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Pro-Inflammatory Interleukin-1 Genotypes Potentiate the Risk of Coronary Artery Disease and Cardiovascular Events Mediated by Oxidized Phospholipids and Lipoprotein (a)

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Abstract

Objective—To assess the influence of pro-inflammatory IL-1 genotype status on the risk of CAD, defined as >50% diameter stenosis, and cardiovascular events mediated by OxPL and Lp(a).

Background—Oxidized phospholipids (OxPL) are pro-inflammatory, circulate on lipoprotein (a) [Lp(a)] and mediate coronary artery disease (CAD). Genetic variations in the interleukin-1 (IL-1) region are associated with increased inflammatory mediators.

Methods—IL-1 genotypes, OxPL on apolipoprotein B-100 (OxPL/apoB) and Lp(a) levels were measured in 499 patients undergoing coronary angiography. The composite genotype termed $IL-1(+)$ was defined by three single nucleotide polymorphisms (SNPs) in the IL-1 gene cluster associated with higher levels of pro-inflammatory cytokines. All other IL-1 genotypes were termed IL- $1(-)$.

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Results—Among IL-1(+) patients, the highest quartile of OxPL/apoB was significantly associated with a higher risk of CAD compared to the lowest quartile (OR 2.84, $P=0.001$). This effect was accentuated in patients 60 years old (OR 7.03, P<0.001). In IL-1(−) patients, OxPL/ apoB levels showed no association with CAD. The interaction was significant for OxPL/apoB (OR 1.99, P=0.004) and Lp(a) (OR 1.96, P<0.001) in IL-1(+) versus IL-1(-) groups for patients 60 years old but not for patients >60 years old. In IL-1(+) patients ≤ 60 years old, after adjusting for established risk factors, high sensitivity C-reactive protein and $Lp(a)$, OxPL/apoB remained an independent predictor of CAD. IL-1(+) patients above the median $OxPL/apoB$ presented to the cardiac catheterization laboratory a mean of 3.9 years earlier $(P=0.002)$ and had worse 4-year event-free survival (death, MI, stroke, and revascularization) compared to other groups (P=0.006).

Conclusion—Our study suggests that IL-1 genotype status can stratify population risk for CAD and cardiovascular events mediated by OxPL. These data suggest a clinically-relevant biological link between pro-inflammatory IL-1 genotypes, oxidation of phospholipids, Lp(a) and genetic predisposition to CAD and cardiovascular events.

Keywords

lipoproteins; oxidation; atherosclerosis; lipoprotein (a); oxidized phospholipids; IL-1; polymorphism; haplotype; inflammation; genetic risk stratification

INTRODUCTION

The presence of chronic arterial inflammation in response to atherogenic stimuli provides a framework in understanding the development and destabilization of atherosclerotic plaques. Oxidized lipids play a central role in mediating a variety of immune, pro-inflammatory and plaque destabilizing processes that further amplify inflammatory responses(1). Underlying this inflammatory cascade is the production and secretion of cytokines, growth factors and metalloproteinases, such as interleukin-1 (IL-1), tumor necrosis factor α and C-reactive protein (CRP)(2). Genetic variations in the IL-1 gene family (chromosome 2q13 region), which include pro-inflammatory cytokines IL-1α, IL-1β and the anti-inflammatory IL-1 receptor antagonist (IL-1Ra)(3–5) are commonly found in the human population, affect proinflammatory gene regulation(6) and have been associated with elevated levels of proinflammatory mediators $(7-10)$. The interplay of various single nucleotide polymorphisms within this IL-1 family determines the overall net effect on pro- or anti-inflammatory responses.

The majority of published studies have shown an association of IL-1 and cardiovascular disease, including early myocardial infarction/acute coronary syndromes (8,11–16) coronary artery disease (CAD)(17–20), acute ischemic stroke(21–23), restenosis following coronary stenting(24) and venous thrombosis(25). The Canakinumab Anti-inflammatory Thrombosis Outcomes Study (CANTOS) will test the hypothesis that treating patients with persistent elevation of CRP post myocardial infarction with a human monoclonal antibody that neutralizes IL-1β antibody will reduce cardiovascular events(26).

Oxidized phospholipids (OxPL) are pro-inflammatory(27), mediate atherothrombosis and are abundant in pathologically-defined human vulnerable plaques(28). Plasma levels of

specific OxPL on apolipoprotein B-100 (apoB) particles (OxPL/apoB) are elevated in patients with coronary, carotid and peripheral artery disease(29), as well as in acute coronary syndromes(30), and following percutaneous coronary intervention(31). Importantly, they predict the occurrence of cardiac death, myocardial infarction and stroke in unselected populations(32–34). Additionally, they reclassify up to one third of patients in intermediate Framingham risk categories into either higher or lower categories(33). In human plasma, OxPL are preferentially carried by $Lp(a)$ lipoprotein (a) $[Lp(a)]$, compared to other apoB-100 particles (reviewed in Taleb et al (35)). OxPL are also covalently bound by plasminogen, but early data suggest different pathophysiological implications when OxPL are on Lp(a) versus plasminogen (36).

Since OxPL mediate pro-inflammatory responses on endothelial cells and monocytes/ macrophages(27), it is possible that the risk they confer on atherothrombosis is potentiated by genetic predisposition to inflammation. In the present study, we hypothesized that the risk of CAD conferred by OxPL/apoB and Lp(a) may be influenced by IL-1 genotypes known to be associated with enhanced inflammatory responses.

METHODS (A full description of the Methods is available in the

Supplement)

Study design

The study was prospectively designed to test the association of CAD with specific IL-1 genotype groups known to be associated with higher inflammatory responses. The study design has been described previously in detail(37). Briefly, 504 eligible, consecutive patients undergoing clinically indicated coronary angiography were recruited. We focused our analyses on angiographically significant disease defined as diameter stenosis (DS) >50%. Two patients had incomplete OxPL/apoB data and 3 patients incomplete IL-1 data, therefore 499 patients were available for the present analysis. Four hundred sixty-six patients (92.5%) followed for up of 4.0 years (interquartile range, 3.9–4.2 years)]. The follow-up events consisted of 20 deaths (6 cardiac), 14 myocardial infarctions, 26 coronary revascularizations (15 percutaneous intervention only, 9 coronary artery bypass surgery only, and 2 with both), and 10 strokes.

Genetic analyses

Single nucleotide polymorphisms (SNPs) were genotyped at two loci in the gene for IL-1β, IL1B(-511; C>T; $rs16944$) and IL1B(+3954; C>T; $rs1143634$); and at one locus in the gene for IL-1α, IL1A (+4845; G>T; rs17561)(38).

IL-1 composite genotype patterns used for association with biochemical and clinical parameters

We designed the study to evaluate the relationship between CAD and IL-1 genotypes that are associated with differential expression of interleukin-1β (IL-1β). Four single-nucleotide polymorphisms (SNPs) in the promoter region of IL1B have been shown to be functional at the molecular level and operate in haplotype context to alter transcriptional activity of IL-1β(6). The functional IL1B SNPs define four predominant haplotypes that as pairs

observed together account for significantly different clinical levels of IL-1β protein in tissue fluid samples(10). All possible composite genotype combinations of the 3 SNPs used in the study provided an efficient tagging of the composite genotypes resulting from combinations of the functional IL1B promoter haplotypes that define differential expression of IL-1β protein(10). Table 1 shows the composite genotypes in this study that defined the $IL-1(+)$ group, which are associated with over-expression of IL-1 β , and the IL-1(−) group, which are the composite genotypes that have not been associated with over-expression of IL-1β. The IL-1(+) and IL-1(−) groups were defined and published (Francis S.E., Crossman D.C., Duff G.W., Kornman K. S., Stephenson K. 2003. Diagnostics for cardiovascular disorders. United States Patent # 6,524,795; Filed November 1, 1999; granted February 25, 2003) prior to data analysis.

RESULTS

Baseline Characteristics of the Study Group

Table 2 displays the baseline characteristics of the entire study group and of the IL-1(+) and IL-1(−) groups. IL-1(+) patients represented 59.9% of the population. There were no significant differences in any parameters between IL-1(+) and IL-1(-) patients, including extent of CAD, except a trend towards more previous myocardial infarction (18% vs. 12%, P=0.08) and higher hsCRP (3.1 mg/L vs. 2.3 mg/L, P=0.057) in the IL-1(+) patients. IL-1 status was not different between groups in the extent of CAD (no disease, mild disease, 1-, 2- and 3-vessel CAD) when analyzed by age 60 years old (P=0.88) and >60 years old (P=0.36). Similar results were obtained when IL-1 status was evaluated as $>50\%$ diameter stenosis (DS) and analyzed by age ≤ 60 years old (P=0.51) and >60 years old (P=0.47).

CAD Risk of OxPL is Mediated by IL-1 Genetic Differences

Odds ratios (OR) for CAD in each quartile of OxPL/apoB were calculated in all patients, in IL-1(+) and IL-1(-) patients, and further analyzed by age (all ages, 60 years old and >60 years old). In the entire cohort, a significant relationship was present between OxPL/apoB and CAD (>50% DS): the OR was 1.96 (95% confidence interval (CI), 1.18–3.26, P=0.009) for fourth quartile compared to first quartile (Table 3), and the OR for trend 1.25 (1.06–1.46, P=0.007].

Analyzing patients by genotype, a significant association was present between increasing OxPL/apoB levels and risk for CAD in IL-1(+) patients [OR 2.84 (1.45–5.55, P=0.001) for fourth quartile compared to first quartile], whereas no significant relationship was present in IL-1(−) patients (Table 3). The genotype effect was strongly accentuated in IL-1(+) patients ≤60 years old (OR 7.03 (2.50–19.77, P<0.001) but not in IL-1(−) patients ≤60 years old (OR 0.80 (0.26–2.49, P=0.71). In patients >60 years old, the association between OxPL/apoB levels and risk for CAD was not significant in either IL-1(+) or IL-1(−) patients.

Similar to the OxPL/apoB results, the association between $Lp(a)$ and risk for CAD was observed primarily in IL-1(+) patients (Table 4), with the strongest genotype effect present in patients 60 years of age (OR 9.00 (3.00–27.03, P<0.001).

Interaction tests were performed comparing IL-1(+) vs. IL-1(−) patients. P-values for the interaction of OxPL/apoB were P=0.007 for IL-1(+) vs. IL-1(-) patients 60 years of age and P=0.70 for IL-1(+) vs. IL-1(−) patients >60 years of age. P-values for the interaction of Lp(a) were P=0.019 for IL-1(+) vs. IL-1(-) patients 60 years of age and P=0.77 for IL-1(+) vs. IL-1(−) patients >60 years of age.

Multivariable Analysis of CAD Risk in the Different Genetic Strata

Multivariate logistic regression analysis was performed to adjust for factors known to affect risk of CAD. Figure 1 shows ORs for sex, OxPL/apoB, hsCRP, current smoking, LDL-C, hypertension, triglycerides, Lp(a), and HDL-C when all are included in a single logistic binary regression model. In patients 60 years old and IL-1(+), $OxPL/apoB$ (log2), male sex and hsCRP ($log2$) were independent predictors of CAD, whereas $Lp(a)$ was not a significant predictor (Figure 1A). The association of OxPL/apoB [(OR 1.83 (1.10–3.05, P=0.02] to CAD remained similar without hsCRP in the model. When the 44 patients with myocardial infarction within 60 days prior to coronary angiography were excluded, the data remained qualitatively similar, except that hsCRP was no longer a predictor of CAD (OR 1.23 (0.89– 1.68, P=0.21). Baseline hsCRP levels in these patients were significantly elevated compared to patients without myocardial infarction, as described previously (33). In patients 60 years old and IL-1(−), male sex, LDL-C, and hypertension were independent predictors (Figure 1B).

In patients >60 years old and IL-1(+), male sex and HDL-C were independent predictors of CAD, but not OxPL/apoB (Figure 2A). In patients >60 years old and IL-1(+), male sex, and hypertension were associated with higher risk (Figure 2B).

To further explore further the relationship between $OxPL/apoB$ or $Lp(a)$ levels and IL-1 genotype relative to risk for CAD, we stratified patients by IL-1 genotype and developed regression models to assess the relationship of OxPL/apoB and Lp(a) levels to CAD risk. The relationship of the OR values for CAD is expressed as function of the magnitude of differences in OxPL/apoB and Lp(a) levels in IL-1(+) and IL-1(−) patients (Figure 3). The OR for CAD was highly sensitive to differences in levels of both OxPL/apoB and Lp(a) in IL-1(+) patients, but no association was present in IL-1(−) patients.

IL-1 Genotype Effect on OxPL Risk for CAD and C-Reactive Protein Levels

Since some of the IL-1 gene variations included in the genetic patterns used in this study have been previously associated with elevated CRP (7,10) we evaluated whether the IL-1 genotype influence on the OxPL association with CAD was influenced by hsCRP levels. The relationship of OxPL/apoB to CAD in IL-1 (+) individuals 60 years of age was analyzed in the multivariate logistic regression framework for patients with hsCRP above and below the median hsCRP level in this study population (2.86 mg/L). The OR for the OXPL/apoB association with CAD in IL-1(+) patients with hsCRP > 2.86 mg/L was 3.36 $(1.21-9.40, P=0.02]$ and in those with hsCRP <2.86 mg/L the OR was 1.43 (0.62-3.31, P=0.40). Removing the 44 patients with recent MI yielded similar results, with an OR of 4.57 (CI 1.06–19.67, P=0.042] for the OxPL/apoB association with CAD in IL-1(+) patients with hsCRP above the median and 1.21 (CI 0.50–2.90, P=0.68] for those below the median.

Relationship of IL-1 Genotype to Age at Presentation to the Cardiac Catheterization Laboratory

Having established the relationship of OxPL/apoB and Lp(a) with CAD in IL-1(+) but not IL-1(−) individuals, particularly those at a younger age, we evaluated whether age at the time of cardiac catheterization was related to IL-1 composite genotype. IL-1(+) patients above the median of OxPL/apoB presented to the cardiac catheterization laboratory a mean of 3.9 years younger than IL-1(−) patients (58.0 vs. 61.9, P=0.006). Similarly, IL-1(+) patients above the median of $Lp(a)$ presented a mean of 3.5 years younger than IL-1(−) patients (58.8 vs. 62.1, P=0.019). In contrast, there was no significant IL-1 genotype effect on the age at presentation to the cardiac catheterization laboratory for patients below the median of OxPL/apoB (58.9 vs. 60.7, P=0.18) or Lp(a) (58.7 vs. 59.9, P=0.40).

Relationship of IL-1 Genotype to CAD events

In the overall group, cardiovascular events were not significantly different between $IL-1(+)$ and IL-1(−) patients (p=0.56). However, Kaplan-Meier curves revealed that IL-1(+) patients with OxPL/apoB above the median had the worst 4-year event-free survival (death, MI, stroke, revascularization) ($P=0.002$ compared to other 3 groups, Figure 4A). The p-value among 4 groups for death was $P=0.069$ and for death/MI P=0.016. The interaction test for IL-1 group by OxPL/apoB group was P=0.002 for event-free survival. For $Lp(a)$, IL-1(+) patients with $Lp(a)$ above the median exhibited worst 4-year event-free survival (P=0.034 compared to other 3 groups, Figure 4B). The p-value among 4 groups for death was $P=0.054$ and for death/MI P=0.011. The interaction test for IL-1 group by $Lp(a)$ group was P=0.014 for event-free survival. There were not enough events to analyze by age cutoffs.

DISCUSSION

This study demonstrates that genetic differences in the IL-1 gene cluster, known to be associated with inflammatory responsiveness, strongly influence the presence of angiographically-determined CAD and CAD events mediated by OxPL/apoB and Lp(a). Patients with pro-inflammatory $IL-1(+)$ genotypes were at a continuum of risk for the presence of CAD whereas patients with IL-1(−) genotypes seemed to be insensitive to risk for CAD mediated by increasing OxPL/apoB or Lp(a) levels. These findings were accentuated in subjects with elevated hsCRP levels. This study provides evidence of a biological link between genetic predisposition to inflammation, oxidation of phospholipids and genetically-mediated elevated $Lp(a)$ levels. It also highlights a possible effect of specific genetic factors in accelerating atherogenesis, development of CAD on angiography and mediation of cardiovascular events.

The genes encoding the pro-inflammatory cytokines interleukin-1 alpha (IL-1α) and interleukin-1 beta (IL-1β) are among the first to be activated in the course of an inflammatory response, and play a major role in both acute and chronic inflammation(4). Plasma levels of IL-1α and IL-1β show reproducible inter-individual differences. Furthermore, IL-1 gene patterns that are highly prevalent in the population, 60% of Caucasians as noted in this study, have been associated with variations in the levels or expression of IL-1 α (39), IL-1 β (8) and the endogenous antagonist, IL-1 receptor antagonist

(IL-1Ra)(40). The IL-1 composite genotypes used in this study were derived from combinations of the predominant functional haplotypes in the promoter region of the gene for IL-1β (6) and other SNPs in the IL-1α and β genes that have been associated with proinflammatory responses(10,41). IL-1β haplotypes exhibit allele-specific differences in nuclear protein binding and transcription rates(6). $IL-1(+)$ genotypes are associated with enhanced generation of IL-1 β when mononuclear cells are stimulated(8) and have been associated with higher IL-1 β levels in plasma(40). Some of the three composite genotypes that comprise the $IL-1(+)$ pattern for this study have been associated with significantly elevated hsCRP levels in plasma compared with $IL-1(-)$ pattern(7,8,10,42,43). It should be noted that although the IL-1 genotype association with elevated IL-1β expression is also significant in gastric mucosa, the genotypes associated with elevated expression appear to be different from those reported for peripheral blood mononuclear cells(44,45).

L-1Ra is an important component of the net IL-1 biological activity of this system, as signaled through the IL-1 receptor type 1, and has been implicated in atherosclerotic cardiovascular diseases(3). Variants in the gene for IL-1Ra (IL1RN) have been associated with lower expression and circulating levels of IL-1Ra(9,46,47)) and with cardiovascular disease outcomes in some but not all studies(14,20,48). Several variants in IL1RN and other genes in the IL-1 cluster on chromosome 2q13-14 are in linkage disequilibrium with the specific IL1A and IL1B markers used in this study. For example in a population cohort of 839 unrelated Caucasians who tested positive for the IL-1 genotype patterns used in the current study, 64.5% were also homozygous for the T allele of IL1RN (+2018; rs419598) compared to 35.0% of those who tested negative (data not shown). Future studies with larger data sets may allow the analysis of contributions by other variants in the IL-1 region, in light of the strong linkage disequilibrium.

Vascular wall cells, such as endothelial cells and smooth muscle cells, as well as macrophages and monocytes can produce IL-1β and IL-1Ra and these cytokines are also present in human atherosclerotic lesions(3,17,19,49). It was shown that IL-1β promoter haplotype pairs are associated with higher levels of $IL-1\beta$ in plasma and from stimulated peripheral blood monocytes from patients, as well as elevated levels of CRP(10). In addition, the IL-1(+) genotype patterns used in the current study tag haplotypes that include the T allele of IL1A(-889; rs1800587), which has been shown to alter transcription factor binding sites in the IL1A gene (50) and was associated with increased levels of IL-1α protein in human gingival fluid samples (51). Transgenic mouse models with variations in IL-1 genotypes further support the causal role of IL-1 in atherogenesis(reviewed in (3,26)). In IL-1 receptor antagonist knockout mice, unopposed IL-1 biological activity resulted in spontaneous arterial inflammation with massive infiltration of macrophages and CD4+, interferon γ + T-cells at branch points in mid and large arteries(52,53). Decreases in IL-1 biological activity in apoE-deficient mice decreased the rate and extent of atherosclerosis formation(54,55). In contrast, increases in IL-1 activity increased atherosclerotic lesion size with more macrophages within lesions(56). Furthermore, anakinra, a recombinant form of human IL-1Ra improves vascular function in patients with rheumatoid arthritis(57).

In experimental studies, oxidized phospholipids interact with cells in the vessel wall and promote pro-inflammatory and pro-atherogenic properties. For example, in a large-scale

gene expression analysis involving 9,600 cDNA targets, IL-1β was one of the differentially over-expressed genes when macrophages were loaded with OxLDL, which is known to be enriched in OxPL detected by E06, compared to acetylated-LDL loading(58). OxLDL stimulation of coronary artery smooth muscle cells also led to significant over-expression of IL-1β(59). More specifically stimulation of endothelial cells and macrophages with OxPL leads to prominent expression of IL-1 α and IL-1 β (60,61), and in turn, stimulation of endothelial cells with IL-1α leads to the generation of such OxPL(62). Thus, it is reasonable to hypothesize that the polymorphisms of the IL-1 family might influence the expression of inflammatory responses to OxPL. Indeed, supporting data shows that IL-1 genetic variations have been associated with acute coronary events, CAD and stroke(11–16,20– 23,25,57,63,64).

In clinical studies elevated OxPL/apoB levels predict new CVD events(29,33,35,65). This study has expanded our understanding of the underlying mechanisms behind this risk by showing that the enhanced risk of CAD and CAD events mediated by OxPL/apoB and Lp(a) is particularly potent in IL-1 $(+)$ patients. Interestingly, this risk of CAD persisted despite $Lp(a)$ in the model, suggesting that in certain patient populations, such as patients $\langle 60 \rangle$ years old, $OxPL/apoB$ may be a better predictor than $Lp(a)$. Patients with underlying genetic predisposition to inflammation and dyslipidemia have exposure to cardiovascular risk from birth, which may explain why IL-1(+) patients 60 years old with elevated $Lp(a)$ and $OxPL/$ apoB levels are at particularly elevated risk for premature CAD. Consistent with the role of life-long exposure to genetic predisposition to inflammation and genetically determined $Lp(a)$ levels, it was demonstrated in this study that IL-1(+) patients with $Lp(a)$ or OxPL/ apoB levels above the median presented for coronary angiography several years earlier than those in the lowest quartiles.

It is noteworthy that in this population, the IL-1 genotype effect on risk of CAD was more pronounced in patients above the median of hsCRP, a biomarker of inflammation generated secondary to cytokines such as IL-6 and IL-1. Similarly, the LPA gene contains an IL-6 response element(66) and patients with inflammatory disorders such as rheumatoid arthritis have elevated Lp(a) levels, which are reduced on treatment with the IL-6 receptor antagonist antibody to cilizumab $(67,68)$. The CANTOS trial will be instrumental in testing whether inhibition of inflammatory responses leads to a lower rate of cardiovascular events. The data from this study suggests that patients with the $IL-1(+)$ genotype and elevated OxPL/apoB and/or Lp(a) levels are a particularly high risk subset that may maximally benefit from therapies aimed at inhibiting IL-1β and IL-1α responses.

Limitations of this study include that patients were selected from a population referred for coronary angiography for clinical indications and thus the data may not be generalizable to broader populations. This study also included predominantly Caucasian patients whose IL-1 genotypes and genetic associations may differ in other ethnic groups and it will be important to study these associations in other populations.

In conclusion, this study demonstrates that the previously demonstrated contribution of OxPL/apoB and Lp(a) on angiographically documented CAD and CAD events is conditional on pro-inflammatory IL-1 genotypes. This novel paradigm links the etiology of

atherogenesis attributed to OxPL and Lp(a) from genetics to clinical expression of CAD. If confirmed and validated in prospective populations, these findings may facilitate our understanding of atherogenesis and provide enhanced tools for diagnosis and treatment of cardiovascular disease.

METHODS

Study design

The study design has been described previously in detail(1). Briefly, 504 eligible, consecutive patients (>97% Caucasian), age 18 to 75, undergoing clinically indicated coronary angiography who consented for the study were recruited between June and December 1998. The study was prospectively designed to test the association of CAD with specific IL-1 genotype groups known to be associated with higher inflammatory responses. Patients with prior coronary revascularization and diabetes mellitus were excluded to avoid potential enrichment with cases that may have confounding etiological factors. The angiographic analysis was previously described in detail(1). The extent of angiographically documented CAD was quantified as follows: normal coronary arteries (smooth, with either no stenosis or a stenosis of <10 percent of the luminal diameter), mild disease (10–50% diameter stenosis (DS) in one or more coronary arteries or their major branches), or one vessel, two-vessel, or three-vessel disease, defined as DS> 50% of the luminal diameter in one, two, or three coronary arteries or their major branches. We focused some of our analyses on angiographically significant disease defined as DS>50%. For some of the analyses (Tables 2 and 3 and figures 1–3), we compared patients with no or mild disease to obstructive disease. Two patients had incomplete OxPL/apoB data and 3 patients incomplete IL-1 data, therefore 499 patients were available for the present analysis.

Four hundred sixty-six patients (92.5%) were contacted by a follow-up questionnaire or by telephone in September 2002 [median follow-up of 4.0 years (interquartile range, 3.9–4.2 years)]. The remaining 38 patients either refused to participate in the follow-up (n=18) or could not be contacted $(n=20)$. The medical records of the patients who had an event were obtained and reviewed to ascertain the type of event or the cause of death. The follow-up events of these patients were described previously (2,3)and consisted of 20 deaths (6 cardiac), 14 myocardial infarctions, 26 coronary revascularizations (15 percutaneous intervention only, 9 coronary artery bypass surgery only, and 2 with both), and 10 strokes.

Laboratory analyses

Apolipoproteins B-100 and AI, Lp(a), total cholesterol, HDL cholesterol (HDL-C) and triglycerides were measured with commercially available kits. LDL cholesterol (LDL-C) was estimated using the Friedewald formula. High sensitivity CRP (hsCRP) (lower range 0.15 mg/L) was measured as previously described(1). The content of OxPL per apoB-100 particle ($OxPL/apoB$) and $Lp(a)$ were measured as previously described(1,4).

Genetic analyses

DNA was extracted and genotyping was performed at the Division of Genomic Medicine, University of Sheffield, UK. All genetic analyses were performed blinded to clinical and

angiographic data. Genotyping was performed by a 5′ nuclease assay (Taqman[™]; Hoffman-LaRoche, Inc.) based on the 5['] nuclease activity of Taq Polymerase and the detection by FRET of the cleavage of two probes, designed to match and hybridize to either allele copy during PCR. The probe and primer sequences and cycling conditions have been previously described(5). Single nucleotide polymorphisms (SNPs) were genotyped at two loci in the gene for IL-1β, IL1B (−511; C>T; rs16944) and IL1B(+3954; C>T; rs1143634); and at one locus in the gene for IL-1α, IL1A (+4845; G>T; rs17561)(6).

Approximately 20% of the samples were evaluated as duplicates, which were blinded to laboratory personnel to test reproducibility of the genotyping methods. There was 100% concordance between duplicate samples.

IL-1 composite genotype patterns used for association with biochemical and clinical parameters

We designed the study to evaluate the relationship between CAD and IL-1 genotypes that are associated with differential expression of interleukin-1β (IL-1β). Four single-nucleotide polymorphisms (SNPs) in the promoter region of IL1B have been shown to be functional at the molecular level and operate in haplotype context to alter transcriptional activity of IL-1β(7). The functional IL1B SNPs define four predominant haplotypes that as pairs observed together account for significantly different clinical levels of IL-1β protein in tissue fluid samples(8). All possible composite genotype combinations of the 3 SNPs used in the study provided an efficient tagging of the composite genotypes resulting from combinations of the functional IL1B promoter haplotypes that define differential expression of IL-1β protein(8). Table 1 shows the composite genotypes in this study that defined the $IL-1(+)$ group, which are associated with over-expression of IL-1 β , and the IL-1(−) group, which are the composite genotypes that have not been associated with over-expression of IL-1β. The IL-1(+) and IL-1(−) groups were defined and published (Francis S.E., Crossman D.C., Duff G.W., Kornman K. S., Stephenson K. 2003. Diagnostics for cardiovascular disorders. United States Patent # 6,524,795; Filed November 1, 1999; granted February 25, 2003) prior to data analysis.

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Figure 1. Multivariable analysis derived odds ratios for CAD associated with selected risk factors among patients ≤60 years old stratified by genotype

CI=confidence interval, LDL=low-density lipoprotein (per increase of 25 mg/dl), hsCRP=C-reactive protein (per doubling), OxPL/apoB (per doubling), Lp(a) (per doubling), HDL=high-density lipoprotein (per increase of 10 mg/dl), and triglycerides (per doubling).

Figure 2. Multivariable analysis derived odds ratios for CAD associated with selected risk factors among patients >60 years old stratified by genotype

CI=confidence interval, LDL=low-density lipoprotein (per increase of 25 mg/dl), hsCRP=C-reactive protein (per doubling), OxPL/apoB (per doubling), Lp(a) (per doubling), HDL=high-density lipoprotein (per increase of 10 mg/dl), and triglycerides (per doubling). Age is measured per decade. Current smoking was deleted as a factor for those >60 years old because of negligible sample size of smokers in this category.

Figure 3. Odds ratios (OR) (solid line) and 95% confidence intervals (dashed lines) for CAD were calculated in a logistic regression model

In this model, risk associated with an incremental increase of each risk factor ranging from 0 (i.e., an odds ratio of 1) to the value equal to the difference between the 75th and 25th percentiles of the risk factors. The analysis was performed on patients 60 years of age stratified as IL-1(+) or IL-1(-).

Event-free survival free period in years of death, MI, stroke and revascularization was plotted for 4 groups based on IL-1 genotype and OxPL/apoB (A) and Lp(a) (B) median split by the Kaplan-Meier method and compared with a log-rank test.

Table 1

Composite Genotypes Used in Study

T*indicates that the second allele in the genotype can be either a G or a T;

****indicates that the genotype at that locus can be GG, GT, TT

Table 2

Baseline Characteristics of the Study Group

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Table 3

Odds Ratios for CAD (>50% DS) According to Quartiles for Oxidized Phospholipid/ApoB in IL-1 Genotype Positive and IL-1 Genotype Negative Odds Ratios for CAD (>50% DS) According to Quartiles for Oxidized Phospholipid/ApoB in IL-1 Genotype Positive and IL-1 Genotype Negative Patients, According to All Ages, 60 years Old and 60 Years Old Patients, According to All Ages, ⁶⁰ years Old and ⁶⁰ Years Old

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Table 4

Odds Ratios for CAD (>50% DS) According to Quartiles for Lp(a) in IL-1 Genotype Positive and IL-1 Genotype Negative Patients, According to All Odds Ratios for CAD (>50% DS) According to Quartiles for Lp(a) in IL-1 Genotype Positive and IL-1 Genotype Negative Patients, According to All Ages, 60 years Old and 60 Years Old Ages, 60 years Old and 60 Years Old

