorical biochemical and clinical variables were determined with the Student’s t-test and $\chi^2$-analysis, respectively. A p-value<0.05 was considered statistically significant (GraphPad Software Inc, San Diego, CA, USA). Though being conservative, Bonferroni correction was used to determine the significance of the biochemical and clinical variables. Power calculations were estimated using Quanto v1.2 [38].

Acknowledgments

We thank Dr. Bart de Strooper (Department of Molecular and Developmental Genetics, VIB, Leuven, Belgium) for helpful support, Dr. Kenji Shirotani and Dr. Christian Haass (Laboratory for Alzheimer’s and Parkinson’s Disease Research, Ludwig-Maximilians-University, Munich, Germany) for the human APH1B wild-type plasmid, Dr. Guido David (Department of Molecular & Developmental Genetics, VIB, Leuven, Belgium) for the anti-Syndecan3 antibody 2E9 and Dr. Bruce Jenkins (Department of Cellular Animal Physiology, Radboud University Nijmegen, The Netherlands) for critical reading of the manuscript.

Author Contributions

Conceived and designed the experiments: KMJvL TD GJMM. Performed the experiments: KMJvL TD MvZ JEvS CW MDT. Wrote the paper: KMJvL TD MvZ JEvS CW MDT GJMM. Contributed reagents/materials/analysis tools: CW MDT. The Netherlands) for critical reading of the manuscript.

References


