Promoter Polymorphism in the Endotoxin Receptor (CD14) Is Associated With Increased Carotid Atherosclerosis Only in Smokers

The Carotid Atherosclerosis Progression Study (CAPS)

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Background and Purpose—The risk of atherosclerosis from endotoxemia is increased in smokers. Endotoxin is a potent mediator of inflammation, and smokers have elevated plasma levels of endotoxin. The endotoxin receptor CD14 can enhance the endotoxin-neutralization capacity of plasma. A functional polymorphism in the promoter region of the CD14 gene (CD14$^{159C/T}$) was studied to determine its impact on common carotid artery (CCA) intima-media thickness (IMT) and any interactions with environmental inflammatory stimuli.

Methods—A community population (n=992; aged 50 to 65 years) underwent genotypic examination for the CD14$^{159}$ polymorphism by restriction fragment length polymorphism analysis.

Results—The CC genotype was associated with increased CCA IMT. The age- and sex-adjusted odds ratio for IMT above the 75th percentile was 1.63 (95% CI, 1.19 to 2.24; $P=0.002$) and 1.70 (95% CI, 1.18 to 2.44; $P=0.004$) after additional adjustment for conventional risk factors. This gene effect was found only in current smokers and ex-smokers. Multivariate analysis in this group (n=503) increased the odds ratio to 2.02 (95% CI, 1.23 to 3.34; $P=0.006$). No significant interactions were found in nonsmokers or with alcohol consumption.

Conclusions—The CD14$^{159}$ polymorphism is associated with increased CCA IMT in smokers from a general population. CD14 may modulate the inflammatory effects of smoking in atherogenesis. (Stroke. 2003;34:600-604.)

Key Words: antigens, CD14 ■ atherosclerosis ■ cigarette smoking ■ polymorphism
been published elsewhere. All members of a German primary healthcare service population aged 40 years or older (n = 15,879) who lived within a radius of 50 km from 5 study sites in western Germany were invited to participate. Within a predefined time limit, 5,460 agreed to participate. The first consecutive 1,000 subjects in the group aged 50 to 65 years (mean age, 57.9 ± 4.4 years; 51.5% women) were included in this study. This number was chosen to allow us to detect a difference in IMT of 0.05 mm with a power of 0.9 and a significance of 0.01. Risk factors determined included the following: pack-years of smoking, current smoking status (defined as current smoker/ex-smoker or never-smoker), body mass index (BMI), mean systolic and diastolic blood pressure, and history of arterial hypertension, diabetes mellitus, or coronary heart disease. Socioeconomic status was measured with the use of a 4-point scale previously applied to German populations for coronary risk factor studies. Average alcohol intake was determined by a standardized questionnaire. Inform consent on the use of samples for analysis was obtained from all participants before entry, and the study was approved by the ethical review committee of the University of Dusseldorf Hospital.

Biochemical Measurements

Fasting blood samples were taken for estimation of serum cholesterol, glycosylated hemoglobin A1c, and fibrinogen. Total serum cholesterol was determined enzymatically with the use of a commercial kit (Boehringer). LDL cholesterol was measured with the heparin-calcium precipitation method and HDL cholesterol with the phosphotungstic acid precipitation method. Glycosylated hemoglobin (glyc-Hb-%) was determined by the IMM method (Abbott). HbA1c concentration was calculated according to the formula HbA1c = (glyc-Hb-% + 1.76)/1.49. Fibrinogen was determined from citrated plasma by the Clauss method (Multifibren, Behringwerke). C-reactive protein (CRP) concentration was measured by a high-sensitivity in-house enzyme-linked immunosorbent assay (range, 0.6 to 40 μg/L).

Ultrasound Imaging

The method used to determine CCA IMT has been described in detail before. In brief, we used a 7.5- to 10.0-MHz linear array transducer (P700SE, Phillips Medical System). IMT measurements were performed off-line with the use of automated imaging processing software that has been described previously. Blood/intimal and medial/adventitial interfaces were automatically detected with the use of a gray value-based edge detection algorithm. The mean length of the arterial segment in which IMT was determined was 14.35 mm for the left CCA and 12.85 mm for the right CCA. Interobserver reliabilities were assessed in a sample of 15 subjects (54 arterial segments) in whom IMT was measured by 4 “blinded” observers. Linear regression analyses revealed high correlation coefficients (r = 0.92 to 0.99), and, according to the method described by Bland and Altman, the ±2 SD of the difference between 2 observers varied between 0.03 and 0.06 mm. Intraobserver test reliability was determined from repetitive examinations of 35 subjects (102 arterial segments) by 3 independent observers. Linear regression showed high coefficients (r = 0.91 to 0.98), and the ±2 SD of the difference between the 2 examinations varied between 0.04 and 0.06 mm.

Laboratory Methods

DNA was available for 992 subjects. DNA was extracted from whole blood with the use of Nucleon kits (Tepnel Life Sciences). The polymorphism underwent genotypic analysis by polymerase chain reaction, resulting in a 497-base pair (bp) product, followed by restriction enzyme digestion with HaeIII (Bioline), producing a fragment of 199 bp, plus fragments of 298 bp for the T allele or 155 and 143 bp (appearing as a single band) for the C allele. Products were visualized on agarose gel stained with ethidium bromide. Genotypes were confirmed by sequencing. Polymerase chain reaction conditions and primers were selected according to the methods of Baldini et al.

Statistical Analysis

Data were analyzed with the use of SPSS (version 10). We analyzed the relationship between genotype and CCA IMT in 2 ways. First, we used CCA IMT as a continuous variable using linear regression. The mean of the right and left CCA IMT values was skewed, and therefore the reciprocal IMT was used to normalize the distribution. Geometric mean IMT values are given in the text for clarity. For the second analysis, we calculated odds ratios for IMT above the 75th percentile using multiple logistic regression. This second analysis was performed because previously published studies suggested that the relationship between IMT and risk of future vascular events is nonlinear and is strongest at higher values of IMT. In both analyses, a genotype-smoking interaction term was included to look for evidence of gene-environment interaction. The effects of genotype on CCA IMT were examined for additive (number of alleles), dominant (carriage of C allele versus TT homozygotes), and recessive (CC homozygotes versus carriage of the T allele) relationships. Age, BMI, mean systolic and diastolic blood pressures, and LDL/HDL cholesterol were normally distributed. We categorized pack-years of smoking by 10-year intervals. In this community population CRP was negatively skewed, with many subjects below the limits of measurement, and therefore CRP was categorized into quartiles.

Results

CCA IMT and Cardiovascular Risk Factors

Associations between cardiovascular risk factors and CCA IMT are shown in Table 1. On univariate analysis, age, sex, pack-years of smoking, BMI, history of arterial hypertension, history of diabetes mellitus, and CRP were all strongly associated with mean CCA IMT. Association with LDL and HDL cholesterol and alcohol intake >30 g/d was weaker but still significant. In multivariate analysis, age, sex, mean systolic blood pressure, low socioeconomic status, and CRP all remained significantly associated with mean CCA IMT.

CD14 Polymorphism and Cardiovascular Risk Factors

The genotype distribution was 24.8% for CC, 50.8% for CT, and 24.4% for TT. This was in Hardy-Weinberg equilibrium (P = 0.999). Analysis of the relationships between genotype and the aforementioned cardiovascular risk factors revealed no significant associations.

CCA IMT and Genotype

When IMT was analyzed as a continuous variable, the C allele of the CD14 polymorphism was associated with increased CCA IMT. This finding was significant when we used an additive model (allele frequency) (P = 0.049) and for CC homozygotes versus CT/TT combined (P = 0.022) (Table 2).

Analysis of IMT by highest quartile showed that the CC genotype was significantly more common in the top quartile; 33.3% of the CC genotype was found in this quartile compared with 23.7% and 23.1% of the CT and TT genotypes, respectively (P = 0.009 for CC compared with TT and P = 0.011 for linear trend). The odds ratio for IMT above the 75th percentile was 1.63 (95% CI, 1.19 to 2.24; P = 0.002) for CC compared with both the other genotypes combined. After multivariate analysis controlling for conventional risk factors, the odds ratio for the CC genotype was not weakened at 1.70 (95% CI, 1.18 to 2.44; P = 0.004).
**TABLE 1.** Univariate and Multivariate Associations Between Vascular Risk Factors and Reciprocal Mean Common Carotid Artery Intima-Media Thickness (mm)

<table>
<thead>
<tr>
<th></th>
<th>Univariate Correlation Coefficients*</th>
<th>P</th>
<th>Multivariate Standardized Coefficients</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, y</td>
<td>-0.277</td>
<td>&lt;0.0005</td>
<td>-0.215</td>
<td>&lt;0.0005</td>
</tr>
<tr>
<td>Female</td>
<td>0.168</td>
<td>&lt;0.0005</td>
<td>0.114</td>
<td>0.004</td>
</tr>
<tr>
<td>Body mass index, kg/m²</td>
<td>-0.162</td>
<td>&lt;0.0005</td>
<td>-0.055</td>
<td>0.137</td>
</tr>
<tr>
<td>Arterial hypertension</td>
<td>-0.147</td>
<td>&lt;0.0005</td>
<td>-0.020</td>
<td>0.565</td>
</tr>
<tr>
<td>Mean systolic blood pressure</td>
<td>-0.285</td>
<td>&lt;0.0005</td>
<td>-0.250</td>
<td>&lt;0.0005</td>
</tr>
<tr>
<td>Mean diastolic blood pressure</td>
<td>-0.185</td>
<td>&lt;0.0005</td>
<td>0.039</td>
<td>0.465</td>
</tr>
<tr>
<td>Diabetes mellitus</td>
<td>-0.085</td>
<td>0.007</td>
<td>-0.018</td>
<td>0.586</td>
</tr>
<tr>
<td>LDL cholesterol, mmol/L</td>
<td>-0.99</td>
<td>0.002</td>
<td>-0.032</td>
<td>0.335</td>
</tr>
<tr>
<td>HDL cholesterol, mmol/L</td>
<td>0.175</td>
<td>&lt;0.0005</td>
<td>0.060</td>
<td>0.114</td>
</tr>
<tr>
<td>Pack-years of smoking (10-y categories)</td>
<td>-0.154</td>
<td>&lt;0.0005</td>
<td>-0.070</td>
<td>0.157</td>
</tr>
<tr>
<td>Smoking status</td>
<td>-0.076</td>
<td>0.017</td>
<td>-0.010</td>
<td>0.842</td>
</tr>
<tr>
<td>Lowest socioeconomic status</td>
<td>0.035</td>
<td>0.292</td>
<td>0.070</td>
<td>0.039</td>
</tr>
<tr>
<td>CRP, mg/L</td>
<td>-0.129</td>
<td>&lt;0.0005</td>
<td>-0.083</td>
<td>0.013</td>
</tr>
<tr>
<td>Alcohol intake &gt;30 g/d</td>
<td>-0.058</td>
<td>0.082</td>
<td>-0.022</td>
<td>0.528</td>
</tr>
</tbody>
</table>

*Pearson (parametric variables)/Spearman’s Rho (nonparametric) correlation coefficients.

**Environment Interactions**

There was a significant interaction between CD14 genotype and smoking ($P$ for interaction=0.008). Specifically, the relationship between genotype and IMT was stronger in smokers and absent in those who had never smoked (Table 3 and Figure). Additionally, there was evidence of a graded relationship between the number of pack-years smoked and the effect of CD14 genotype on IMT. Increasing pack-years of smoking resulted in a linear increase in IMT with carriage of the T allele. In contrast, there was no linear relationship in the TT homozygotes ($P=0.704$, adjusted for cardiovascular risk factors). The relationship with smoking was not affected by potential confounding of factors, including exercise, total energy expenditure per day, or use of antihypertensive treatment.

No significant associations were shown between increased IMT, CD14 genotype, and BMI or level of alcohol consumption.

**Discussion**

This study found that the C allele of the functional CD14 (endotoxin receptor) –159C/T polymorphism was associated with increased CCA IMT in a general community population but that this association was limited to smokers. The C allele has previously been associated with lower levels of circulating sCD14, and individuals with lower levels of sCD14 have reduced capacity to neutralize endotoxin. Interestingly, this association was limited to smokers, who are known to have increased endotoxin exposure. These findings support a potential role for this polymorphism in modulating endotoxin-mediated atherosclerosis and demonstrate a potentially important gene-environment interaction between smoking and CD14 genotype in the pathogenesis of early atherosclerosis.

Our study is one of the first to demonstrate gene-environment interactions in the pathogenesis of carotid atherosclerosis. There are a number of pathophysiologic explanations for the interaction with smoking. Previous work has shown that TT homozygotes for the CD14 –159 polymorphism have elevated levels of sCD14 and that carriage of the T allele results in upregulation of transcription of CD14. Increases in sCD14 can decrease monocyte response to endotoxin by clearance via lipoproteins. This leads to a decreased inflammatory response. A strong correlation between sCD14 and the endotoxin-neutralizing capacity of

**TABLE 2.** Association Between the CD14 Polymorphism and Mean CCA-IMT Analyzed According to Smoking Status

<table>
<thead>
<tr>
<th>Subject Group</th>
<th>Mean CCA-IMT (mm)</th>
<th>Additive No. of C Alleles</th>
<th>Dominant CC/CT vs TT</th>
<th>Recessive CC vs CT/TT</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>CC</td>
<td>CT</td>
<td>TT</td>
<td>$P_a$ $P_m$ $P_a$ $P_m$ $P_a$ $P_m$</td>
</tr>
<tr>
<td>All</td>
<td>0.768</td>
<td>0.749</td>
<td>0.748</td>
<td>0.049 0.255 0.363 0.955 0.022 0.057</td>
</tr>
<tr>
<td>Nonsmokers</td>
<td>0.752</td>
<td>0.738</td>
<td>0.756</td>
<td>0.047 0.284 0.212 0.087 0.491 0.935</td>
</tr>
<tr>
<td>Ever smokers</td>
<td>0.789</td>
<td>0.758</td>
<td>0.738</td>
<td>0.002 0.011 0.023 0.072 0.006 0.021</td>
</tr>
</tbody>
</table>

*Significance values are shown for additive (allele frequency), dominant (carriage of C allele vs TT), and recessive (CC vs T allele carriage) models and also after adjustment for all cardiovascular risk factors (see text).

$P_a$ indicates univariate $P$ value; $P_m$ multivariate $P$ value.
plasma has also been demonstrated.23 Data from the Bruneck atherosclerosis study showed that subjects with high endotoxin levels were at risk of increased IMT only if they also had increased inflammatory markers.11 Individuals with the CC genotype express lower levels of CD1421 and therefore may also be less able to clear endotoxin and other CD14 ligands, resulting in chronic low-grade inflammation. Conversely, carriage of the T allele upregulates CD14 expression and may enable a more robust response to acute challenge but better clearance of ligand and reduced chronic inflammation. The effect of smoking on IMT may arise from the bioactive endotoxin found in cigarette smoke.9 The increased risk of lower respiratory tract infection seen in smokers24 may also increase the antigenic load in this group. Risk of atherosclerosis from endotoxemia has been found to be increased in current and past smokers compared with nonsmokers.10 A genetic predisposition that reduces clearance of endotoxin would therefore be expected to enhance the inflammatory consequences of smoking. The CC genotype may be such a genotype. The measurement of endotoxin alone may not be sufficient as an indication of potential CD14 stimulation. The CD14 receptor is known to respond to a range of factors and may enable a more robust response to acute challenge but better clearance of ligand and reduced chronic inflammation. These findings support a role for the CD14 endotoxin receptor in atherosclerosis. Genetic variation in the endotoxin

### Table 3. Risk of an Increased IMT Above the 75th Percentile Conferrred by the CC Genotype, Analyzed According to Smoking Status

<table>
<thead>
<tr>
<th>Subject Group</th>
<th>Age and Sex Adjusted</th>
<th>Multivariate</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>OR 95% CI</td>
<td>OR 95% CI</td>
</tr>
<tr>
<td>All</td>
<td>1.58 1.14–2.19</td>
<td>1.69 1.20–2.39</td>
</tr>
<tr>
<td>Ever smokers</td>
<td>1.79 1.13–2.85</td>
<td>2.02 1.23–3.34</td>
</tr>
<tr>
<td>Nonsmokers</td>
<td>0.73 0.45–1.17</td>
<td>0.74 0.46–1.22</td>
</tr>
</tbody>
</table>

Significance values are shown after age and gender adjustment and after adjustment for all cardiovascular risk factors (see text).
receptor may act to mediate the risk of smoking on vascular disease.

Acknowledgments

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References


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