


REVIEW ARTICLE

Fibrinogen α C domain: Its importance in physiopathology

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Abstract: Fibrinogen, involved in coagulation, is a soluble protein composed of two sets of disulfide-bridged $\text{A}\alpha$, $\text{B}\beta$, and γ -chains. In this review, we present the clinical implications of the α C domain of the molecule in Alzheimer's disease, hereditary renal amyloidosis and a number of thrombotic and hemorrhagic disorders. In Alzheimer's disease, amyloid beta peptide ($\text{A}\beta$) is increased and binds to the α C domain of normal fibrinogen, triggering increased fibrin(ogen) deposition in patients' brain parenchyma. In hereditary renal amyloidosis, fibrinogen is abnormal, with mutations located in the fibrinogen α C domain. The mutant α C domain derived from fibrinogen degradation folds incorrectly so that, in time, aggregates form, leading to amyloid deposits in the kidneys. In these patients, no thrombotic tendency has been observed. Abnormal fibrinogens with either a point mutation in the α C domain or a frameshift mutation resulting in absence of a part of the α C domain are often associated with either thrombotic events or bleeding. Mutation of an amino acid into cysteine (as in fibrinogens Dusart and Caracas V) or a frameshift mutation yielding an unpaired cysteine in the α C domain is often responsible for thrombotic events. Covalent binding of albumin to the unpaired cysteine via a disulphide bridge leads to decreased accessibility to the fibrinolytic enzymes, hence formation of poorly degradable fibrin clots, which explains the high incidence of thrombosis. In contrast, anomalies due to a frameshift mutation in the α C connector of the molecule, provoking deletion of a great part of the α C domain, are associated with bleeding.

KEYWORDS

Alzheimer's disease, dysfibrinogenemia, fibrinogen, fibrinogen α C domain, renal amyloidosis

Essentials

- The C-terminal domain of the fibrinogen α chain (α C domain) is implicated in different severe diseases via clotting abnormalities or amyloid deposits.
- Certain anomalies of the fibrinogen molecule lead to amyloid deposits in the kidney, inducing renal insufficiency.
- In contrast, in Alzheimer's disease, fibrinogen is normal, but due to an inflammatory process, fibrinogen crosses into the brain and interacts with $\text{A}\beta$, leading to formation of pathological deposits.

Abbreviations: α C domain, C-terminal portions of fibrin(ogen) $\text{A}\alpha$ chains, residues 220-610; α 2AP, α 2 antiplasmin; t-PA, tissue-type plasminogen activator; AEF, amyloidosis-enhancing factor; AD, Alzheimer's disease; SNP, single-nucleotide polymorphism; α E, extended fibrinogen α chain; VTE, venous thromboembolism; PE, pulmonary embolism; BBB, blood-brain barrier; NSAIDs, nonsteroidal anti-inflammatory drugs.

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1 | INTRODUCTION

Fibrinogen is a soluble plasma glycoprotein comprising two sets of three chains, disulfide-bridged ($A\alpha$ - $B\beta$ - γ)₂. It consists of one central E domain containing the N terminal portions of the $A\alpha$, $B\beta$ and γ chains, two lateral D domains connected to the E domain by coiled coils formed by parts of the three chains ($A\alpha$ 50-160, $B\beta$ 81-192, and γ 24-134), and two $A\alpha$ C-terminal domains ($A\alpha$ 220-610), (α C domains) located outside the D domains (Figure 1).^{1,2}

Fibrinogen is converted by thrombin into insoluble fibrin during blood clot formation. First, thrombin catalyzes the release of fibrinopeptides A and B from the $A\alpha$ and $B\beta$ chains, respectively, to form fibrin monomer. Fibrinopeptide A is released from the N-terminal part of the $A\alpha$ chain, making accessible a polymerization site "A" that interacts with the complementary "a" site located in the γ chain (T374-E396).³ The resulting fibrin monomers interact with each other in a half-staggered manner to produce two-stranded protofibrils.⁴ Release of fibrinopeptide B, located at the N-terminus of the fibrinogen $B\beta$ chain, unmasks polymerization site "B" to interact with its complementary site "b" located in the C-terminal portion of the $B\beta$ chain, thereby generating fibrin fibers that are associated laterally.⁵ In parallel, FXIII activated by thrombin (FXIIIa) catalyzes formation of ϵ -(γ -glutamyl) lysyl covalent bonds between two γ chains and several α chains of adjacent fibrin molecules, and crosslinks α 2-antiplasmin (α 2AP), the major plasmin inhibitor, to fibrin.⁶ It was further shown that factor XIII also mediates α 2AP ligation to plasma fibrinogen on $A\alpha$ chains prior to initiation of clotting. This process plays an important role in down-regulating the rate of fibrinolysis.⁷ Using a homozygous case of dysfibrinogenemia characterized by an amino acid substitution located at the peptide bond on the $A\alpha$ chain that is normally cleaved by thrombin, it was shown that clotting of fibrinogen may sometimes occur in absence of fibrinopeptide A release.⁸⁻¹⁰

Recently, it was evidenced that fibrinogen α C domain has several roles in coagulation, mediating its activity during various physiological and pathological processes. α C domain is composed of residues $A\alpha$ 220-610 consisting of a flexible, unstructured α C connector ($A\alpha$ 221-391) and a relatively compact C-terminal portion of fibrinogen $A\alpha$ chain ($A\alpha$ 392-610).¹¹

In fibrinogen, the two α C domains interact both intramolecularly (ie, with each other) and with the central E region, preferentially

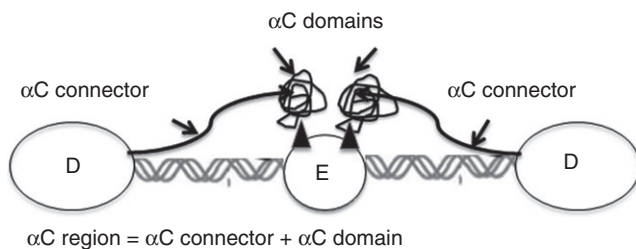


FIGURE 1 Schema of fibrinogen structure showing relationship of α C domains (α C connectors and α C compact domains) to the D and E domains

through the N termini of the $B\beta$ chains.^{2,12} Initially folded on the N-terminal part of the fibrinogen molecule, the 2 α C domains open outward after fibrinopeptide B (FPB) cleavage,^{1,12} revealing novel cryptic sites for plasminogen and t-PA binding within residues $A\alpha$ 392-610 of the α C domains^{13,14} and for α 2 anti plasmin binding within residues $A\alpha$ 504-610.¹⁵ Sites also become available for self-association of the α C domains into α C polymers,¹⁶ occurring by formation of a hydrogen bond network through their N-terminal subdomains via β -hairpin swapping. This structure is reinforced by interaction of their C-terminal subdomains with the α C connectors, providing the proper orientation of their reactive residues for efficient cross-linking by factor XIIIa.¹⁶ Lateral aggregation may occur in the absence of α C regions, but their presence enhances it. Clots made from fibrinogen lacking α C domains comprise fibers that are thinner and denser, and have more branch points than normal controls¹⁶; anomalies located in this region of the molecule can induce anomalies in aggregation of the protofibrils.

After clot formation, fibrinolysis occurs. The fibrinolytic system comprises an inactive proenzyme, plasminogen, which is converted by tissue-type plasminogen activator (t-PA) into plasmin, which degrades fibrin. Plasminogen activation is regulated by molecular interactions between its main components, ie, by the binding of plasminogen and t-PA to fibrin.¹⁷ Conformational changes upon conversion of fibrinogen into fibrin result in the unmasking of multiple sites that expose fibrin to the action of fibrinolytic enzymes. These include the plasminogen and t-PA binding sites in the α C domain ($A\alpha$ 392-610) as described above,^{13,14} in addition to sites found in other regions of the molecule. In 1988, Mirshahi et al¹⁸ showed, using their own monoclonal antibodies, that the $A\alpha$ 148-197 and γ 86-302 regions were involved in t-PA binding to fibrin. Later, Medved et al¹⁹ found that the conformational change upon conversion of fibrinogen to fibrin results in the exposure of specific epitopes involved in t-PA binding to fibrin; these epitopes are located in $A\alpha$ 148-160 and γ 312-324.

1.1 | Implications of the α C domains in several diseases

It was shown that mutation(s) in the α C domain of fibrinogen may be responsible for severe coagulation disorders,¹² and more recently this domain was also implicated in amyloidosis generation, eg, in Alzheimer's disease,²⁰ and familial renal amyloidosis.²¹

Amyloidosis is caused by abnormal deposition of proteins in soft tissues, and amyloid deposits are primarily made up of protein fibers known as amyloid fibrils. These amyloid fibrils are formed when normally soluble proteins or peptides aggregate and then remain in the tissues instead of being cleared away. Amyloidosis results from a disorder of protein folding characterized by a conformational change of native globular proteins into fibrils with a β -sheet appearance (ie, β strands connected laterally by two or three backbone hydrogen bonds, forming a twisted pleated sheet) that deposit in various organs.²² In amyloidoses, the deposits contain normal blood proteins and another factor not present in plasma, the amyloidosis-enhancing factor (AEF),

which is probably generated at the site of amyloid deposition and acts in accelerating the pre-amyloid phase.²³

1.2 | Fibrinogen α C domain in Alzheimer's disease

Alzheimer's disease (AD) is a neurodegenerative disorder that involves vascular pathology^{20,24}; it is characterized by extraneuronal deposition of the amyloid β peptide ($A\beta$) in the form of plaques and by intraneuronal deposition of the microtubule-associated Tau protein in the form of filaments. Tau interacts with microtubules by mediating microtubule assembly and stability, but in AD, Tau is hyperphosphorylated, which decreases its biological activity.²⁵ $A\beta$ peptide is generated from the transmembrane protein APP (amyloid precursor protein), which seems to be a dependence receptor.^{26,27} Such receptors activate programmed cell death pathways in absence of their specific ligand(s) or trophic factor(s), and promote cell survival in their presence.²⁷ Limited proteolysis of APP, first by β -secretase and then by γ -secretase complex produces the hydrophobic $A\beta$ peptide,²⁸ which aggregates to form neurotoxic, stable $A\beta$ oligomers.²⁹ These aggregates are evident in the initial microscopic deposition of $A\beta$ in the form of early (diffuse) plaques in AD brains.³⁰ Polymerization of the $A\beta$ peptide into protease-resistant fibrils is a significant step in AD pathogenesis.³¹

Interaction of $A\beta$ peptide with fibrinogen leads to its oligomerization, and several authors have reported the crucial involvement of fibrinogen in the pathophysiology of AD—especially its association with cerebral amyloid angiopathy.³² Fibrinogen is not normally found in the brain, nevertheless it accumulates in the extravascular space in brains of AD patients.²⁰ In these patients, deposition of the $A\beta$ oligomers is responsible for endothelial cell damage leading to blood-brain barrier leakage,³³ attested by a diffuse pattern of staining for fibrinogen with considerable fibrinogen immunoreactivity appearing in association with $A\beta$ deposits.³⁴ This fibrinogen-associated $A\beta$ accumulates around or inside blood vessels in the brain,³⁴ and is thought to be responsible for vascular dysfunction through provoking the degeneration of vessel wall components, affecting cerebral blood flow and worsening cognitive decline³⁵ indeed, fibrinogen that strongly interacts with $A\beta$ peptide was found to be deposited together with $A\beta$ peptide at the sites of cerebral amyloid angiopathy. In addition, $A\beta$ is a prothrombotic factor, triggering thrombin generation via FXII-dependent activation of FXI, and hence is responsible for the chronic formation of fibrin, suggesting a new mechanism for neuronal dysfunction.³⁶ Thus, fibrinogen does not normally cross the blood–brain barrier but, due to the cerebrovascular pathology, it does accumulate in the damaged brain vasculature and parenchyma of AD mice.³⁷ Fibrin(ogen) deposition is due to interaction of $A\beta$ with fibrinogen; the binding sites of fibrinogen on $A\beta$ are located in the C-terminus of the β -chain (β 396– β 407)³² and in the α C domain.³⁸ Fibrin clots formed in the presence of $A\beta$ peptide are structurally abnormal and resist degradation.³⁹ Binding of $A\beta$ to fibrin(ogen) renders fibrin clots more resistant to degradation via two mechanisms: (a) specific binding of $A\beta$ to the α C domain of fibrinogen followed, upon thrombin action, by fibrin polymerization into a tight network resistant to

fibrinolysis;³⁸ and (b) $A\beta$ overlaid on preformed clots binds to fibrin and delays lysis.³⁹

Mounting evidence thus implicates fibrin(ogen) in AD pathogenesis. Indeed, abnormal deposition and persistence of fibrin(ogen) in AD brains resulting from $A\beta$ -fibrin(ogen) binding would be expected to enhance $A\beta$ deposition and increase neuroinflammation and neurodegeneration.⁴⁰ In patients, Narayan et al⁴¹ recently demonstrated that there is a significant increase in fibrinogen in brain microarray sections from AD cases compared to controls. Moreover, a novel $A\beta$ –fibrinogen interaction inhibitor rescues both thrombosis and cognitive decline in AD mice.⁴²

As aptly summarized by Cortes-Canteli et al,⁴³ AD is a multifactorial disorder with a vascular component, and increasing evidence suggests that fibrinogen and fibrin clot formation contribute to this disorder.⁴⁴ Fibrin(ogen) was observed to be present in areas where neurons were degenerating, and decreasing the fibrinogen levels reduced neuronal death in AD mice. Furthermore, fibrin is also abnormally present intra- and extra-vascularly in different areas of the brains of patients with AD, as well as in the brains of AD mice where it increases over time and correlates with the level of $A\beta$ deposition. Large vessels lined with fibrin or capillaries that are completely blocked by its deposition will alter the cerebral blood flow, especially if these vascular occlusions occur chronically over the course of many years. This may play a substantial role in the cerebral hypoperfusion seen in AD patients.^{43,44}

1.3 | Fibrinogen α C domain anomalies in renal hereditary amyloidosis

The renal hereditary amyloidoses are a rare but clinically important group of disorders that are inherited in an autosomal-dominant fashion. Variants of the α C domain of fibrinogen cause the most common type of hereditary renal amyloidosis in Europe and, possibly, in the United States as well.⁴⁵ Absence of bleeding disorders and normal clot formation indicate that the mutations do not significantly affect clotting function. Mutation induces improper folding of the mutant α C fragment derived from fibrinogen degradation so that, as shown by X-ray fiber diffraction and electron microscopy, fibrinogen amyloid fibrils similar to other chemical types of amyloid accumulate as a β -sheet structure; the end result is amyloid deposition in the kidneys.⁴⁶

Various renal amyloidogenic mutations in fibrinogen have been described in the literature.^{47–53} These deposits disrupt kidney structure and cause abnormal kidney function, which tends to become progressively more abnormal as amyloid deposits accumulate with time. In these patients, renal histology was characteristic: almost complete glomerular obliteration by amyloid deposition. The disease is characterized by variable penetrance and is associated with hypertension, nephrotic syndrome, proteinuria, and renal failure. Age at onset of symptoms varies from 13 to 70 years. In all cases the clotting times of the variants responsible for renal amyloidosis was normal, except in that reported by Uemichi et al,⁵¹ where thrombin time was slightly prolonged and fibrinogen level was low.

Known amyloidogenic fibrinogen point mutations implicated in the disease are all located in the α C domain: these include R554L⁴⁷; E526V,⁴⁸ the mutation that most commonly causes renal amyloidosis; E540V, P552H, and T538K, mutations described by Gillmore et al⁴⁹; E524K, E526K, G555F, and R554H, described by Rowczenio et al.⁵⁰ Reported amyloidogenic frameshift mutations associated with the disease include: a single-nucleotide deletion at the third base of codon 524 of the fibrinogen A α -chain gene (4904 del G) resulting in premature termination of the protein at codon 548⁵¹; a point deletion at position 4897 of the fibrinogen A α -chain gene producing a frameshift at codon 522 with truncation at codon 548⁵²; a frameshift mutation found in a young Korean girl that is responsible for an A α (517-522) deletion-insertion of a 31 amino-acid stop.⁵³

Biochemical analysis of amyloid fibrils from kidneys of the patient with the R554L mutation detected amino acid residues 500-580 of fibrinogen A α chain.⁴⁷ Amyloid fibrils from patients with the E526V mutation contain a similar length peptide fragment from the variant fibrinogen A α chain only, despite the fact that patients' plasmas contain approximately equal amounts of normal and variant A α chains;⁴⁹ and amyloid fibrils from the patient with a single-nucleotide deletion producing a frameshift at codon 522 are composed of a 49 amino acid fragment of the A α chain (residues 499-521) followed by a novel sequence created by the frameshift in the patient.⁵¹

1.4 | Fibrinogen α C domain anomalies in coagulation disorders

1.4.1 | Variant haplotypes located in the α C domain

Among the several haplotypes of the A α chain associated with a single nucleotide polymorphism (SNP), only one induces an amino acid modification in the α C domain, the α -fibrinogen T312A polymorphism. The frequency of this variant by self-reported race is 5.1% in white patients and 13.5% in black patients.⁵⁴ The α -fibrinogen T312A variant has been shown to influence clot structure through increased factor XIII cross-linking, since this polymorphism occurs in a region important for FXIII-dependent cross-linking processes, leading to the formation of fibrin clots that could predispose to clot embolization.^{55,56} However, the effect of this common variant on risk of venous thromboembolism (VTE) is unclear for some authors.⁵⁷

Another variant commonly encountered is Fib 420, characterized by extended α chains (α E) representing 1%-2% of the circulating fibrinogen content. Fib 420 (α E B β γ)₂, is a normal human variant fibrinogen with α E subunits that are 50% longer than those of the common A α subunit due in part to an extra 236 amino acids encoded by exon VI and a variant posttranslational processing, including N-glycosylation. Additional amino acids are located between G635 and the terminal Q847. Several lines of evidence suggest that the α E chain is less susceptible to proteolytic degradation than the common A α chain.⁵⁸

1.4.2 | Dysfibrinogenemias associated with mutations in the α C domain

Fibrinogen anomalies in the α C domain often lead to coagulation disorders with highly variable clinical manifestations, from severe bleeding or thrombosis to asymptomatic (Tables 1-4). Some patients presenting an α C domain anomaly suffer from a bleeding diathesis because of the formation of fibrin clots that exhibit reduced functional properties but, paradoxically, thromboembolic disorders are detected in many other patients. These latter may arise due to the formation of fibrin clots resistant to fibrinolysis by plasmin, secondary to defective t-PA or plasminogen binding to fibrin, or else to abnormal plasminogen activation on the fibrin surface. Spontaneous abortion is another common clinical complication. The study of such cases has improved our understanding of the fibrinogen–fibrin structure, and of the mechanisms of polymerization and fibrinolysis. Characteristics of published mutations are summarized in Tables 1-4, respectively, corresponding to four types of mutations reported in the literature: single amino-acid substitution in the α C domain; 39-amino-acid duplication in the connector region of the α C domain; truncations affecting both the α C connector and the α C compact domain; and truncations of the α C compact domain alone.

1.4.3 | Mutants characterized by an amino acid substitution

The first reported case of this type was Dusart syndrome (Table 1), discovered in one of our patients who presented a severe familial thromboembolic disease and for whom we focused on thrombosis caused by abnormal fibrin structure, since clots from this patient were very tight and could not be degraded by fibrinolytic enzymes.⁵⁹ The thromboembolic disease was attributed to impaired fibrin-enhanced plasminogen activation responsible for a defect in fibrin degradability⁶⁰ and to an unusual clot rigidity inducing the formation of a brittle clot, therefore resulting in a high incidence of embolism.⁶¹ Further investigation of this fibrinogen variant showed that the anomaly is due to an R554C mutation in the α C domain of fibrinogen that has not been associated with amyloid formation.⁶² This contrasts with the observation of Benson et al,⁴⁷ who detected a fibrinogen variant with a different mutation at the same residue (R554L), but which is associated with renal amyloidosis without thrombotic disorder. Plasma Dusart fibrinogen was found to be disulfide-linked to albumin, possibly at A α C554; removal of the α C domain from fibrinogen Dusart by limited plasmin digestion nearly normalized fibrin polymerization.⁶³ These observations support the conclusion that the fibrinogen α C domain plays an important role in lateral fibril association. Whether it is the presence of cysteine at A α 554 or the albumin molecules bound to the fibrinogen at this position that causes the defective function, cannot be deduced. Since the initial discovery, five further cases of distinct families affected by Dusart syndrome have been reported; all had an impressive history of thrombosis, which was sometimes fatal.⁶⁴⁻⁶⁸ These six cases lend

TABLE 1 Dysfibrinogenemia due to an amino-acid substitution in the fibrinogen α C domain

Name of abnormal fibrinogen	Genotype	Anomaly in the α C domain	Clinical syndrome	Reference
Fibrinogen Dusart	Heterozygous	Mutation of A α 554 R to C	Thromboembolism	59-63
5 other cases of Fibrinogen Dusart:		Idem		64-68
Fibrinogen Dusart Chapel Hill 1	Heterozygous		Thromboembolism	64
Fibrinogen Dusart German family 2	Heterozygous		Thromboembolism	65
Fibrinogen Dusart 3	Heterozygous		Thromboembolism	66
Fibrinogen Dusart 4	Heterozygous		Venous & arterial thrombosis	67
Fibrinogen Dusart 5	Heterozygous		Thrombosis in portal vein	68
Fibrinogen San Diego	Heterozygous	Mutation of A α 554 R to H	Moderate thromboembolism	69
Fibrinogen Caracas V	Heterozygous	Mutation of A α 532 S to C	Thromboembolism	70
Fibrinogen Bordeaux	Heterozygous	Mutation of A α 439 R to C	Thrombosis	71
Fibrinogen Sumperk II	Double Heterozygous	Double Mutation A α 13 G to E and A α 314 S to C	Mild bleeding	72
Fibrinogen Caracas II	Heterozygous	Mutation of A α 434 S to N-glycosylated N	Asymptomatic	73
Fibrinogen Grand Lyon III	Heterozygous	Mutation of A α 496 D to N	Asymptomatic	74
Fibrinogen Seoul II	Heterozygous	Mutation of A α 328 Q to P	Myocardial infarct	75
Fibrinogen Sumida	Heterozygous	Mutation of A α 472 C to S	Asymptomatic	76
Fibrinogens of several origins	Homozygous	Mutation of A α 519 G to R	Unknown	77
	Homozygous			
	Homozygous	Mutation of A α 524 E to K	Unknown	77
	Homozygous			
	Unknown	Mutation of A α 526 E to K	Unknown	77
	Unknown	Mutation of A α 526 E to V (Christchurch IV)	Asymptomatic	77
	Unknown	Mutation of A α 540 E to V	Unknown	77
	Unknown	Mutation of A α 552 P to H	Unknown	77

TABLE 2 Dysfibrinogenemia due to an elongation of the α C domain of fibrinogen

Name of abnormal fibrinogen	Genotype	Anomaly in the α C domain	Clinical syndrome	Reference
Fibrinogen Champagne Mont d'Or	Heterozygous	39 amino acid WXXGSSGPGSTGN duplication in the connector domain starting at position 272	Thromboembolism	78

support to the concept of thromboembolic diseases due to defective fibrin lysis arising from anomalies in the α C domain of fibrinogen.

Other anomalies (n = 15) in the α C domain of the fibrinogen molecule have been described and are presented in Table 1A.⁶⁹⁻⁷⁷ Among these cases, four presented thrombotic disorders, another presented mild bleeding (fibrinogen Sumperk II),⁷² four of them were asymptomatic (Caracas II,⁷³ Grand Lyon III,⁷⁴ Sumida,⁷⁶ and Christchurch IV⁷⁷), and for the six others the clinical syndrome was unknown. Mutation of an α C domain amino acid to cysteine

is associated with thrombotic disorders in the six fibrinogens Dusart (A α R554C) of several origins,⁶⁴⁻⁶⁸ as well as in Caracas V (A α K532C)⁷⁰ and Bordeaux (A α R439C)⁷¹; the unpaired cysteine, not being able to form a disulfide bridge, binds covalently to free -SH groups of albumin, resulting in formation of abnormally thin fibrin fibers that are resistant to plasmin degradation.⁶³ Fibrinogen Sumperk II (double heterozygous mutation A α G13E and S314C) presented only mild bleeding.⁷² Fibrinogen Seoul II (A α G328P) had a myocardial infarction.⁷⁵ In fibrinogen Sumida,⁷⁶ the functionally

TABLE 3 Dysfibrinogenemia due to a frameshift mutation in the fibrinogen α C-connector ($A\alpha$ 221-391) resulting in a truncation affecting both the connector itself and the $A\alpha$ compact domain

Name of abnormal fibrinogen	Genotype	Anomaly in the α C domain	Clinical Syndrome	Reference
Fibrinogen Egyptian	Homozygous	$A\alpha$ (221)Q stop	Bleeding tendency	77
Fibrinogen Bulgaria	Homozygous	$A\alpha$ (229)W stop	Bleeding tendency	77
Fibrinogen Algerian	Homozygous	$A\alpha$ (276)W stop	Bleeding tendency	77
Fibrinogen Chinese	Homozygous	$A\alpha$ (293) frameshift-stop	Unknown	77
Fibrinogen Iran III	Unknown	$A\alpha$ (297) frameshift-stop	Bleeding	77
Fibrinogen France VII	Homozygous	$A\alpha$ (297)G stop	Unknown	77
Fibrinogen France XII	Unknown	$A\alpha$ (315)W stop	Bleeding & Thrombosis	77
Fibrinogen Turkey	Homozygous	Idem	Idem	77
Fibrinogen Tunisia	Homozygous	$A\alpha$ (323)G frameshift stop	Bleeding	77
Fibrinogen Germany	Homozygous	$A\alpha$ (327)N frame shift stop	Bleeding	77
Fibrinogen Keokuk	Heterozygous	Lack of $A\alpha$ (328-610), $A\alpha$ (328)Q stop Double heterozygous: Keokuk mutation plus $A\alpha$ intron 4 G-to-T mutation	Asymptomatic Bleeding with severe hypofibrinogenemia, and thrombotic episodes secondary to surgery accompanied by infusion of normal fibrinogen	79
Fibrinogen Otago	Homozygous	Lack of $A\alpha$ (272-610). Insertion of cytosine at position 4133 producing a frameshift which translates as 3 new amino acids Q268-E-P before termination at position 271	Bleeding and miscarriages	80

important disulfide-bridged loop $A\alpha$ C442-C472 is abolished by the $A\alpha$ C472S mutation, and although the unpaired C442 binds covalently to albumin, markedly impairing lateral aggregation of protofibrils, there are no clinical manifestations—indeed, clot lysis by plasminogen and t-PA is normal.

1.4.4 | A mutant characterized by elongation of the α C domain

The patient with fibrinogen Champagne au Mont d'Or (Table 2) developed a spontaneous deep venous thrombosis complicated by pulmonary embolism (PE). But further evidence is needed to determine whether the connector prolongation predisposes to venous thrombosis by impairing fibrin degradation.⁷⁸

1.4.5 | Mutants characterized by a truncation in the α C connector domain

Most of the patients (Table 3) that presented a frameshift located in the α C connector ($A\alpha$ 221-391) are homozygous, with a bleeding tendency attributable to either defective factor XIIIa-induced α -chain crosslinks recently identified as Q223-K508, Q223-K539, Q237-K418, Q237-K508, Q237-K539, Q237-K556, Q366-K539, Q563-K539, and Q563-K601,^{77,79,80,93} or else to a decrease in factor XIIIa-mediated crosslinking of PAI-2 to several lysines, including

$A\alpha$ K413 and K457, which are associated with hyperfibrinolysis.⁹⁴ PAI-2 may be undetectable in normal plasma, but it is synthesized by activated monocytes in inflamed tissues,⁹⁴ and aligns along fibrin strands, where it may cross-link with fibrin(ogen).⁹⁵

Only the patient with France XII dysfibrinogenemia⁷⁷ and the double heterozygous Keokuk patient ($A\alpha$ Q328-stop and guanine-to-thymine mutation in Intron 4 of the $A\alpha$ chain, inducing afibrinogenemia)⁷⁹ presented both bleeding and thrombotic episodes secondary to surgery accompanied by infusion of normal fibrinogen. Heterozygosity for both mutations was required for the expression of severe hypodysfibrinogenemia and for clinical symptoms.⁷⁹

Fibrinogen Otago is a homozygous dysfibrinogenemia with truncation of approximately 60% of the $A\alpha$ chain (amino acids 272-610), leading to a markedly decreased plasma fibrinogen level (0.1 g/L) that is responsible for bleeding episodes and multiple miscarriages.⁸⁰

1.4.6 | Mutants characterized by a truncation within the compact domain of the α C domain

This group of 14 patients with frameshift mutations leading to truncation of the α C compact domain presents a wide variety of clinical outcomes (Table 4). Severe thrombotic disorders occurred in two cases of homozygous dysfibrinogenemia, fibrinogen Marburg (lacking $A\alpha$ 461-610)⁸¹ and fibrinogen Milano III (lacking $A\alpha$ 452-610),⁸²

TABLE 4 Dysfibrinogenemia due to truncation caused by a frameshift mutation in the fibrinogen α C compact domain ($A\alpha$ 392-610)

Name of abnormal fibrinogen	Genotype	Anomaly in the α C domain	Clinical Syndrome	Reference
Fibrinogen Marburg	Homozygous	Lack of $A\alpha$ (464-610) [codon $A\alpha$ 461 AAA (K) to TAA (stop)]	Thromboembolism	81
Fibrinogen Milano III	Homozygous	Lack of $A\alpha$ (454-610) & 2 new C-terminal amino acids (W452-S453) [insertion of a thymine in exon V after the ATT triplet coding for $A\alpha$ I451]	Thromboembolism	82
Fibrinogen India	Homozygous	$A\alpha$ (447)T-frameshift-17 amino acids-stop	Bleeding tendency	83
Fibrinogen Multinational	Heterozygous	$A\alpha$ (452)G-frameshift-stop	Unknown	77
Fibrinogen Wilmington	Heterozygous	Cytosine deletion at nucleotide 4727 producing a frameshift at T465 followed by the additional sequence PKMVLTVPRQWI	Bleeding	84
Fibrinogen Guarenas	Heterozygous	Nonsense mutation at G4731T that causes an $A\alpha$ chain truncation at S466	Severe bleeding in the propositus, mild in a brother, asymptomatic in others	85
Fibrinogen Lincoln	Heterozygous	Lack of $A\alpha$ (479-610) & 4 new C-terminal amino acids resulting in a frameshift at A475, followed by H476-C-L-A-stop	Mild bleeding tendency	86
Fibrinogen San Giovanni Rotondo	Heterozygous	Single nucleotide deletion in codon A499. Appearance of a premature codon at position 518 coding for 18 new amino acids with cysteine at last position (SSTLPQLEKHSQVSSHLC)	Asymptomatic	87
Fibrinogen Nieuwegein	Homozygous	Lack of $A\alpha$ 454-610 with deletion of TG cross linking site in the α C domain	Asymptomatic	88
Fibrinogen Multinational	Unknown	$A\alpha$ M476 frameshift stop	Thrombosis	77
Fibrinogen Perth	Heterozygous	Lack of $A\alpha$ 494-610 due to cytosine deletion at nucleotide 4841 & incorporation of 23 new residues (LMKLPSSSTLPQLEKHSQVSSHLC)	Bleeding in some propositus, thrombosis in others	89-91
Fibrinogen Mannheim V	Heterozygous	Nucleotide deletion (C1537delA) resulting in $A\alpha$ H494P mutation followed by 23 amino acids (LMKLPSSSTLPQLEKHSQVSSHLC) before premature truncation after C517	Miscarriages	92

as well as in one case where zygosity status is not indicated that is characterized by an $A\alpha$ M476 frameshift stop.⁷⁷ Patients with other mutations showed a mild bleeding tendency that may be explained by defective factor XIIIa-induced α polymerization.^{77,84-86} A variable penetrance is observed for fibrinogen Guarenas,⁸⁵ since the propositus presented severe bleeding, whereas his brother, who has the same anomaly, presented only mild bleeding, and their mother, likewise affected, was asymptomatic. Patients with still other mutations were asymptomatic.^{87,88} Some patients with Perth fibrinogen presented with thrombosis, and others with bleeding disorders.⁸⁹⁻⁹¹ The patient with fibrinogen Mannheim V presented only with miscarriages.⁹² It is interesting to note that similar sequences with a cysteine in position 517 were found in three different abnormal dysfibrinogenemias, ie, San Giovanni Rotondo,⁸⁷ Perth,⁸⁹⁻⁹¹ and Mannheim V.⁹²

- Perth mutation $A\alpha$ P495-LMKLPSSSTLPQLEKHSQVSSHLC-C517
- Mannheim V mutation $A\alpha$ H494-PLMKLPSSSTLPQLEKHSQVSSHLC-C517

- San Giovanni Rotondo mutation $A\alpha$ A499-SSTLPQLEKHSQVSSHLC-C517

Although they share an identical sequence, and the unpaired cysteine at $A\alpha$ 517 generated fibrinogen-albumin complexes in all three dysfibrinogenemias, the clinical syndromes are different: the propositus with fibrinogen San Giovanni Rotondo is asymptomatic, whereas the patient with fibrinogen Mannheim V had miscarriages—and those with fibrinogen Perth present either thrombotic disorders or a bleeding tendency, as described above.

1.4.7 | Importance of the α C domain in fibrinogen assembly in and/or secretion by hepatocytes

The α C domain seems to be involved in fibrinogen assembly within and/or secretion from hepatocytes, as previously suggested by Ridgway et al⁸⁰ and Jayo et al⁹¹ in the case of fibrinogen Otago (lacking amino acids 272-610), the mother (propositus) was homozygous for the mutation and expressed very low fibrinogen

level (0.06 mg/mL), whereas no circulating A α ^{Otago} chain was found in her heterozygous son, and his fibrinogen level was normal. Likewise, in fibrinogen Marburg an homozygous case of dysfibrinogenemia lacking A alpha 461-610,⁸¹ the fibrinogen level in plasma was very low, while in her heterozygous siblings there is less than 10% of truncated A α chain. In fibrinogens Lincoln,⁸⁶ Wilmington,⁸⁴ and Perth,⁸⁹⁻⁹¹ a low level of abnormal A α chain was found in plasma fibrinogen (ratio of truncated A α to normal A α chain is 0.2:1, which is considerably less than the 1:1 normally expected for heterozygotes). From all these cases, it is suggested that the α C domain is involved in assembly of the fibrinogen molecule in the hepatocyte, since the truncated chains do not compete with the normal ones during assembly of mature fibrinogen. In contrast, the A α C442-C472 loop which is so important in fibrinogen function has little or no effect on chain assembly and secretion, since disruption of this A α intrachain loop (by site-directed mutagenesis C442-C472) did not impact fibrin(ogen) assembly nor secretion in transfected COS cells.⁹⁶

1.4.8 | Importance of unpaired A α cysteine in dysfibrinogenemias

In normal fibrinogen, the α C domains are folded on the N-terminal portion of the fibrinogen molecule and unfold upon fibrin formation, promoting lateral aggregation of protofibrils.² As a result, anomalies in the α C domain (Tables 1 and 4) may be expected to induce anomalies in aggregation of the protofibrils. Interestingly, the mutation of A α R554 leads to different pathologies according to whether R is mutated to L (as in hereditary renal amyloidosis, vide supra) or to C (eg, in Dusart syndrome).

In fact it appears that mutation to C of an amino acid located in the α C domain is important for thrombotic disorders. For example, in certain dysfibrinogenemias (Table 4) the deletion of amino acids A α 465-610 (Nieuwegein), 452-610 (Milano III), 461-610 (Marburg) or 467-610 (Guarenas) results in the presence of an unpaired cysteine (C442), which in normal fibrinogen forms an intrachain disulfide bridge with A α C472. The free -SH group of C442 covalently links to a free -SH group in albumin, which results in disturbed protofibril assembly leading to formation of a tight fibrin network and the acquisition of plasmin resistance relevant to thrombophilia. Thus it would appear that the abnormal network formation observed in such cases is caused by the covalently linked albumin rather than by absence of the carboxyl-terminal part of the A α chain. However, thromboembolisms were only observed in Marburg and Milano III. Other fibrinogens that bind albumin due to an anomaly in the α C domain (Mannheim, San Giovanni Rotondo, Nieuwegein) did not present any thrombotic tendency, and patients with fibrinogen Perth presented either thrombotic or hemorrhagic syndromes. With the exception of families with clear thrombotic genotype (eg, fibrinogen Dusart), in other cases the penetrance of the thrombotic phenotype may vary (eg, fibrinogen Perth), perhaps depending on the amount of albumin that becomes disulphide-bonded to the variant.

In abnormal fibrinogens arising from a frameshift mutation in the α C connector that results in truncation of the A α chain beginning at amino acid positions 272-328 (Table 3), there are no unpaired cysteines available to bind albumin (A α C442 and C472 are absent); this may explain why no thrombosis was reported in these patients.

Sauls et al⁹⁷ have shown that cysteine-fibrinogen (Hcys-fibrinogen) obtained by in vitro incubation of H-cyc thiolactone with purified fibrinogen shows increased resistance to fibrinolysis: H-Cys fibrinogen has additional cysteines (seven in the A α chain, two in the B β chain, three in the γ chain). Of the seven cysteine residues located in the A α chain, three are in the α C domain, which is involved in t-PA and plasminogen binding. Furthermore, these residues are found in the naturally occurring A α mutations R554C in the Dusart fibrinogens⁶² and L532C in Caracas V⁷⁰ where they are characterized by impaired fibrin-stimulated plasminogen activation by t-PA. It therefore seems likely that plasminogen binding in the α C domain may regulate fibrinolysis by making bound plasminogen readily available for ternary complex formation in fibrin.

2 | PERSPECTIVES

From these results it appears that the α C domain of fibrin(ogen) is involved in various pathologies such as AD, renal familial (hereditary) amyloidosis, and coagulation disorders (thromboembolism or bleeding). Normal fibrin(ogen) can be found in AD plaques, whereas mutated α C domain or its fragments have been implicated in the physiopathology of renal amyloidosis and certain coagulation disorders.

Cerebral amyloid angiopathy, responsible for the vascular dysfunction seen in AD, is induced by A β -fibrinogen complex; and depletion of fibrinogen lessens cerebral amyloid angiopathy.²⁰ The blood-brain barrier (BBB) normally prevents uncontrolled entry of blood-borne and blood-derived products into the brain. Indeed, brain capillary endothelial cells are connected by both tight and adherens junctions, forming a continuous endothelial monolayer. This anatomical barrier only permits the passage of small circulating lipid-soluble molecules. In AD, the BBB breakdown associated with vascular dysfunction allows influx into the brain of neurotoxic blood-derived debris, cells, and microbial pathogens, and is associated with inflammatory and immune responses that can trigger multiple pathways of neurodegeneration.⁹⁸ With the failure of several large-scale trials of treatments designed to lower the amyloid load in the brains of AD patients, and since fibrinogen is increased in inflammatory processes, trials with nonsteroidal anti-inflammatory drugs (NSAIDs) have begun. These studies indicate that, by decreasing fibrinogen levels, NSAIDs can attenuate the destructive process if they are started well before clinical signs develop (at least 6 months, and preferably as long as 5 years before the clinical diagnosis of AD).⁹⁹

Because of the life-threatening potential of renal insufficiency in cases of hereditary amyloidosis, double transplantation (kidney and liver) may still offer the best treatment option for eligible patients: by

replacing the source of circulating amyloidogenic fibrin(ogen) with normal (non-amyloidogenic) protein, liver transplantation prevents the formation of amyloid deposits in the transplanted kidney. It has been suggested that preemptive solitary liver transplantation early in the course of the disease might be a viable alternative, avoiding the need for hemodialysis and kidney transplantation.⁴⁵ In contrast, dysfibrinogenemia associated with thrombotic or hemorrhagic disorders can be adequately managed with anticoagulant therapy or blood transfusion, respectively.

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AUTHOR CONTRIBUTION

JS and CS: Researchers, analysis of several dysfibrinogenemias, discovery of Dusart Syndrome (abnormal fibrinogen with a mutation in the C-terminal domain of the A α chain of the molecule that leads to a severe thrombotic disorder due to defective thrombolysis); JS framed and wrote the paper. SM: Researcher, specialist in fibrin degradability, extensively involved in the conception of the paper, and in drafting and preparing the manuscript. SQM: Clinician, research on defective fibrinolytic patterns during formation of fibrin deposits, involved in literature searches and in writing the paper. RV: Research Professor, relationship between clot structure and fibrin degradability, invaluable discussions and suggestions during preparation of manuscript. LLP: Researcher, involved in critical discussions, preparation of manuscript. MM: Researcher, participated in determining which domains of the A α chain are implicated in the binding of plasminogen activator on the fibrinogen molecule, participated in framing and writing the paper.

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