Does Elevated Plasma Fibrinogen Increase the Risk of Coronary Heart Disease?

Evidence from a Meta-Analysis of Genetic Association Studies

George Davey Smith, Roger Harbord, Julie Milton, Shah Ebrahim, Jonathan A.C. Sterne

Objective—The purpose of this study was to assess whether a genetic variant associated with higher fibrinogen levels is associated with increased coronary heart disease (CHD) risk, as a test of the causal influence of fibrinogen on CHD.

Methods and Results—We performed a meta-analysis of case-control and prospective studies of the G-455→A and C-148→T β-fibrinogen promoter region variants, in relation to CHD risk. The 19 studies found included 12,393 cases and 21,649 controls. Fibrinogen levels were robustly related to the genetic variants (mean increase per allele, 0.117 g/L; 95% CI, 0.091–0.142 g/L). However, the genetic variants were unrelated to CHD risk (odds ratio per allele, 0.976; 95% CI, 0.916–1.040). The predicted causal odds ratio for a 1 g/L higher plasma fibrinogen level, given the genetic variant–fibrinogen and genetic variant–CHD associations, was 0.81 (95% CI, 0.46–1.40).

Conclusions—Although imprecise, the predicted causal effect of fibrinogen on CHD is clearly different from the odds ratio of 1.8 (95% CI, 1.6–2.0) for an increase of 1 g/L derived from a meta-analysis of observational studies. This evidence suggests that lowering the fibrinogen level may not, in itself, reduce CHD risk.

Key Words: Mendelian randomization ■ fibrinogen ■ coronary heart disease

The status of plasma fibrinogen as a cardiovascular risk factor remains controversial.1−7 In prospective observational studies and case-control studies, fibrinogen level is predictive of coronary heart disease (CHD) risk, a meta-analysis reporting a relative risk of 1.8 (95% CI, 1.6–2.0) for the top to the bottom third of the fibrinogen distribution.8 However, existing atherosclerosis may increase fibrinogen levels, and, thus, reverse causation will lead fibrinogen to predict future CHD events. There is also substantial confounding, with higher fibrinogen levels being seen in several population subgroups known to have increased CHD risk, for example, cigarette smokers, people from less favorable socioeconomic backgrounds, nondrinkers, and people who engage in less leisure time activity.9 Certain members of the fibrate class of drugs, including clofibrate and bezafibrate, lower fibrinogen levels, and, if fibrinogen were causally related to CHD, should reduce CHD risk to a greater extent than predicted by their cholesterol lowering effect. This has not been seen in randomized, controlled trials.10,11 Thus, it is unclear whether fibrinogen is a causal factor for CHD or merely serves as a marker of both preexisting disease status and other causal factors.

Several authors have explicitly suggested that genetic polymorphisms related to differences in fibrinogen levels could be used to examine whether fibrinogen is a causal factor with respect to CHD.5,6,12 The association between CHD risk and a polymorphism related to increased circulating fibrinogen levels is not susceptible to reverse causation or confounding, because atherosclerosis will not change genetic make-up, nor is it likely that behavioral and socioeconomic confounding factors will be related to the distribution of the polymorphism in question. These properties, that have been referred to as those of “Mendelian randomisation,”13 mean that the association between a genetic polymorphism and a disease outcome provides robust evidence of the causal nature of the factor influenced by the polymorphism, such as circulating fibrinogen level in the present case. The sustained differences in fibrinogen level related to the polymorphism should translate into differences in CHD risk if there is a causal association between fibrinogen and CHD. In studies that relate the polymorphism to fibrinogen level and to CHD risk, if fibrinogen is a causal factor, the polymorphism should be related to CHD risk to the degree predicted by the joint associations of the polymorphism with fibrinogen level and of fibrinogen level with CHD risk.12,13 The most common polymorphism that has been studied in this regard is the G-455→A polymorphism in the promoter region of the β-fibrinogen gene. This polymorphism is consistently associated with differences in fibrinogen levels and, therefore, should be associated with CHD risk if fibrinogen is a causal...
factor. A second variant, C-148→T, is essentially in complete linkage disequilibrium with the G-455→A variant in European-origin and Indian subcontinent origin populations.14 We have, therefore, analyzed these 2 variants together.

Individual studies of the G-455→A polymorphism that have explicitly related this polymorphism to both fibrinogen levels and CHD risk as a test of the causal nature of the fibrinogen–CHD association5,6 have been grossly underpowered.15 For example, in a report of a case-control study provocatively titled “Elevated plasma fibrinogen. Cause or consequence of cardiovascular disease?”,6 a 1 g/L increase in fibrinogen level was associated with a relative risk of myocardial infarction (MI) of 1.45 (95% CI, 1.12–1.88), whereas the association between genotype and MI risk was essentially null. The authors interpreted these results as indicating that fibrinogen was not a cause of MI. However, the predicted risk according to genotype, given the observed associations of fibrinogen with MI and of genotype with fibrinogen, could not be reliably distinguished from the observed relative risk.13

Given the inadequate sample sizes of individual studies, we have performed a meta-analysis of the associations of this polymorphism with CHD risk, examining the polymorphism–CHD and polymorphism–fibrinogen associations and testing these against the expectation based on a causal link between fibrinogen and CHD.

Methods

Search Strategy for Identification of Studies

MEDLINE and EMBASE were searched for articles that might describe association studies of β-fibrinogen and cardiovascular diseases. The following keywords were used in the search: “genotype fibrinogen locus,” “beta gene,” “genotype,” “β-fibrinogen,” “β-fibrinogen gene,” “polymorphism (genetics),” “β-chain gene,” “polymorphisms,” “g-455-a,” “fibrinogen,” “fibrinogen gene,” “blood coagulation factors,” “cardiovascular diseases,” “heart disease,” “coronary disease,” “myocardial infarction,” “ischemia or isch- emia,” “atherosclerosis,” “455G>A,” “G-455-A,” “cardiovascular risk,” and “risk factors”. The search was rerun with C-148→T in place of G-455-A.

Studies were defined as eligible if they were case-control or prospective cohort studies relating fibrinogen polymorphisms (ascertained via genotyping) to CHD, including CHD, angina, MI, coronary atheroma, atherosclerosis, coronary artery disease, ischemic heart disease, and coronary stenosis. Family studies or studies of disease progression were excluded. The title and abstract of each article were scanned, and full article copies of potentially eligible studies or reviews that might contain references to such studies were retrieved. The reference lists of these articles were scanned for additional potentially eligible studies. Where necessary, articles were translated into English.

For each eligible study, we extracted (where available) details of the association between the genotype and end point of interest, genotype and intermediate phenotype (plasma fibrinogen), and intermediate phenotype and end point (CHD). We also recorded study design, case definition, whether cases were incident or prevalent, exclusion criteria, whether the study was restricted to patients with a particular disease and how controls were selected, variables used to adjust estimated associations, whether those doing the genotyping were blind to participants’ disease status, geographic location of the study, details of the gender, age, body mass index, smoking patterns, alcohol consumption of cases and controls, and whether subgroup analyses had been performed.

Because we have combined studies of 2 variants essentially in complete linkage disequilibrium, we used the terminology H1 (haplotype 1) to refer to the G allele of the G-455→A variant or the C allele for the C-148→T variant. H2 refers to the A and T alleles.

Where the numbers of cases and controls in the 3 categories of genotype (H1H1, H1H2, and H2H2) were reported, these were recorded and used for analyses. Studies that did not report all of the categories (because they combined H1H2 with H2H2) contributed only to the meta-analyses for their reported comparison. For all of the studies providing usable data, we derived the mean and SD of fibrinogen levels in cases and controls. All of the units were standardized to grams per liter. Where studies reported geometric means with associated CIs, means and SDs were derived on the assumption that plasma fibrinogen has a log-normal distribution.

A test for Hardy-Weinberg equilibrium was performed on the control group genotype data when this was provided in full, using an exact test. We meta-analyzed the mean difference in fibrinogen between H1H1 and H1H2 controls and also between H1H1 and H2H2 controls. We also analyzed the mean fibrinogen difference per H2 allele assuming a codominant mode of transmission by first fitting a per-allele model to the data from each study using variance-weighted least squares, in which the genotype was coded as 0 (H1H1), 1 (H1H2), or 2 (H2H2), and meta-analyzing the resulting slopes.

We conducted a meta-analysis of the genotype–CHD association corresponding with a codominant mode of transmission. This was derived from the log odds ratio and corresponding SE from a logistic regression analysis of the results from each study with the genotype coded as above. Both fixed-effect meta-analysis (inverse-variance method) and random-effects meta-analysis (Der Simonian and Laird method49) were used. As well as deriving tests for heterogeneity, we quantified the amount of heterogeneity in each meta-analysis using I² statistics.17 Funnel plots of effect size against its SE18 were examined visually for signs of asymmetry, and formal tests of small-study effects were performed using rank correlation19 and regression20 tests.

Results

Characteristics of Included Studies

Table 1 shows the study design, genotype information, and availability of plasma fibrinogen measurements for the 19 included studies.5–7,12,21–35 None of the genotype frequencies showed notable departure from Hardy-Weinberg equilibrium after allowing for the multiplicity of tests.

Association of β-Fibrinogen Genotypes With Plasma Fibrinogen

We examined the difference in mean plasma fibrinogen between genotypes in control participants. Thirteen of the 19 studies measured plasma fibrinogen. However, 4 of these5,25,32,34 did not present the results by genotype in controls in extractable form (we attempted to contact the authors but with limited success). Of the remaining 9 studies, 2 small studies6,27 presented plasma fibrinogen in H1H2 and H2H2 subjects combined, but these 2 studies contributed only 4% of the remaining 10,656 control subjects. Figure 1 shows the results for the 7 studies that presented extractable plasma fibrinogen data for each genotype. The results are homogeneous with the exception of 1 study,22 with only 1 H2H2 control subject, that gave results incompatible with the others, and in which all of the plasma fibrinogen results appeared anomalously high. If we exclude this anomalous study, compared with control subjects with H1H1 genotypes, mean fibrinogen levels are higher by 0.12 g/L (95% CI, 0.08–0.15 g/L) in H1H2 controls and by 0.24 g/L (95% CI, 0.16–0.31 g/L) in H2H2 controls. This gives evidence that the
β-fibrinogen gene is codominant, with the difference in mean plasma fibrinogen between those with H2H2 and H1H1 genotypes being twice that between H1H2 and H1H1 genotypes. By fitting such a per-allele model within each of the 6 homogeneous studies and meta-analyzing the results (I^2 = 0 so fixed-effect and random-effects models equivalent), we obtained a final estimate that each H2 allele gives a mean increase in plasma fibrinogen of 0.117 g/L (95% CI, 0.091–0.142 g/L). There was no indication of funnel plot asymmetry from visual inspection or formal tests (P = 0.71 by rank correlation test and P = 0.74 by regression test).

**Association of β-Fibrinogen Genotype With CHD**

In light of the above evidence that β-fibrinogen has a codominant effect on plasma fibrinogen levels, it was assumed that a “per-allele” model also applies to the association of β-fibrinogen genotype with cardiovascular disease, that is, that the odds ratios for comparison of H1H2 to H1H1 and

<table>
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<th>Study</th>
<th>Study Design</th>
<th>Cases</th>
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<th>Poly-morphism</th>
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<td>339</td>
<td>148</td>
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The total no. of cases and controls with genotype data in some studies are slightly lower than the total no. of cases and controls because of genotyping failure.

*Only combined H1H2+H2H2 numbers given.
†Plasma fibrinogen results presented with H1H2+H2H2 combined.
‡Only 1 H2H2 control so SD of plasma fibrinogen cannot be computed for this genotype.
H2H2 to H1H2 individuals are the same. Of the 19 studies, 16 combined H1H1 and H1H2 subjects in their results and, thus, cannot be included in this analysis. Results for the other 18 studies are presented in Figure 2. Nearly all of the studies are consistent with the null hypothesis that the polymorphism has no effect on CHD risk, with the possible exception of 2 studies,22,30 1 of which22 also gave anomalous results for the association with plasma fibrinogen. The other30 gives an association in the opposite direction from that which might be expected. As a sensitivity analysis, Table 2 shows the results of random-effects meta-analyses excluding 1 or both of these studies. There was no impression of asymmetry in the funnel plot, nor formal evidence of small study effects (P > 0.41 by rank correlation test and P = 0.93 by regression test, with all of the studies included). The 2 studies of the C-148→T variant produced a per-allele OR of 1.03 (95% CI, 0.97–1.10), whereas the 16 studies of the G-455→A variant produced an equivalent OR of 0.96 (95% CI, 0.89–1.04). There is no strong statistical evidence to suggest these are different (P = 0.27, permutation test).

Predicted Association of Plasma Fibrinogen With CHD From Mendelian Randomization

Table 2 shows the predicted OR for a 1 g/L increase in plasma fibrinogen, calculated assuming a linear-logistic relationship between plasma fibrinogen level and odds of CHD and that each H2 allele gives an increase in plasma fibrinogen of 0.117 g/L by raising the odds ratio per H2 allele to the power of 1/0.117. Allowing for the uncertainty in the association between genotype and plasma fibrinogen makes little difference to the width of the CIs (maximum increase in width of CIs for log odds ratios is 3.2%, in model 3), because the uncertainty in this estimate is small compared with the uncertainty in the association between genotype and CHD. The predicted odds ratio for a 1 g/L increase in plasma fibrinogen is 0.81 (95% CI, 0.46–1.40) for model 1, which includes all of the studies.

Discussion

In this meta-analysis, we demonstrate that a common variant in the promoter region of the β-fibrinogen gene is associated...
with a robust difference in circulating fibrinogen levels. If fibrinogen were a causal factor for CHD, the expectation would be that carriers of such a variant would be at increased risk of CHD. However, there is no strong evidence of any association between carriage of the variant and CHD risk, and when the joint associations of variant with fibrinogen and variant with CHD risk were combined to yield a predicted estimate of the causal influence of fibrinogen on CHD, the odds ratio was less than unity, although with relatively wide CIs. A meta-analysis of prospective observational studies of the association between fibrinogen and CHD found that an increase of 1.0 g/L in long-term usual mean fibrinogen was associated with a risk ratio of 1.8 (95% CI, 1.6–2.0). Comparing this with our predicted estimate from all studies of 0.81 (95% CI, 0.46–1.40) shows strong evidence that the estimates differ ($P=0.005$, 2-sample $z$-test).

It has been suggested that methods for reducing fibrinogen levels should be sought, because they may have the potential to reduce CHD risk. However, these data cast doubt on this proposition. This is in line with findings from randomized, controlled trials of those fibrates that reduce fibrinogen level but do not have a greater effect on CHD than that predicted by their cholesterol-lowering action. Furthermore, although CHD risk factors, such as cholesterol level, blood pressure, and smoking, are associated with CHD risk both within populations and between populations, the same is not consistently true for fibrinogen. Although 1 study within Europe suggests a positive ecological association between nephelometric fibrinogen levels and CHD rates, another study found higher fibrinogen levels in a low-CHD risk African country than in countries with much higher rates of CHD. Finally, 1 study finding a positive association between fibrinogen and CHD risk demonstrated that adjustment for a wide range of confounding factors essentially abolished this association.

One study carried out in China reported an order of magnitude greater effect of genotype on fibrinogen and a nominally significant association between genotype and CHD risk. Linkage disequilibrium between the G-455 $\rightarrow$ A and C-148 $\rightarrow$ T variants may be lower in this population. However, it is the C-148 $\rightarrow$ T variant that has been shown to be more directly associated with fibrinogen than the G-455 $\rightarrow$ A variant, and, thus, in a population where there is less linkage disequilibrium between the variants, the G-455 $\rightarrow$ A variant would be expected to be less strongly related to outcomes, rather than more strongly related. The small sample size of the Chinese study, or particular methodological issues, may have generated this markedly outlying finding. A study carried out in South Korea generated findings similar to those of the overall meta-analysis. More data from non-European origin populations would be of value, however.

Limitations of the “Mendelian randomization” approach illustrated in this article need to be considered. Confounding of the genotype–CHD association could occur if the genotype were in linkage disequilibrium with other genetic variants that influenced CHD risk through processes other than fibrinogen level. If this were the case, then the genotype would be expected to be related to other CHD risk factors, but the studies that examined this found it not to be the case. A second possibility is that the variant associated with fibrinogen has pleiotropic effects on other metabolic or physiological systems that influence CHD risk. Again, this would be expected to reveal itself through an association between the variant and other CHD risk factors. Such pleiotropic effects may, however, occur through mechanisms that have not been investigated in these studies.

Publication bias could influence evidence on genetic variant–disease associations, but this would be expected to lead to overestimates, rather than underestimates, of any effects. We found no evidence of an association between study size and the strength of either genotype–CHD or genotype–fibrinogen associations, although such tests have limited power when the number of studies is modest.

Canalization, in which there is compensation to altered gene expression during development, could occur such that elevated fibrinogen levels expressed throughout the developmental period may not have the same biological effects on the cardiovascular system as fibrinogen levels that become elevated during later stages of life. This proposition is difficult to test outside animal models, and we know of no evidence to either support or refute it.

Perhaps the most serious drawback to the Mendelian randomization approach applied in this article is the need for very large sample sizes. Even in this meta-analysis, which included 12,393 cases and 21,649 controls, CIs around the estimated association between plasma fibrinogen and CHD risk, given the joint associations of genetic variant and fibrinogen and genetic variant and CHD risk, were wide. We have estimated previously that 30,000 cases and 30,000 controls would be required to produce an appropriately precise estimate. Given this, the central effect estimate is the best available, and it suggests that there may be no causal association between fibrinogen and CHD risk.

References


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<thead>
<tr>
<th>Model</th>
<th>Odds Ratio per H2 Allele, Random-Effects Model (95% CI)</th>
<th>$I^2$ (% Variation Attributable to Heterogeneity)</th>
<th>Predicted Odds Ratio for a 1 g/L Increase in Plasma Fibrinogen (95% CI)</th>
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<td>(1) All studies</td>
<td>0.976 (0.916–1.040)</td>
<td>39%</td>
<td>0.81 (0.46–1.40)</td>
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<td>(2) Excluding Yu</td>
<td>0.995 (0.949–1.043)</td>
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<td>0.96 (0.63–1.44)</td>
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<td>(3) Excluding Ma</td>
<td>0.973 (0.920–1.028)</td>
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<td>(4) Excluding Yu and Ma</td>
<td>0.995 (0.954–1.038)</td>
<td>0%</td>
<td>0.96 (0.66–1.39)</td>
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</table>
Davey Smith et al  Elevated Plasma Fibrinogen and Coronary Heart Disease 2233


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