

Analysis of gene-environment interaction in coronary heart disease: fibrinogen polymorphisms as an example

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Several epidemiological studies have shown that an increase in fibrinogen levels is associated with the risk of cardiovascular disease. Recently, it has been demonstrated that the levels of fibrinogen can be genetically determined. Overall the studies show a strong association between two polymorphisms of the fibrinogen β -chain gene and fibrinogen plasma concentration. Few studies have, in contrast, found an association between such polymorphisms and the risk of ischemic vascular disease.

Rather than directly affecting the levels of proteins or the risk of disease, polymorphisms can amplify the effect of environmental or intermediate conditions on the final phenotype. The genetic control of fibrinogen has to be considered together with environmental factors: fibrinogen genotypes may interact with cigarette smoking, gender, physical activity, use of drugs and infections in determining the increase in fibrinogen levels and perhaps the risk of ischemic heart disease. Three examples are presented supporting the concept that, in multifactorial diseases, genetic variability influences the risk of disease by determining a different individual susceptibility to environmental risk factors.

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Fibrinogen and cardiovascular disease

Among the components of the coagulation system, high levels of fibrinogen have been strongly associated with occlusive vascular disorders¹⁻³.

A number of fibrinogen properties are relevant in the process that leads to thrombosis, such as its role as a substrate for fibrin formation, as a mediator of platelet aggregation^{4,5} and as a determinant of plasma viscosity⁶.

The first evidence of such association was provided in the early 80's by Meade et al.^{1,7} in the Northwick Park Heart Study. Long-term prospective studies followed these findings. Ernst and Resch⁸ published a meta-analysis of six of these studies on a total of 845 cases of coronary heart disease (CHD). Afterwards, several of these studies have reported additional follow-up results and many other studies have been performed. Danesh et al.⁹ reviewed them more recently in a meta-analysis: fibrinogen levels in the top third were associated with an odds ratio of 1.8 (95% confidence interval 1.6-2.0). Increased fibrinogen level also clusters with other risk factors¹⁰⁻¹². Furthermore, increased fibrinogen levels can be considered as one of the links between

these environmental factors and the risk of CHD.

However, more recently the study of genetic determinants has offered a new perspective in this complex scenario of interactions.

Genetic polymorphisms and plasma fibrinogen levels

Fibrinogen is a 340-kD dimeric glycoprotein; each dimer consists of three different polypeptide chains known as α , β and γ chains, linked by disulfide bonds. The three polypeptide chains are encoded by three different genes clustered within a 50 kb region located in the distal third of the long arm of chromosome 4q23-32^{13,14}.

All three genes have an interleukin (IL)-6 responsive element^{15,16} near to the site of the start of transcription. Fibrinogen levels arise following an acute phase response; it is therefore possible that changes in this region may affect the rate of transcription. *In vitro* studies have suggested that β -chain synthesis limits the rate of the production of mature fibrinogen¹⁷. As a consequence, most of the studies have focused on the β chain. Many polymorphisms have been

identified, however the two most studied were those detected by BclII and HaeIII restriction enzymes. Overall, the studies show a strong association between β -chain fibrinogen genotypes and its plasma concentrations¹⁸⁻²⁸. On the other hand, the relation between these polymorphisms and the risk of CHD is still debated.

BclII polymorphism of the β -fibrinogen gene. Several studies have reported a DNA variation of the β -fibrinogen gene, detected at the 3' region, by the BclII restriction enzyme (BclII polymorphism), as influencing the levels of fibrinogen. This is a biallelic polymorphism, with a frequency of the rare B2 allele of 0.18 in the general population.

The rare B2B2 genotype has been consistently associated with levels of fibrinogen 15-20% higher than B1B1 genotype^{19,22,28,29}. The involvement of BclII fibrinogen polymorphism in the risk of ischemic vascular disease has been confirmed by some studies, although others gave negative results³⁰.

-455 G/A polymorphism of the β -fibrinogen gene. The BclII polymorphism was found to be in linkage disequilibrium with the G/A sequence variation at position -455, detected in the promoter region, by the HaeIII restriction enzyme^{21,26}.

Due to its position in the β -fibrinogen gene, it is conceivable that this polymorphism may have an effect on transcription. It is, indeed, located in the promoter, close to responsive elements (IL-6 and the hepatocyte nuclear factor-1 elements)¹⁶. Therefore, this polymorphism has been selected for study by many investigators^{18,20-27,30-48}.

Among 22 publications between 1991 and 2000, all the studies^{22,23,26,27,35-48} but four³⁰⁻³³, are consistent with the finding that the A⁻⁴⁵⁵ allele, which is present in about 20% of the general population, is associated with increased levels of fibrinogen of about 0.30 g/l as compared with homozygotes for the G allele. On the contrary, only few studies have found an association between -455 G/A polymorphism and the risk of CHD^{32,39,44,46,47}. In particular, out of 13 studies in which the relation between -455 G/A polymorphism and the risk of CHD was evaluated, only 5 reported the presence of an association.

The inhomogeneity of the findings published suggests two types of considerations:

- the number of subjects included in the different studies is never sufficient to detect any rational association. Indeed, considering the results of the meta-analyses of fibrinogen, it can be assumed that an increase in 1 g/l of fibrinogen accounts for a relative risk of 1.8 for CHD. Nevertheless, homozygosity for the A⁻⁴⁵⁵ allele increases of about 0.30 g/l the levels of fibrinogen, which, assuming linearity in the logarithm of relative risk, corresponds to a relative risk of about 1.20. To have the power of 80% to detect such an increase, a case control study should recruit about 11 600 cases and a corre-

sponding number of controls. This size has never been reached in the studies published until now;

- since the effects of genetics on multifactorial diseases could not be expected to be strong by definition, it would be difficult to reveal it by studying CHD as a bulk of patients not further subtyped. Studying more homogeneous subgroups of patients can help to better define the role of genetics. This could be indeed, the case of patients with familial myocardial infarction or at young age or with very well defined clinical phenotypes. Moreover, rather than directly affecting the levels of proteins or the risk of disease, polymorphisms can amplify the effect of environmental or intermediate conditions on the final phenotype. Stressing gene-environment interactions can be finally a suitable approach to highlight the role of genetics.

Gene-environment interaction and changes in plasma fibrinogen levels

Individuals have different ability to maintain homeostasis and this can be due to genetic variations: an individual with a genetic predisposition might have a stronger response when exposed to a specific stimulus, which translates in the synthesis of higher levels of fibrinogen. As a consequence, he can have a greater thrombotic risk in respect to one who makes a moderate response to environmental stimuli (Fig. 1).

Fibrinogen is an acute phase protein and its levels rise in response to infections, inflammations and trauma⁴⁹, and to other factors such as hypertension, age, obesity, serum cholesterol level, hormonal changes and diabetes⁵⁰⁻⁵⁴. The within-individual variation of fibrinogen levels is high because of its sensitivity to environmental factors; however, the genetic control of fibrinogen has to be considered together with environmental factors: it has been shown that fibrinogen genotypes may interact with cigarette smoking, gender, physical activity, use of drugs in determining the increase in fibrinogen levels^{35,36,40,55} and perhaps the risk of ischemic heart disease.

We shall mention in the next paragraphs three different examples of gene-environment interaction, that can modulate either the level of fibrinogen or the risk of CHD.

Fibrinogen polymorphisms and gender. Among others, a stronger association has been found between -455G/A or BclII polymorphisms and fibrinogen levels in women than in men^{26,35,36}.

Fibrinogen levels vary according to sex and menopausal status. They are lower in premenopausal women with respect to men of the same age, and increase after menopause. Hormone replacement therapy, however, may revert the effect of menopause on fibrinogen levels. The overall effect of the -455 G/A polymorphism is also different in males and females.

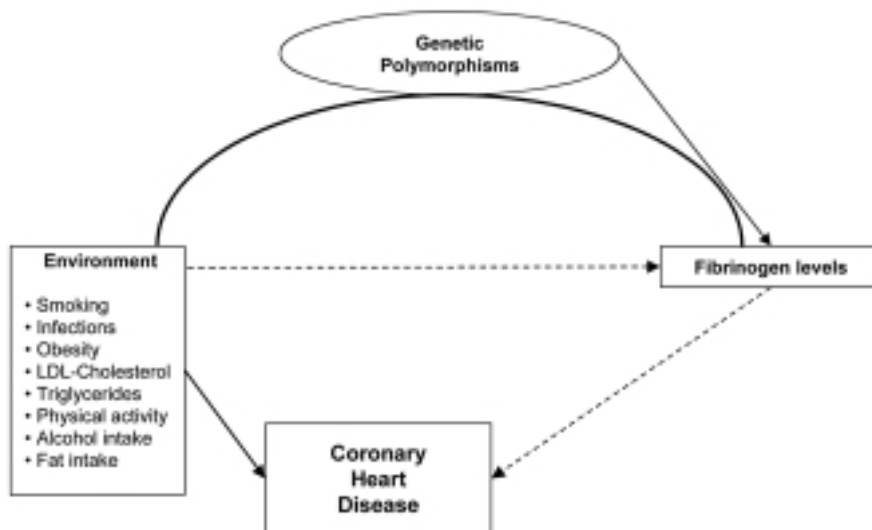


Figure 1. Interaction between genetic and environmental factors in determining levels of fibrinogen and the risk of coronary heart disease.

Indeed, the effect of the A allele on fibrinogen levels is additive in men, while it appears to be dominant in women with no additional effect on fibrinogen levels in the homozygotes. After stratification for menopausal status and hormone replacement therapy, the dominant effect of the A allele was evident only in postmenopausal women not taking hormones. In both premenopausal and postmenopausal women treated with hormone replacement therapy, the effect of the A allele was additive, as observed in men³⁶.

These findings suggest that hormones or other gender-specific factors modulate the increase in fibrinogen probably by down-regulating hepatic fibrinogen synthesis. The presence of genetic variance at the promoter levels can differently regulate the repression of the fibrinogen gene transcription. On the basis of these results, the interaction with gender should be always taken into consideration in studying the effect of fibrinogen polymorphisms on the risk of CHD.

Fibrinogen polymorphisms and physical training.

Several studies have shown that a moderate physical activity decreases the levels of fibrinogen. A decrease in plasma fibrinogen concentration has also been reported in elderly men after physical training programs and in physically active postmenopausal women⁵⁶.

An inverse dose-response relationship has been described between regular physical exercise and CHD risk. Reduction in fibrinogen could, at least in part, be responsible for such an association. Some of the benefits of regular exercise, however, are lost under very intensive training, especially in those with a sedentary lifestyle.

The association between physical activity and plasma fibrinogen may vary according to fibrinogen genotypes.

Physical exercise may acutely enhance the fractional catabolic rate of fibrinogen and the degradation rate

of the α -chain. However, these effects are evident only in carriers of the B2 allele of BclII β -chain polymorphism. Vaisanen et al.⁵⁷ showed that physical activity levels explained up to 9% of variance in the carriers of the B2 genotype, while the effect was only marginal in the carriers of the common B1 fibrinogen genotype. Similar results were shown for polymorphisms in the α -chain gene of fibrinogen. This is a polymorphic site within codon Aa312 which can be detected by RsaI restriction enzyme, resulting in a more frequent Thr or less common Ala phenotype.

Although no association was found between such polymorphism and plasma fibrinogen, in control populations low levels of fibrinogen were described in postmenopausal women, homozygous for the Thr allele, if physically most active, but not in carriers of the Ala allele⁵⁸. Moreover, in a controlled randomized study, an interaction between physical activity and fibrinogen genotype was also demonstrated in middle-aged men⁵⁶. Among the men assigned to a regular exercise training of low intensity for 3 years, individual changes in anaerobic threshold, an index of fitness, explained 48% of fibrinogen variance only in the Thr homozygotes.

Montgomery et al.⁴⁰ have demonstrated that an acute rise in fibrinogen levels occurs in response to intensive exercise. The increase lasted several days, probably due to a continuous fibrinogen production. This phenomenon is strongly influenced by the G/A -455 polymorphism of the fibrinogen gene. In particular, a gradient of increasing acute fibrinogen response was seen across the GG, GA, and AA genotypes, respectively. After 2 days of strenuous military exercise, 156 male British army recruits showed an increase in fibrinogen levels as compared to the concentration at pre-training. Levels were maximally increased at the second day after exercise. This effect, however, was stronger in the AA homozygotes as compared with heterozygotes and GG homozygotes.

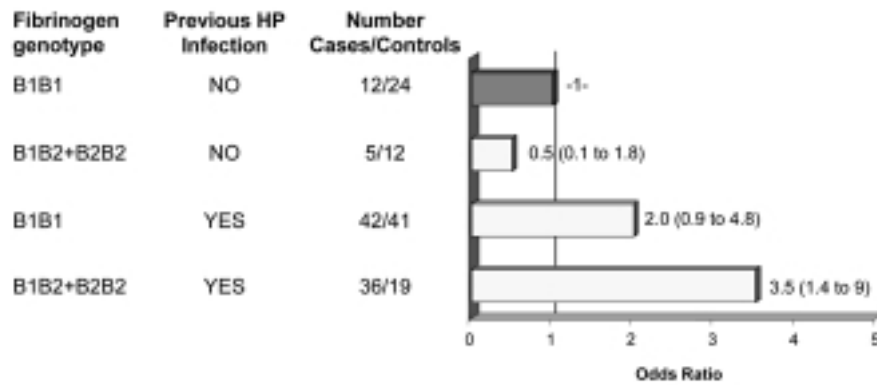


Figure 2. Combined effect of fibrinogen genotype and *Helicobacter pylori* (HP) infection on myocardial infarction risk.

This finding suggests the possibility of a greater response of β -chain promoter to cytokines, whose increase can also be induced by a strenuous physical training. The G/A change at position -455, indeed, is in an almost complete linkage disequilibrium with a T/C polymorphism at position 148 of the promoter. The latter is close to a consensus sequence that confers responsiveness to IL-6 in *in vitro* experiments.

More recently, however, it has been demonstrated that the G to A substitution at position -455 increases by itself the basal rate of transcription in HepG2 cells.

Fibrinogen polymorphism and *Helicobacter pylori* infection. *Helicobacter pylori* (HP) infection has recently been associated with a higher risk to develop ischemic heart disease, although the results are controversial⁵⁹⁻⁶⁴. Zito et al.²⁹ confirmed such an association in a case-control study. They found that HP infection accounts for a 4-fold increase in the risk of myocardial infarction. In that study the cases, patients who had suffered from a first episode of myocardial infarction, showed fibrinogen levels higher than controls. A clear association was found between HP infections and fibrinogen levels both in cases and in controls. Fibrinogen levels were also associated with the BcII fibrinogen polymorphism, carriers of B2 allele showing higher fibrinogen levels as compared to B1 homozygous subjects.

HP is a life-long bacterial infection and it is conceivable that the infectious stimulus could chronically increase the plasma levels of acute phase reactants, such as fibrinogen, with the possible mediation of certain cytokines. In fact, IL-6 and tumor necrosis factor- α levels were found increased in patients with HP-associated gastritis^{59,60,64,65}.

Carriership of the B2 allele of the BcII polymorphism amplifies the effect of seropositivity for HP²⁹ on the risk of myocardial infarction (Fig. 2). Indeed, patients with both seropositivity for HP and carriers of the B2 genotype showed an additional increase in the risk of myocardial infarction as compared to subjects affected by HP but homozygous for the B1 allele.

Since both seropositivity for HP and BcII polymorphism are associated with fibrinogen levels and an interaction between them has been described in determining fibrinogen levels, the gene-environment interaction reported to increase the risk of myocardial infarction could be probably explained by cumulative effects of both factors on fibrinogen levels.

Conclusions

The role of a typically acute phase reactant such as fibrinogen in CHD risk has been deeply studied in recent years through the evaluation of some of its genetic determinants: as highlighted in the three above examples, the interindividual responses to variables like gender or to environmental stimuli like physical exercise or infections may be genetically determined and genetic variability underlies the differences in biological reactions which plausibly contribute to the differences in CHD risk. These examples strongly support the concept that, in multifactorial diseases (like CHD) genetic variability, rather than playing any causal role, influences the risk of disease by determining a different individual susceptibility to environmental risk factors.

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