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

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Lakka, Timo A., Tuomo Rankinen, Treva Rice, Arthur S. Leon, D. C. Rao, James S. Skinner, and Claude Bouchard. Quantitative trait locus on chromosome 20q13 for plasma levels of C-reactive protein in healthy whites: the heritage family study. *Physiol Genomics* 27: 103–107, 2006. First published July 5, 2006; doi:10.1152/physiolgenomics.00054.2005.—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 assay. 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, $P = 0.00014$), D20S869 (LOD score 2.75, $P = 0.0002$), 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, $P = 0.001$). We also detected suggestive linkage on chromosome 5p13 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.

genes; genomic scan; immune system; inflammation; health, risk factors, exercise training, and genetics

C-REACTIVE PROTEIN (CRP) is a sensitive marker of systemic low-grade inflammation and is currently recommended as the principal inflammatory marker in research and clinical practice (34). Increased plasma levels of CRP have been found to predict the risk of cardiovascular and metabolic diseases, such as coronary heart disease (23, 40), ischemic stroke (7), peripheral artery disease (39), hypertension (42), and Type 2 diabetes (16), independently of traditional risk factors. Elevated plasma

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.

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

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included coronary heart disease, stroke, peripheral vascular disease, severe obesity, hypertension, hypercholesterolemia, hypertiglyceridemia, 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 (IMMULITE 2000 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*

	Whites	Blacks
Number of subjects	444	220
Age, yr	36.4 (14.5)	34.0 (11.5)
Sex, % female	50.5	64.1
Generation, % offspring	60.8	70.5
Use of hormones, %*	20.5	14.5
Smoking status		
Never, %	61.3	70.9
Former, %	24.1	19.6
Current, %	14.6	9.6
Alcohol intake, g/wk	6.3 (10.9)	2.5 (5.6)
Body mass index, kg/m ²	25.9 (4.9)	27.9 (5.7)
Maximal oxygen uptake, ml/kg/min	32.9 (8.8)	27.1 (7.2)
Plasma glucose, mmol/l	5.1 (0.6)	5.1 (0.6)
Plasma insulin, pmol/l	66.0 (40.5)	81.1 (65.5)
Plasma LDL cholesterol, mmol/l	3.0 (0.8)	2.9 (0.7)
Plasma HDL cholesterol, mmol/l	1.04 (0.26)	1.08 (0.30)
Plasma triglycerides, mmol/l	1.40 (0.80)	1.05 (0.63)
Systolic blood pressure, mmHg	116.3 (10.9)	123.1 (11.8)
Diastolic blood pressure, mmHg	66.1 (8.1)	72.7 (8.3)

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, $P = 0.0002$),

Table 2. Baseline CRP (mg/l) by race, sex, and generation

	Whites			Blacks		
	<i>n</i>	Median	Interquartile Range	<i>n</i>	Median	Interquartile Range
All	444	1.21	0.58–2.69	220	1.54	0.65–3.82
Fathers	90	1.44	0.86–2.51	23	1.92	1.29–4.25
Mothers	84	2.04	0.99–4.54	42	2.69	0.73–5.49
Sons	130	0.78	0.36–1.56	56	1.05	0.46–2.11
Daughters	140	1.15	0.53–2.82	99	1.58	0.65–4.25

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, $P = 0.001$). We also detected suggestive linkage on chromosome 5p13 for marker D5S1470 (LOD score 2.23, $P = 0.0007$).

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.

CRP is principally produced by the liver, and proinflammatory cytokines induce the expression and release of CRP during the inflammatory process (48). CRP is a sensitive marker of systemic low-grade inflammation, and currently available assays allow the accurate measurement of very low plasma CRP levels in healthy individuals (34). Another advantage of CRP as a measure of low-grade inflammation is the small seasonal and diurnal variation in individuals with a stable lifestyle (29). Plasma CRP levels are increased in many proinflammatory conditions, such as smoking, overweight and obesity, diabetes, dyslipidemia, elevated blood pressure, the metabolic syndrome, the use of estrogen and progestogens, and chronic infections and inflammatory diseases (34). On the other hand, weight loss, regular physical activity, moderate alcohol consumption, and the use of lipid-lowering medications, including statins, fibrates, and niacin, appear to reduce CRP levels (34).

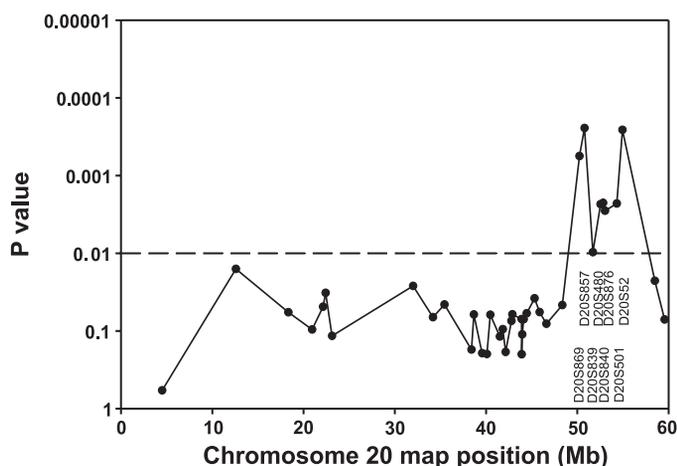


Fig. 1. Linkages for plasma C-reactive protein levels on chromosome 20 in whites.

Table 3. Linkages for plasma CRP levels in whites

Chromosome	Marker	Map Position, Mb	SIBPAL Empirical <i>P</i> Value	Merlin Variance Component LOD Score (<i>P</i> value)
5p13	D5S1470	32.53779	0.0007	2.23 (0.0007)
20q13	D20S869	50.24202	0.0008	2.75 (0.0002)
20q13	D20S857	50.79369	0.0002	2.87 (0.00014)
20q13	D20S839	51.70721	0.0075	1.84 (0.002)
20q13	D20S480	52.54275	0.0025	2.59 (0.0003)
20q13	D20S840	52.83278	0.0026	2.18 (0.0008)
20q13	D20S876	53.03317	0.0030	2.07 (0.001)
20q13	D20S501	54.32661	0.0026	2.55 (0.0003)
20q13	D20S52	54.94566	0.0002	3.18 (0.00006)

LOD, logarithm of odds.

To minimize confounding, we adjusted data for independent correlates of CRP within each race, sex, and generation subgroup. Moreover, due to the design of the HERITAGE Family Study, we only included healthy sedentary individuals who did not have chronic diseases or were not taking regularly medications, such as lipid-lowering drugs, that could have affected the inflammatory process. However, we cannot exclude the possibility that some of the subjects used aspirin or other anti-inflammatory analgesics, although this is an unlikely explanation for the results. We therefore believe that the observed linkage for CRP on chromosome 20q13 is a true finding and not due to confounding.

The maximal heritability for plasma CRP levels in whites was comparable to that observed in previous studies (32, 48), and the number of sibling pairs was large enough for reliable linkage analyses. However, we did not detect a heritable component for CRP levels in blacks. A possible explanation for this is the limited statistical power in blacks due to the smaller number of sibling pairs. Therefore, we performed linkage analyses in whites only.

To our knowledge, no previous genome-wide linkage scan reports are available for plasma CRP levels. Interestingly, however, there is accumulating evidence of linkage on chromosome 20q13 for cardiovascular and metabolic diseases and their risk factors that have been associated with inflammation, such as obesity (11, 12, 25, 26, 31), Type 2 diabetes (5, 18, 21, 22, 27, 30, 35, 44, 51), fasting plasma insulin levels (26), plasma HDL cholesterol levels (33, 43), and systolic blood pressure (20). A quantitative trait locus (QTL) for body fatness in the Pennsylvania study (25) spanned across five markers (D20869, D20857, D20S839, D20S840, D20S876), all of which showed linkage with CRP in the present study. A QTL for Type 2 diabetes in the Finland United States Investigation of Noninsulin-Dependent Diabetes Mellitus Genetics (FUSION) study (18) also included three markers (D20S480, D20S840, D20S857), which were linked with CRP in our study. Elevated CRP levels have been associated with obesity (15, 50), an increased risk of developing Type 2 diabetes (16), elevated insulin levels (15, 50), reduced HDL cholesterol levels (15), and increased blood pressure (42). These associations may be partly due to the effect of genes located on chromosome 20q13 that are involved in the inflammatory process. Other genomic scans in healthy individuals and in those who already have diseases that are associated with

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

Putative candidate genes for inflammation on chromosome 20q13 include NFAT1, C/EBP β , and ADA. NFAT1 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/EBP β 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/EBP β gene is located 1.3 Mb from the NFAT1 gene at 49.5 Mb. C/EBP β is important in the induction of CRP expression by interleukin (IL)-6 (3). C/EBP β 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 adenosine 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.

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REFERENCES

1. **Abecasis GR, Cardon LR, and Cookson WO.** A general test of association for quantitative traits in nuclear families. *Am J Hum Genet* 66: 279–292, 2000.
2. **Abecasis GR, Cherny SS, Cookson WO, and Cardon LR.** Merlin—rapid analysis of dense genetic maps using sparse gene flow trees. *Nat Genet* 1: 97–101, 2002.
3. **Agrawal A, Cha-Molstad H, Samols D, and Kushner I.** Transactivation of C-reactive protein by IL-6 requires synergistic interaction of CCAAT/enhancer binding protein beta (C/EBP beta) and Rel p50. *J Immunol* 166: 2378–2384, 2001.
4. **Bouchard C, Leon AS, Rao DC, Skinner JS, Wilmore JH, and Gagnon J.** The HERITAGE family study. Aims, design, and measurement protocol. *Med Sci Sports Exerc* 27: 721–729, 1995.
5. **Bowden DW, Sale M, Howard TD, Qadri A, Spray BJ, Rothschild CB, Akots G, Rich SS, and Freedman BI.** Linkage of genetic markers on human chromosomes 20 and 12 to NIDDM in Caucasian sib pairs with a history of diabetic nephropathy. *Diabetes* 46: 882–886, 1997.
6. **Brull DJ, Serrano N, Zito F, Jones L, Montgomery HE, Rumley A, Sharma P, Lowe GD, World MJ, Humphries SE, and Hingorani AD.** Human CRP gene polymorphism influences CRP levels: implications for the prediction and pathogenesis of coronary heart disease. *Arterioscler Thromb Vasc Biol* 23: 2063–2069, 2003.
7. **Cao JJ, Thach C, Manolio TA, Psaty BM, Kuller LH, Chaves PH, Polak JF, Sutton-Tyrrell K, Herrington DM, Price TR, and Cushman M.** C-reactive protein, carotid intima-media thickness, and incidence of ischemic stroke in the elderly: the Cardiovascular Health Study. *Circulation* 108: 166–170, 2003.
8. **Chagnon YC, Borecki IB, Perusse L, Roy S, Lacaille M, Chagnon M, Ho-Kim MA, Rice T, Province MA, Rao DC, and Bouchard C.** Genome-wide search for genes related to the fat-free body mass in the Quebec family study. *Metabolism* 49: 203–207, 2000.
9. **Cristalli G, Costanzi S, Lambertucci C, Lupidi G, Vittori S, Volpini R, and Camaioni E.** Adenosine deaminase: functional implications and different classes of inhibitors. *Med Res Rev* 21: 105–128, 2001.
10. **Decker EL, Nehmann N, Kampen E, Eibel H, Zipfel PF, and Skerka C.** Early growth response proteins (EGR) and nuclear factors of activated T cells (NFAT) form heterodimers and regulate proinflammatory cytokine gene expression. *Nucleic Acids Res* 31: 911–921, 2003.
11. **Deng HW, Deng H, Liu YJ, Liu YZ, Xu FH, Shen H, Conway T, Li JL, Huang QY, Davies KM, and Recker RR.** A genomewide linkage scan for quantitative-trait loci for obesity phenotypes. *Am J Hum Genet* 70: 1138–1151, 2002.
12. **Dong C, Wang S, Li WD, Li D, Zhao H, and Price RA.** Interacting genetic loci on chromosomes 20 and 10 influence extreme human obesity. *Am J Hum Genet* 72: 115–124, 2003.
13. **Dupuis J, Larson MG, Vasan RS, Massaro JM, Wilson PW, Lipinska I, Corey D, Vita JA, Keaney JF Jr, and Benjamin EJ.** Genome scan of systemic biomarkers of vascular inflammation in the Framingham Heart Study: evidence for susceptibility loci on 1q. *Atherosclerosis* 182: 307–314, 2005.
14. **Elston RC, Buxbaum S, Jacobs KB, and Olson JM.** Haseman and Elston revisited. *Genet Epidemiol* 19: 1–17, 2000.
15. **Festa A, D'Agostino R Jr, Howard G, Mykkanen L, Tracy RP, and Haffner SM.** Chronic subclinical inflammation as part of the insulin resistance syndrome: the insulin resistance atherosclerosis study (IRAS). *Circulation* 102: 42–47, 2000.
16. **Freeman DJ, Norrie J, Caslake MJ, Gaw A, Ford I, Lowe GD, O'Reilly DS, Packard CJ, and Sattar N.** C-reactive protein is an independent predictor of risk for the development of diabetes in the West of Scotland coronary prevention study. *Diabetes* 51: 1596–1600, 2002.
17. **Furstenau U, Schwaninger M, Blume R, Jendrusch EM, and Knepel W.** Characterization of a novel calcium response element in the glucagon gene. *J Biol Chem* 274: 5851–5860, 1999.
18. **Ghosh S, Watanabe RM, Valle TT, Hauser ER, Magnuson VL, Langefeld CD, Ally DS, Mohlke KL, Silander K, Kohtamaki K, Chines P, Balow J Jr, Birznieks G, Chang J, Eldridge W, Erdos MR, Karanjawala ZE, Knapp JL, Kudelko K, Martin C, Morales-Mena A, Musick A, Musick T, Pfahl C, Porter R, and Rayman JB.** The

- Finland-United States investigation of non-insulin-dependent diabetes mellitus genetics (FUSION) study. I. An autosomal genome scan for genes that predispose to type 2 diabetes. *Am J Hum Genet* 67: 1174–1185, 2000.
19. **Horsley V and Pavlath GK.** NFAT: ubiquitous regulator of cell differentiation and adaptation. *J Cell Biol* 156: 771–774, 2002.
 20. **Jacobs KB, Gray-McGuire C, Cartier KC, and Elston RC.** Genome-wide linkage scan for genes affecting longitudinal trends in systolic blood pressure. *BMC Genet* 4, Suppl 1: S82, 2003.
 21. **Ji L, Malecki M, Warram JH, Yang Y, Rich SS, and Krolewski AS.** New susceptibility locus for NIDDM is localized to human chromosome 20q. *Diabetes* 46: 876–881, 1997.
 22. **Klupa T, Malecki MT, Pezolesi M, Ji L, Curtis S, Langefeld CD, Rich SS, Warram JH, and Krolewski AS.** Further evidence for a susceptibility locus for type 2 diabetes on chromosome 20q13.1-q132. *Diabetes* 49: 2212–2216, 2000.
 23. **Koenig W, Sund M, Frohlich M, Fischer HG, Lowel H, Doring A, Hutchinson WL, and Pepys MB.** C-Reactive protein, a sensitive marker of inflammation, predicts future risk of coronary heart disease in initially healthy middle-aged men: results from the MONICA (monitoring trends and determinants in cardiovascular disease) Augsburg cohort study, 1984 to 1992. *Circulation* 99: 237–242, 1999.
 24. **Lawrence MC, Bhatt HS, and Easom RA.** NFAT regulates insulin gene promoter activity in response to synergistic pathways induced by glucose and glucagon-like peptide-1. *Diabetes* 51: 691–698, 2002.
 25. **Lee JH, Reed DR, Li WD, Xu W, Joo EJ, Kilker RL, Nanthakumar E, North M, Sakul H, Bell C, and Price RA.** Genome scan for human obesity and linkage to markers in 20q13. *Am J Hum Genet* 64: 196–209, 1999.
 26. **Lembertas AV, Perusse L, Chagnon YC, Fislser JS, Warden CH, Purcell-Huynh DA, Dionne FT, Gagnon J, Nadeau A, Lusic AJ, and Bouchard C.** Identification of an obesity quantitative trait locus on mouse chromosome 2 and evidence of linkage to body fat and insulin on the human homologous region 20q. *J Clin Invest* 100: 1240–1247, 1997.
 27. **Luo TH, Zhao Y, Li G, Yuan WT, Zhao JJ, Chen JL, Huang W, and Luo M.** A genome-wide search for type II diabetes susceptibility genes in Chinese Hans. *Diabetologia* 44: 501–506, 2001.
 28. **McCaffrey PG, Luo C, Kerppola TK, Jain J, Badalian TM, Ho AM, Burgeon E, Lane WS, Lambert JN, Curran T, Verdine GL, Rao A, and Hogan PG.** Isolation of the cyclosporin-sensitive T cell transcription factor NFATp. *Science* 262: 750–754, 1993.
 29. **Meier-Ewert HK, Ridker PM, Rifai N, Price N, Dinges DF, and Mullington JM.** Absence of diurnal variation of C-reactive protein concentrations in healthy human subjects. *Clin Chem* 47: 426–430, 2001.
 30. **Mori Y, Otabe S, Dina C, Yasuda K, Populaire C, Lecoeur C, Vatin V, Durand E, Hara K, Okada T, Tobe K, Boutin P, Kadowaki T, and Froguel P.** Genome-wide search for type 2 diabetes in Japanese affected sib-pairs confirms susceptibility genes on 3q, 15q, and 20q and identifies two new candidate Loci on 7p and 11p. *Diabetes* 51: 1247–1255, 2002.
 31. **Norman RA, Tataranni PA, Pratley R, Thompson DB, Hanson RL, Prochazka M, Baier L, Ehm MG, Sakul H, Foroud T, Garvey WT, Burns D, Knowler WC, Bennett PH, Bogardus C, and Ravussin E.** Autosomal genomic scan for loci linked to obesity and energy metabolism in Pima Indians. *Am J Hum Genet* 62: 659–668, 1998.
 32. **Pankow JS, Folsom AR, Cushman M, Borecki IB, Hopkins PN, Eckfeldt JH, and Tracy RP.** Familial and genetic determinants of systemic markers of inflammation: the NHLBI family heart study. *Atherosclerosis* 154: 681–689, 2001.
 33. **Peacock JM, Arnett DK, Atwood LD, Myers RH, Coon H, Rich SS, Province MA, and Heiss G.** Genome scan for quantitative trait loci linked to high-density lipoprotein cholesterol: the NHLBI family heart study. *Arterioscler Thromb Vasc Biol* 21: 1823–1828, 2001.
 34. **Pearson TA, Mensah GA, Alexander RW, Anderson JL, Cannon RO III, Criqui M, Fadl YY, Fortmann SP, Hong Y, Myers GL, Rifai N, Smith SC Jr, Taubert K, Tracy RP, and Vinicor F.** Markers of inflammation and cardiovascular disease: application to clinical and public health practice: a statement for healthcare professionals from the Centers for Disease Control and Prevention and the American Heart Association. *Circulation* 107: 499–511, 2003.
 35. **Permutt MA, Wasson JC, Suarez BK, Lin J, Thomas J, Meyer J, Lewitzky S, Rennich JS, Parker A, DuPrat L, Maruti S, Chayen S, and Glaser B.** A genome scan for type 2 diabetes susceptibility loci in a genetically isolated population. *Diabetes* 50: 681–685, 2001.
 36. **Ramji DP and Foka P.** CCAAT/enhancer-binding proteins: structure, function and regulation. *Biochem J* 365: 561–575, 2002.
 37. **Rao A, Luo C, and Hogan PG.** Transcription factors of the NFAT family: regulation and function. *Annu Rev Immunol* 15: 707–747, 1997.
 38. **Rice T, Borecki IB, Bouchard C, and Rao DC.** Commingling analysis of regional fat distribution measures: the Quebec family study. *Int J Obes Relat Metab Disord* 16: 831–844, 1992.
 39. **Ridker PM, Cushman M, Stampfer MJ, Tracy RP, and Hennekens CH.** Plasma concentration of C-reactive protein and risk of developing peripheral vascular disease. *Circulation* 97: 425–428, 1998.
 40. **Ridker PM, Rifai N, Rose L, Buring JE, and Cook NR.** Comparison of C-reactive protein and low-density lipoprotein cholesterol levels in the prediction of first cardiovascular events. *N Engl J Med* 347: 1557–1565, 2002.
 41. **SAGE.** *Statistical Analysis for Genetic Epidemiology* (computer program package). Cork, Ireland: Statistical Solutions, 2002.
 42. **Sesso HD, Buring JE, Rifai N, Blake GJ, Gaziano JM, and Ridker PM.** C-reactive protein and the risk of developing hypertension. *JAMA* 290: 2945–2951, 2003.
 43. **Soro A, Pajukanta P, Lilja HE, Ylitalo K, Hiekkalinna T, Perola M, Cantor RM, Viikari JS, Taskinen MR, and Peltonen L.** Genome scans provide evidence for low-HDL-C loci on chromosomes 8q23, 16q24.1–242, and 20q1311 in Finnish families. *Am J Hum Genet* 70: 1333–1340, 2002.
 44. **Stoffel M, Le Beau MM, Espinosa R III, Bohlander SF, Le Paslier D, Cohen D, Xiang KS, Cox NJ, Fajans SS, and Bell CI.** A yeast artificial chromosome-based map of the region of chromosome 20 containing the diabetes-susceptibility gene, MODY1, and a myeloid leukemia related gene. *Proc Natl Acad Sci USA* 93: 3937–3941, 1996.
 45. **Szmitko PE, Wang CH, Weisel RD, de Almeida JR, Anderson TJ, and Verma S.** New markers of inflammation and endothelial cell activation: part I. *Circulation* 108: 1917–1923, 2003.
 46. **Vatay A, Bene L, Kovacs A, Prohaszka Z, Szalai C, Romics L, Fekete B, Karadi I, and Fust G.** Relationship between the tumor necrosis factor alpha polymorphism and the serum C-reactive protein levels in inflammatory bowel disease. *Immunogenetics* 55: 247–252, 2003.
 47. **Verma S, Szmitko PE, and Yeh ET.** C-reactive protein: structure affects function. *Circulation* 109: 1914–1917, 2004.
 48. **Vickers MA, Green FR, Terry C, Mayosi BM, Julier C, Lathrop M, Ratcliffe PJ, Watkins HC, and Keavney B.** Genotype at a promoter polymorphism of the interleukin-6 gene is associated with baseline levels of plasma C-reactive protein. *Cardiovasc Res* 53: 1029–1034, 2002.
 49. **Volanakis JE.** Human C-reactive protein: expression, structure, and function. *Mol Immunol* 38: 189–197, 2001.
 50. **Yudkin JS, Stehouwer CD, Emeis JJ, and Coppack SW.** C-reactive protein in healthy subjects: associations with obesity, insulin resistance, and endothelial dysfunction: a potential role for cytokines originating from adipose tissue? *Arterioscler Thromb Vasc Biol* 19: 972–978, 1999.
 51. **Zouali H, Hani EH, Philippi A, Vionnet N, Beckmann JS, Demenais F, and Froguel P.** A susceptibility locus for early-onset non-insulin dependent (type 2) diabetes mellitus maps to chromosome 20q, proximal to the phosphoenolpyruvate carboxykinase gene. *Hum Mol Genet* 6: 1401–1408, 1997.