Clot properties and cardiovascular disease

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Summary
Fibrinogen is cleaved by thrombin to fibrin, which provides the blood clot with its essential structural backbone. As an acute phase protein, the plasma levels of fibrinogen are increased in response to inflammatory conditions. In addition to fibrinogen levels, fibrin clot structure is altered by a number of factors. These include thrombin levels, treatment with common cardiovascular medications, such as aspirin, anticoagulants, statins and fibrates, as well as metabolic disease states such as diabetes mellitus and hyperhomocysteinaemia. In vitro studies of fibrin clot structure can provide information regarding fibre density, clot porosity, the mechanical strength of fibres and fibrinolysis. A change in fibrin clot structure, to a denser clot with smaller pores which is more resistant to lysis, is strongly associated with cardiovascular disease. This pathological change is present in patients with atherosclerotic disease as well as venous diseases, and is also found in a moderate form in relatives of patients with cardiovascular disease. Pharmacological therapies, aimed at both the treatment and prophylaxis of cardiovascular disease, appear to result in positive changes to the fibrin clot structure. As such, therapies aimed at ‘normalising’ fibrin clot structure may be of benefit in the prevention and treatment of cardiovascular disease.

Keywords
Fibrin, fibrinogen, clot structure, cardiovascular disease

Introduction
Fibrinogen, with circulating plasma levels of 1.5–4.0 mg/ml under normal conditions (1), is the third most abundant (after albumin and the immunoglobulins) of all human plasma proteins. At 340 kDa, it is a large glycoprotein, made up of two identical subsets, each consisting of three polypeptides (α-, β- and γ-chains), supported by a total of 29 disulphide bonds. All six chains converge at the central part of the molecule, the E-region, where the cleavage sites for thrombin are located (2, 3). This E-region is connected by two coiled-coil regions, where the α- β- and γ-chains intertwine and form alpha-helical coil structures, to two D-regions, which contain the binding pockets that are important in polymerisation (4). Both the β- and γ-chains end in the D-region, whilst the α-chain protrudes from the D-region, forming a long flexible αC region of over 350 amino acid residues (see Fig. 1) (5). Fibrinogen is primarily synthesised in the liver, where the chains are assembled rapidly in the endoplasmic reticulum, producing a complete molecule in as little as 5 minutes (6).

Fibrinogen is an acute phase protein with plasma levels of fibrinogen increasing rapidly in inflammatory conditions. Fibrinogen expression is strongly up-regulated in response to pro-inflammatory agents such as interleukin-6 and other cytokines, with increased gene transcription leading to higher circulating fibrinogen levels (7, 8). Elevated plasma levels of fibrinogen have been associated with a wide variety of thrombotic diseases, from cardiovascular disease (CVD) (1, 9, 10), stroke (1), peripheral vascular disease (11) and abdominal aortic aneurysm (12), to pulmonary embolism (13). In addition to the potential effect of fibrinogen on thrombus formation and stability in these disease states, there is evidence to suggest that fibrinogen is also important in atherosclerosis. Fibrinogen has been shown to be present within atherosclerotic plaques, indicating a potential role for fibrinogen in their development and/or stability (14, 15). Despite the clear links between fibrinogen levels and CVD, whether this association represents cause or effect remains a subject of debate. Studies attempting to link genotype, phenotype and disease failed to show an association between a fibrinogen polymorphism that results in increased plasma fibrinogen levels and myocardial infarction (16). In addition, whilst fibrinogen is present in atherosclerotic plaques, plasma levels of fibrinogen do not necessarily correlate with indicators of atherosclerosis (17). A recent multi-ethnic meta-analysis
of functional genotypes for circulating fibrinogen levels also failed to show strong evidence of a causal association between circulating fibrinogen levels and CVD (18).

**Conversion of fibrinogen to fibrin – fibrin clot formation**

Vascular injury leads to activation of the coagulation cascade, which culminates in the generation of thrombin, and the conversion of soluble fibrinogen into insoluble fibrin. The fibrin fibre network provides the clot with essential structure, stability and strength, leading to haemostasis and preservation of vascular integrity.

Fibrinogen is converted to fibrin by thrombin cleavage of two fibrinopeptides A, and two fibrinopeptides B from the Aα- and Bβ-chains, respectively (4, 19). The cleavage of these short, acidic N-terminal peptides exposes polymerisation sites, and results in a change in solubility, causing the molecules to polymerise and form fibrin fibres. At a molecular level, thrombin first cleaves the fibrinopeptide A between Arg16 and Gly17 (20), exposing a binding site on the fibrin E-region which is specific for a binding pocket in the D-region. By this mechanism, one fibrin molecule can bind to two other fibrin molecules, which in turn can each bind to another fibrin molecule and so on, producing a fibrin polymer, or protofibril, comprised of staggered and overlapping fibrin molecules, as illustrated in Figure 1 (19-22). Fibrinopeptide B is also cleaved by thrombin, but at a much slower rate compared to fibrinopeptide A. This latter cleavage results in two important events; it exposes a second binding site in the E-region (which is specific for a binding pocket in the fibrin D-region), and also results in the release of the αC-region, such that its active domain becomes available for intermolecular interactions in fibrin. Both of these actions facilitate the lateral aggregation of the protofibrils into fibrin fibres (see Figure 1) (22).

**Factor XIII**

Alongside the cleavage of the fibrinopeptides from fibrinogen molecules, thrombin also activates factor XIII (FXIII), a member of the transglutaminase family of enzymes. FXIII consists of two A subunits, which contain the active site of the enzyme, and two B subunits, which protect the hydrophobic A subunits. The activation of FXIII is a two step process, with thrombin cleaving a 37 amino acid residue from the FXIII-A subunit, before calcium induces dissociation of the B subunits, exposing the activated FXIII-A and producing the active enzyme (FXIIIa) (23). This activation process is enhanced in the presence of fibrin. FXIIIa covalently cross links fibrin, resulting in fibrin clots with increased density, reduced pore size and thinner fibres, with increased resistance to lysis (24). FXIII cross links the α- and γ-, but not the β-chains, of fibrin, with the α-chain and γ-chain cross linking playing independent roles in fibrin clot structure. γ-chain cross linking occurs first, soon after protofibril formation, and affects fibre density (25).

α-chain cross linking increases fibre tautness, increases clot stiffness and reduces clot deformation (25), and plays an important role in the regulation of fibrinolysis (26-28), in part by reducing the accessibility of the coiled coil region of fibrin to plasmin (29). Inter-chain cross linking between the γ- and α-chain also occurs (30). In addition to cross linking between fibrin molecules, FXIIIa also cross links other proteins into the fibrin clot that are important for increasing the resistance to fibrinolysis. It incorporates α2-antiplasmin into the fibrin α-chain, by cross linking Gln14 of α2-antiplasmin to Lys303 of the fibrinogen α-chain, providing one of the main mechanisms by which the clot produces resistance to lysis (31). About 70% of α2-antiplasmin is cleaved between Pro12-Asn13 producing Asn-α2-antiplasmin which is cross linked 13-times faster to fibrin by FXIII than full-length α2-antiplasmin whilst retaining its full capacity to inhibit plasmin (32). Thrombin-activatable fibrinolysis inhibitor (TAFI) is also cross linked into the fibrin clot by FXIIIa (33) via a Gln residue located at position 2 in the TAFI activation peptide. Its counterpart fibrin Lys residue, to which TAFI is cross linked, is currently unknown, and the effects of cross linked TAFI on resistance of the fibrin network to fibrinolysis remain to be fully characterised. Finally, plasminogen activator inhibitor-2 (PAI-2), an inhibitor of fibrinolysis occurring during pregnancy, is also cross linked to fibrin by FXIIIa, via Gln83/86 in PAI-2 and several Lys residues in the fibrin α-chain (34).

**Mechanisms that determine fibrin clot structure**

Fibrinogen levels have an effect on the polymerisation pattern and thus overall clot structure, with increasing fibrinogen concentrations leading to an increased number and size of fibrin fibres (35, 36). However, fibrinogen levels alone do not account for all of the differences in fibrin clot structure that have been observed in in vitro studies. Specifically, the concentration of thrombin present when a fibrin clot is formed has a significant effect on clot structure. Low concentrations of thrombin produce fibrin clots with thick, loosely woven fibres, whilst high levels of thrombin produce clots that are composed of thinner, more tightly packed fibres (37, 38). Along with FXIII, other proteins of the coagulation cascade have been shown to have thrombin-dependent and -independent effects on fibrin clot structure. In plasma, but also in a purified system, increasing levels of factor XIIa (FXIIa) were associated with increasing fibrin fibre density. The relevance of this in-vivo was demonstrated by staining thrombi from human carotid arteries, which showed colocalization of FXII with areas of dense fibrin deposition, implying a role for FXIIa in in-vivo clot modulation (39).

Importantly, some of the most common pharmacological therapies for thrombosis have an effect on fibrin clot structure. In addition to its effects on platelets, aspirin, used widely in both primary and secondary prevention of CVD, results in the acetylation of fibrinogen. Addition of aspirin in vitro leads to a looser fibrin clot structure, with larger pores and thicker fibres, which is less resistant to lysis (40-42). Similar changes in clot structure have been
observed in *ex vivo* plasma clots from healthy subjects after taking aspirin (40). However, changes in fibrin clot structure with aspirin treatment do not always occur. Patients on aspirin with severe coronary artery disease (43) for example, and patients with aspirin treatment failure (44) (that is patients having cardiovascular events whilst on aspirin), continue to have a rigid *ex vivo* fibrin clot structure, with thinner fibres and increased resistance to fibrinolysis. Homocysteinylation of the fibrinogen molecule, as occurs in patients with hyperhomocysteinaemia, also has a marked effect on fibrin clot structure, with a decrease in permeability, shorter, thicker fibrin fibres, and increasing resistance to lysis (45), as observed in both *in vitro* and *in vivo* models (46). This effect is reversible; in a study of humans treated for hyperhomocysteinaemia with folic acid, alongside the return to normal plasma homocysteine levels there was an increase in *ex vivo* fibrin clot permeability and a decreased resistance to lysis (47).

There is evidence of a heritability to fibrin clot structure, with the first degree relatives of patients with peripheral arterial disease (48), coronary artery disease (49) and venous thromboembolism (50) demonstrating *ex vivo* fibrin clots with thicker fibres, increased fibre branching, decreased permeability and increased resistance to lysis compared with controls; changes that are apparent in disease states but not in the normal healthy population. The exact reason for this is not clear, although it is suggested that cholesterol levels in these relatives may contribute to their change in clot structure (48). Furthermore, a study in apparently healthy twins has shown a significant heritability of 40–45% of the complex phenotype of fibrin clot structure (51). It appears that fibrin clot structure can be influenced by common genetic variations in both fibrinogen and FXIII. The fibrinogen Bβ-chain has a functional single nucleotide polymorphism (SNP) Arg448Lys, which is associated with the severity of coronary artery disease and the development of stroke. At a molecular level *in vitro*, 448Lys fibrinogen results in a more compact clot structure, with thinner fibres, smaller pores and stiffer clots, which are more resistant to lysis than 448Arg fibrinogen (52). Also in the β-chain is the −455G/A SNP, which in a recent meta-analysis was shown to be independently associated with both ischaemic stroke and coronary artery disease (53), and has also been associated with abdominal aortic aneurysm (54). The Aα-chain of fibrinogen contains the Thr312Ala polymorphism, which has been shown to influence clot structure by increasing FXIII cross-linking, and through the formation of thicker fibres in the fibrin clot (55). Several studies have found a link between this polymorphism and venous thromboembolism (VTE), with the change to FXIII cross-linking associated with 312Ala fibrinogen being thought to result in a clot which is more susceptible to embolisation (56-58). A more recent study investigating chronic thromboembolic pulmonary hypertension

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**Figure 1:** Diagrammatic representation of the molecular structure of fibrinogen, and fibrin formation. Fibrinogen is composed of 2Aα-, 2Bβ- and 2γ-chains, which are arranged in a symmetrical dimer. The central E-region contains the N-termini of all six chains. From here, a coiled-coil region connects the six chains to the D-region, which contains the C-termini of the Bβ- and γ-chains. The C-termini of the Aα-chains protrude beyond the D-region, and interact with the E-region. Cleavage of Fibrinopeptide A by thrombin results in polymerisation into protofibrils. Subsequent cleavage of Fibrinopeptide B releases the C termini of the γ-chains, which then interact and result in lateral aggregation.
found a strong association between Thr312Ala and this disease, alongside an increase in fibrin resistance to lysis (59).

Given its pivotal role in cross linking of the fibrin clot, changes in FXIII also have an effect on fibrin clot structure. The Val34Leu polymorphism of FXIII accelerates thrombin activation of FXIII and affects the cross-linked fibrin structure, with clots formed in the presence of 34Leu FXIII having thinner fibres and smaller pores than those formed with Val34 FXIII (23, 60). This relationship is altered with high fibrinogen concentrations, with the structure of clots formed in the presence of 34leu FXIII remaining relatively stable, whilst those formed with Val34 FXIII reducing in pore size with increasing concentrations of fibrinogen (61). This may offer some explanation as to the apparent protective effect of this polymorphism against CVD, as at the higher concentrations of fibrinogen associated with CVD, the 34Leu FXIII results in a clot with a favourable structure compared with Val34 FXIII. Multiple studies have shown a protective effect of Val34Leu against coronary artery disease (62, 63) and VTE (58, 64), although any role in protection against stroke remains a matter of debate (62, 65).

In addition to these functional SNPs, 8–15% of plasma fibrinogen contains a variant γ-chain, γ′ (66), which arises from the altered splicing of the γ-chain mRNA, and leads to the substitution of the C-terminal 4 amino acid residues of the γA-chain with a new stretch of 20 amino acid residues in γ′. This new sequence reportedly contains binding sites for FXIII (67) and thrombin (68). Clots produced with fibrinogen γ′ have thinner fibres and an increased resistance to lysis (69, 70). The effects of γ′ on clot structure are independent of thrombin and FXIIIa, and occur early in the process of clot formation, resulting in a clot that is heterogeneous in structure, mechanically weaker, but also more resistant to lysis (71). As a result of these effects of fibrinogen γ′ on fibrin clot structure, it is unsurprising that recent studies have identified positive associations between fibrinogen γ′ levels and CVD (72, 73).

**Fibrin clot structure and fibrinolysis**

Plasmin, generated from plasminogen, is the main enzyme responsible for fibrinolysis of the fibrin fibres. The presence of fibrin enhances the conversion of plasminogen to plasmin by providing a catalytic surface to which both tissue plasminogen activator (tPA) and plasminogen bind. Therefore, fibrin acts as a co-factor in its own breakdown. However, inhibitors of plasmin are also cross linked into the fibrin clot; α2-antiplasmin (74), plasminogen activator inhibitor-2 (PAI-2) (75) and TAFI (33), which serve to help stabilise and maintain the fibrin clot structure.

Changes in the fibrin clot structure are associated with changes in rates of fibrinolysis; denser clots with smaller pores and more closely packed fibres lyse more slowly than clots with larger pores and more loosely packed fibres. Whilst on an individual basis single thick fibres are cleaved at a slightly slower rate compared to thin fibres (76), clots with an increased number of more densely packed thinner fibres are slower to lyse than clots with thick fibres. This is because the difference in fibrinolysis rates based on fibre thickness is overruled by the delay in fibrinolysis due to the increased number of fibrin fibres. The delay in fibrinolysis rates in densely packed clots with thinner fibres is likely due to a combination of mechanisms, including reduced permeation of the fibrinolytic enzymes into the centre of the clot, as well as reduced binding of tPA and plasminogen to densely packed, thin fibres (77, 78).

**Clot properties and CVD**

There is increasing evidence for a consistent association between fibrin clot structure, CVD and (athero)thrombotic disorders (79). The overriding consensus is that patients with CVD demonstrate a tendency to form fibrin clots with densely packed fibres, increased stiffness and enhanced resistance to fibrinolysis. These changes have been observed in patients with both arterial and venous thrombotic disease. The literature provides a plausible mechanistic role for fibrin structure and function in thrombosis, but causality remains to be fully explored and future studies are needed to discover whether or not specific pharmacological intervention targeted at fibrin clot structure may be beneficial in patients with thrombosis.

**Arterial thrombotic disease**

Patients with coronary artery disease display an unfavourable fibrin clot structure. Independent of fibrinogen levels, young myocardial infarction (MI) survivors have stiffer *ex vivo* fibrin clots, with shorter fibres that show increased resistance to lysis (80). Hypofibrinolysis has also been demonstrated in the *ex vivo* fibrin clots of female MI survivors (81). The same is true for elderly patients with more advanced coronary artery disease (82). Also, in the healthy male relatives of patients with a history of premature coronary artery disease, the same *ex vivo* fibrin clot profile, of thicker fibres, smaller pores and an increased resistance to lysis has been found, suggesting a familial basis to clot abnormalities (49). As also found in patients with hyperhomocysteinaemia, the presence of thicker fibres together with smaller pores is perhaps counterintuitive as usually thinner fibres are associated with smaller pore size. Whilst this could be explained by increased fibrinogen levels, some studies have found the presence of thicker fibres to be independent of fibrinogen concentration. Another explanation for the thicker fibres could be that it is related to changes in protofibril packing, with increased relative water content leading to thicker fibres. This latter explanation is, however, entirely speculative and further studies need to be done to elucidate the cause of thicker fibres in patients with CVD and their relatives.

Although known to help normalise fibrin clot structure, risk factor management in this group of patients with standard prophylactic medication is not always effective. Patients who suffered an MI despite treatment with aspirin (44) and clopidogrel (83) continued to show *ex vivo* fibrin clot properties associated with disease, with increased clot density and longer lysis time (44) and increased fibre strength (83). Even if there is some effect, for
patients with advanced coronary artery disease (CAD), taking aspirin does not necessarily bring their fibrin clot structure back in line with control subjects (82), suggesting that perhaps more aggressive or more specific treatment is required to normalise fibrin clot structure in these patients. In addition, other complex diseases can increase risk in patients with coronary artery disease (CAD). Diabetes mellitus (DM) has been shown to further modify fibrin clot structure (84), with CAD patients who also have DM having even denser, more lysis resistant ex vivo fibrin clots than patients with CAD alone (85).

Like CAD patients, patients with ischaemic stroke also display consistent changes in fibrin clot structure. Fibrin clots made in vitro from the plasma of patients with ischaemic stroke have decreased permeability, faster fibrin polymerisation, increased fibre diameter and density, and are more resistant to lysis (86-88). Interestingly, in a study of cryptogenic stroke, those patients who suffered stroke as a result of a patent foramen ovale developed clots that were more permeable and lysed more quickly than those patients with pure arterial strokes, although both types of stroke were associated with denser clots with increased resistance to fibrinolysis compared to control subjects (87). Since strokes in patients with patent foramen ovale may be associated with venous thrombosis and paradoxical embolisation, these findings suggest that the pathological change in clot structure in venous disease may differ from arterial disease. However as a note of caution there were differences in the number of smokers between the two groups of patients in this study, which also may have played a role in the observed differences in clot structure (87).

The pathological arterial fibrin clot structure, of denser clots with smaller pores that are more resistant to lysis, is also found in patients with abdominal aortic aneurysms (89). Patients with larger aneurysms showed denser ex vivo fibrin clots that were more resistant to fibrinolysis than patients with smaller aneurysms, which in turn were denser and more resistant to lysis compared to controls. These data suggest that abnormal fibrin clot structure is present even in the early development of aneurysmal disease. However, as with CAD, whether these changes in fibrin structure and function demonstrate cause or effect remains to be established.

### Venous thrombotic disease

Similar to arterial disease, there is evidence of altered fibrin clot structure in patients with venous thromboembolic (VTE) disease. Patients with VTE produce clots that are less permeable, denser and have increased lysis time compared with controls (50). Again, like in arterial disease, there is evidence of heritability, with healthy first degree relatives of VTE patients showing similar structure, although to a slightly less severe extent as compared to the patients (50). Perhaps even more interesting is the evidence for a difference in fibrin clot structure in those patients with pulmonary embolism (PE), who develop clots that are more permeable, less compact and lyse more effectively than patients who had deep-vein thrombosis (DVT) without PE (50). Further to this, patients with PE have accelerated acquisition of viscoelastic clot properties compared with DVT patients (90). These differences between DVT and PE patients may contribute to our understanding of the mechanisms of clot structure that are involved in determining whether or not a deep vein thrombus produces emboli.

### Pharmacological treatment and clot structure

Pharmacological therapies used for both the treatment and prophylaxis of thromboembolic disease result in changes in fibrin clot structure and function. These are summarised in Table 1.

**Table 1: Pharmacological therapies used in the treatment and prophylaxis of thromboembolic disease, and their effect on fibrin clot structure.**

<table>
<thead>
<tr>
<th>Drug</th>
<th>Class</th>
<th>Effect on Clot Structure</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Unfractionated Heparin</td>
<td>Indirect thrombin inhibitor (binds to anti-thrombin)</td>
<td>Increased clot porosity, more susceptible to fibrinolysis</td>
<td>92</td>
</tr>
<tr>
<td>Low Molecular Weight Heparin</td>
<td>Indirect factor Xa inhibitor (binds to anti-thrombin)</td>
<td>Increased clot porosity, more susceptible to fibrinolysis</td>
<td>93</td>
</tr>
<tr>
<td>Fondaparinux</td>
<td>Indirect, selective factor Xa inhibitor</td>
<td>Looser fibrin network, larger pores, less branches, more susceptible to fibrinolysis</td>
<td>94</td>
</tr>
<tr>
<td>Rivaroxaban</td>
<td>Direct Factor Xa inhibitor</td>
<td>Looser clot structure, more susceptible to fibrinolysis</td>
<td>95</td>
</tr>
<tr>
<td>Apixaban</td>
<td>Direct Factor Xa inhibitor</td>
<td>Decreased density of fibrin clot structure (larger pores)</td>
<td>96</td>
</tr>
<tr>
<td>Dabigatran, Argatroban, Bivalirudin Lepirudin</td>
<td>Direct thrombin inhibitor</td>
<td>Increased permeability, decreased rigidity, thicker fibres, more susceptible to fibrinolysis</td>
<td>97, 98</td>
</tr>
<tr>
<td>Aspirin</td>
<td>Cyclo-oxygenase inhibitor</td>
<td>Larger pores, thicker fibres, less resistance to fibrinolysis</td>
<td>40–42</td>
</tr>
<tr>
<td>Simvastatin, Atorvastatin</td>
<td>Statin (Hypolipidaemic medication)</td>
<td>Increased permeability, thicker fibres, less resistance to fibrinolysis</td>
<td>91</td>
</tr>
<tr>
<td>Fenofibrate</td>
<td>Fibrate (Hypolipidaemic medication)</td>
<td>Increased permeability, thicker fibres, less resistance to fibrinolysis</td>
<td>91</td>
</tr>
</tbody>
</table>
Conclusion

Fibrin clot structure is the result of a number of complex molecular interactions, all of which are influenced by genetic and environmental factors, including disease states and pharmacological treatments. Despite a lack of clarity in causality, the obvious relationship between fibrin clot structure and CVD is compelling, and certainly warrants further investigation. Pharmacological therapies, aimed at both the treatment and prophylaxis of CVD, appear to result in positive changes to the fibrin clot structure of patients. As such, therapies aimed at ‘normalising’ fibrin clot structure may be of benefit in the prevention and treatment of CVD. Specific therapeutic agents are still needed, and the development of these with in vivo and subsequent in-human testing remains an active avenue of research. The limited evidence on the structural changes that result in embolisation is another area where further research would be warranted and important. In combination, these research avenues may hold the key to new breakthroughs in the prevention and treatment of CVD.

Conflicts of Interest
None declared.

References


98. He S, Blomback M, Bark N, et al. The direct thrombin inhibitors (argatroban, bivalirudin and lepirudin) and the indirect Xa-inhibitor (danaparoid) increase fibrin network porosity and thus facilitate ﬁbrinolysis. Thromb Haemost 2010; 103: 1076-1084.