Quantitative trait locus on chromosome 20q13 for plasma levels of C-reactive protein in healthy whites: the HERITAGE Family Study

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Submitted 1 March 2005; accepted in final form 5 June 2006

C-REACTIVE PROTEIN (CRP) is a sensitive marker of systemic low-grade inflammation. Increased plasma levels of CRP predict the risk of cardiovascular and metabolic diseases. Although genetic factors account for 30–40% of individual differences in plasma CRP levels, genomic regions contributing to CRP levels remain unknown. We performed a genome-wide linkage scan for plasma CRP levels in healthy whites from the HERITAGE Family Study. CRP was measured with a high-sensitivity method. Multipoint linkage analyses were performed in 280 sibling pairs with 654 markers using regression and variance components-based methods. Data were adjusted for independent correlates of plasma CRP. We showed the strongest evidence of linkage for plasma CRP levels on chromosome 20q13. Markers which gave suggestive linkages in this region were D20S52 [logarithm of odds (LOD) score 3.18, P = 0.00006], D20S857 (LOD score 2.87, P = 0.0014), D20S869 (LOD score 2.75, P = 0.0002), D20S840 (LOD score 2.59, P = 0.0003), D20S501 (LOD score 2.55, P = 0.0003), D20S840 (LOD score 2.18, P = 0.0068), and D20S876 (LOD score 2.07, P = 0.001). We also detected suggestive linkage on chromosome 13 for marker D5S1470 (LOD score 2.23, P = 0.0007). Chromosome 20q13 may contribute to plasma CRP levels in healthy whites. This region contains genes that are important in the inflammatory process and may play a role in the development of chronic inflammatory diseases. The present findings may be useful in the ongoing effort to search for genes contributing to inflammation and to identify individuals at an increased risk of chronic inflammatory diseases.

METHODS

Study design and subjects. The HERITAGE Family Study is a multicenter exercise intervention trial carried out by a consortium of five universities in the United States and Canada (4). The study was designed to investigate the contribution of exercise training to changes in risk factors for Type 2 diabetes and cardiovascular diseases and the role of genetic factors in cardiovascular, metabolic, and hormonal responses to exercise training in white and black families. The study protocol was approved by each of the Institutional Review Boards of the HERITAGE Family Study research consortium. Written informed consent was obtained from each participant.

The subjects came from families that included the biological mother and father (≥65 yr of age) and their offspring (≥17 yr of age). The white families had at least two offspring; the black families were smaller. The subjects were required to be sedentary, defined as not having participated in regular physical activity during the previous 6 mo. Moreover, we disallowed subjects who had chronic diseases that could have prevented their participation in a structured exercise training program or affected the inflammatory process. The diseases CRP levels have also been associated with features of the metabolic syndrome, including increased body adiposity, insulin resistance, increased plasma triglyceride levels, reduced plasma high-density lipoprotein (HDL) cholesterol levels, elevated blood pressure, and endothelial dysfunction (15, 50). Recent evidence suggests that CRP not only is a marker of systemic inflammation but also actively contributes to arterial wall inflammation, endothelial dysfunction, and atherothrombosis (45, 47). Moreover, CRP is an important component of the innate immune system, providing host defense by activating the classical complement pathway (49).

Cardiovascular and metabolic diseases and their risk factors have been associated with increased plasma CRP levels, whereas healthy lifestyle changes and cholesterol-lowering medications appear to reduce CRP levels (34). Genetic factors have been found to account for ∼30–40% of individual differences in plasma CRP levels (32, 48). The Framingham Heart Study showed no evidence of linkage for CRP, whereas linkages were found for two other biomarkers of inflammation, monocyte chemoattractant protein-1 and soluble intercellular adhesion molecule-1 (13). However, some polymorphisms in genes involved in the inflammatory process have been associated with CRP levels (6, 46, 48). As genomic regions contributing to plasma CRP levels remain unknown, we performed a genome-wide linkage scan for plasma CRP levels in healthy white men and women from the Health, Risk Factors, Exercise Training, and Genetics (HERITAGE) Family Study.

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included coronary heart disease, stroke, peripheral vascular disease, severe obesity, hypertension, hypercholesterolemia, hyperglycemia, Type 1 or Type 2 diabetes, other endocrinological diseases, autoimmune or collagen vascular diseases, respiratory diseases, gastrointestinal diseases, urinary tract or genital diseases, neurological or neuromuscular diseases, psychiatric diseases, hematological diseases, cancer in the past 5 yr except skin cancer therapeutically controlled, and musculoskeletal diseases. Also, the subjects were not allowed to take regularly medications, such as cholesterol-lowering drugs, that could have affected the inflammatory process.

We excluded eight subjects whose CRP value separated by ≥4 SD from the mean or by ≥1 SD from the next highest value. The final study sample with complete data on CRP and all other variables needed for the analyses included 444 whites (220 men, 224 women) from 96 nuclear families and 220 blacks (79 men, 141 women) from 106 nuclear families. The number of sibling pairs for the linkage analyses was 280 in whites and 79 in blacks.

**Measurement of CRP.** Plasma CRP was measured with a high-sensitivity solid-phase chemiluminescent immunometric assay (IM-ULTRA, High Sensitivity CRP, Diagnostic Products, Los Angeles, CA) implemented on an automated immunoassay instrument (Diagnostic Products). In 48 randomly selected subjects, the intraclass correlation between two CRP measurements during the same study visit was 0.98, and the coefficient of variation was 6.4%.

**Assessment of confounding factors.** The method for assessing smoking, alcohol intake, the use of hormone replacement therapy or oral contraceptives, body mass index, maximal oxygen uptake, plasma low-density lipoprotein (LDL) cholesterol, HDL cholesterol, triglycerides, glucose, and insulin, as well as systolic and diastolic blood pressure, has been presented previously (4).

**Data adjustment.** Because of skewed distributions, logarithmic transformation was used for CRP, insulin, HDL cholesterol, and triglycerides. CRP was regressed on its independent correlates by stepwise multiple regression analysis, as explained in detail previously (38). The analyses were performed separately within the race-by-sex-by-generation subgroups, and the variables included in the models were smoking status, the use of hormone replacement therapy or oral contraceptives, maximal oxygen uptake, body mass index, and up to a third-degree polynomial in age. Only significant (P < 0.05) terms were retained. The significant terms were body mass index and the use of hormone replacement therapy or oral contraceptives in white daughters and body mass index in white fathers, mothers, and sons and in black sons, daughters, and mothers. No terms were significant in black fathers. The residuals, or the raw scores if no terms were significant, were then standardized to zero mean and unit variance within each subgroup and constituted the final phenotypes.

**Molecular methods.** A total of 654 markers with an average spacing of 4.7 Mb were used. The marker density was higher on chromosome 20 because fine mapping was done in this region for another study conducted in our laboratory ~5 yr ago. The additional microsatellite markers on chromosome 20 were genotyped also on the HERITAGE samples, but no fine mapping has been done for any trait in this region. Polymerase chain reaction (PCR) conditions and genotyping methods have been described in detail previously (8). Automatic DNA sequencers from LI-COR were used to detect the PCR products, and genotypes were scored semiautomatically with the SAGA software. Mendelian inheritance was checked, and markers showing incompatibilities were regenotyped (<10%). Microsatellite markers were selected mainly from the Marshfield panel, version 8a. Map locations were taken from the National Center for Biotechnology Information (NCBI) physical map, build 35.1.

**Genetic analyses.** Maximal heritability was estimated using the variance components method as implemented in the QTDT program (1). Total phenotypic variance was broken into genetic, environmental, and residual variance, and the maximal heritability was calculated as the proportion of the total variance explained by the genetic component.

### Table 1. Characteristics of the subjects

<table>
<thead>
<tr>
<th></th>
<th>Whites</th>
<th>Blacks</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of subjects</td>
<td>444</td>
<td>220</td>
</tr>
<tr>
<td>Age, yr</td>
<td>36.4 (14.5)</td>
<td>34.0 (11.5)</td>
</tr>
<tr>
<td>Sex, % female</td>
<td>50.5</td>
<td>64.1</td>
</tr>
<tr>
<td>Generation, % offspring</td>
<td>60.8</td>
<td>70.5</td>
</tr>
<tr>
<td>Use of hormones, %</td>
<td>20.5</td>
<td>14.5</td>
</tr>
<tr>
<td>Smoking status</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Never, %</td>
<td>61.3</td>
<td>70.9</td>
</tr>
<tr>
<td>Former, %</td>
<td>24.1</td>
<td>19.6</td>
</tr>
<tr>
<td>Current, %</td>
<td>14.6</td>
<td>9.6</td>
</tr>
<tr>
<td>Alcohol intake, g/wk</td>
<td>6.3 (10.9)</td>
<td>2.5 (5.6)</td>
</tr>
<tr>
<td>Body mass index, kg/m²</td>
<td>25.9 (4.9)</td>
<td>27.9 (5.7)</td>
</tr>
<tr>
<td>Maximal oxygen uptake, ml/kg/min</td>
<td>32.9 (8.8)</td>
<td>27.1 (7.2)</td>
</tr>
<tr>
<td>Plasma glucose, mmol/l</td>
<td>5.1 (0.6)</td>
<td>5.1 (0.6)</td>
</tr>
<tr>
<td>Plasma insulin, pmol/l</td>
<td>66.0 (40.5)</td>
<td>81.1 (65.5)</td>
</tr>
<tr>
<td>Plasma LDL cholesterol, mmol/l</td>
<td>3.0 (0.8)</td>
<td>2.9 (0.7)</td>
</tr>
<tr>
<td>Plasma HDL cholesterol, mmol/l</td>
<td>1.04 (0.26)</td>
<td>1.08 (0.30)</td>
</tr>
<tr>
<td>Plasma triglycerides, mmol/l</td>
<td>1.40 (0.80)</td>
<td>1.05 (0.63)</td>
</tr>
<tr>
<td>Systolic blood pressure, mmHg</td>
<td>116.3 (10.9)</td>
<td>123.1 (11.8)</td>
</tr>
<tr>
<td>Diastolic blood pressure, mmHg</td>
<td>66.1 (8.1)</td>
<td>72.7 (8.3)</td>
</tr>
</tbody>
</table>

Values are means (SD) or percentages. *Hormone replacement therapy or oral contraceptives.

The linkage analyses were performed with the SIBPAL program of Statistical Analysis for Genetic Epidemiology (SAGE) 4.5 (14, 41) using the NCBI physical map, build 35.1. The physical map is the only way to place all markers on the same map and guarantees the correct order of the markers, the most important requirement for reliable multipoint linkage analyses. Siblings who share a greater proportion of alleles identical-by-descent (IBD) at the marker locus will show a greater resemblance in the phenotype. The phenotypic resemblance of the siblings, modeled as a weighted combination of squared trait difference and squared mean-corrected trait sum, is linearly regressed on the estimated proportion of alleles that the sibling pair shares IBD at each marker locus. The multipoint estimates of allele sharing IBD were generated using the GENIBD program of the SAGE 4.5. Allele frequencies for the IBD calculations were derived from the parents, e.g., biologically unrelated subjects. For all markers with SIBPAL nominal multipoint P values ≤ 0.01, empirical P values were derived from a maximum of 500,000 permutations. For each replicate, the allele sharing among the sibling pairs was permuted, the test statistic was recalculated, and the proportion of the replicates that is equal to or greater than the statistic calculated from the original observations was determined. The number of replicates for each marker was chosen so that the estimated empirical P value was within 20% of its true value with 95% confidence, as implemented in the permutation algorithm of the SIBPAL program. The multipoint linkage analyses were also performed by variance components linkage analysis with the Merlin program (2).

### RESULTS

The characteristics of whites and blacks are shown in Table 1. The median CRP was higher in blacks than whites, in women than men, in fathers than sons, and in mothers than daughters (Table 2). The maximal heritability for CRP was 39% in whites. Heritability was not detectable in blacks, probably due to the limited number of sibling pairs. We therefore performed linkage analyses in whites only. We showed the strongest evidence of linkage for CRP on chromosome 20q13 between 49 and 58 Mb (Fig. 1). Markers that gave suggestive linkages in this region were D20S52 [logarithm of odds (LOD) score 3.18, P = 0.00006], D20S857 (LOD score 2.87, P = 0.00014), D20S869 (LOD score 2.75, P = 0.0002),
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**DISCUSSION**

The present study supports the previous finding that genetic factors account for ∼30–40% of individual differences in plasma CRP levels in Caucasians (32, 48). The novel finding of the present study is the evidence of linkage for CRP levels on chromosome 20q13 in healthy whites. Chromosome 20q13 contains putative candidate genes for inflammation.

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CRP, C-reactive protein.

D20S480 (LOD score 2.59, \( P = 0.0003 \)), D20S501 (LOD score 2.55, \( P = 0.0003 \)), D20S840 (LOD score 2.18, \( P = 0.0008 \)), and D20S876 (LOD score 2.07, \( P = 0.0011 \)). We also detected suggestive linkage on chromosome 5p13 for marker D5S1470 (LOD score 2.23, \( P = 0.0007 \)).

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inflammation are needed to confirm the linkage results on chromosome 20q13.

Putative candidate genes for inflammation on chromosome 20q13 include NFKB1, C/EBPβ, and ADA. NFKB1 is a member of the nuclear factor of activated T cells (NFAT) family of transcription factors (28), is expressed in most immune system cells, and is important in the transcription of many genes regulating the production of proinflammatory cytokines and the activation of immune system (10, 37). We found evidence of linkage with the marker D20S857 located in the NFAT1 gene at 50.8 Mb. NFAT1 also regulates the transcription of insulin and glucagon genes in the pancreatic β-cells (17, 24), which may partly explain the linkage for Type 2 diabetes on chromosome 20q13 (5, 18, 21, 22, 27, 30, 35, 44, 51). Moreover, NFAT1 regulates the differentiation and development of vascular endothelial cells, skeletal muscle cells, adipocytes, and chondrocytes (19) and could thereby contribute to chronic inflammatory diseases, such as atherosclerosis, diabetes, obesity, and arthritis. C/EBPβ is a member of the CCAAT/enhancer binding protein (C/EBP) family and is one of the key transcription factors in the induction of genes involved in the acute phase response, innate immunity, and inflammation (35). The C/EBPβ gene is located 1.3 Mb from the NFAT1 gene at 49.5 Mb. C/EBPβ is important in the induction of CRP expression by interleukin (IL)-6 (3). C/EBPβ is also involved in the differentiation of adipocytes (36), which could partly explain the linkage for obesity on chromosome 20q13 (11, 12, 25, 26, 31). The inherited deficiency of adenine deaminase (ADA) causes one form of severe combined immunodeficiency disease, in which there is a dysfunction of both B and T lymphocytes, with an impaired cellular immunity and a decreased production of immunoglobulins (9). A milder dysfunction of the ADA gene, which is located at 43.9 Mb, may contribute to the linkage for plasma CRP levels in healthy whites of the present study. However, chromosome 20q13 does not contain CRP, IL-6, or TNF-α genes, the variants of which have been previously reported to be associated with plasma CRP levels (6, 46, 48).

The present genome-wide linkage scan suggests that chromosome 20q13 may contribute to plasma CRP levels in healthy whites. This region contains genes that are important in the inflammatory process and may play a role in the development of chronic inflammatory diseases. The present findings may be useful in the ongoing effort to search for genes contributing to inflammation and to identify individuals at an increased risk of chronic inflammatory diseases.

ACKNOWLEDGMENTS

Gratitude is expressed to Dr. Andre Nadeau and the staff of the Diabetes Research Unit and to the staff of the Lipid Research Center, Laval University Medical Center, Ste-Foy, Quebec, Canada, for their contribution to the HERITAGE Family Study, and to Dr. Jacob Brand for his contribution to the statistical analyses. Some of the results were obtained by using the SAGE statistical package, which is supported by a US Public Health Service Resource Grant (1 P41 RR-03655) from the National Center for Research Resources.

GRANTS

The HERITAGE Family Study is supported by National Heart, Lung, and Blood Institute through Grants HL-45670 (to C. Bouchard); HL-47323 (to A. S. Leon), HL-47317 (to D. C. Rao), HL-47327 (to J. S. Skinner), and HL-47321 (to Jack H. Wilmore). C. Bouchard is partially supported by the Henry L. Taylor endowed Professorship in Exercise Science and Health Enhancement. T. A. Lakka is an Academy Research Fellow of the Academy of Finland and was supported by grants from the Academy of Finland, the Yrjo Jahnsson Foundation, the Paavo Nurmi Foundation, and the University of Kuopio.

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