



The Collagen Family

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Collagens are the most abundant proteins in mammals. The collagen family comprises 28 members that contain at least one triple-helical domain. Collagens are deposited in the extracellular matrix where most of them form supramolecular assemblies. Four collagens are type II membrane proteins that also exist in a soluble form released from the cell surface by shedding. Collagens play structural roles and contribute to mechanical properties, organization, and shape of tissues. They interact with cells via several receptor families and regulate their proliferation, migration, and differentiation. Some collagens have a restricted tissue distribution and hence specific biological functions.

Collagens are the most abundant proteins in mammals (~30% of total protein mass). Since the discovery of collagen II by Miller and Matukas (1969), 26 new collagen types have been found, and their discovery has been accelerated by molecular biology and gene cloning. Several reviews on the collagen family have been published (Miller and Gay 1982; van der Rest and Garone 1991; Kadler 1995; Ricard-Blum et al. 2000, 2005; Myllyharju and Kivirikko 2004; Ricard-Blum and Ruggiero 2005; Kadler et al. 2007; Gordon and Hahn 2010) and even if the question “What is collagen, what is not?” (Gay and Miller 1983) may still be valid, numerous answers have been provided giving new insights into the structure and the biological roles of collagens.

THE COLLAGEN SUPERFAMILY

The collagen superfamily comprises 28 members numbered with Roman numerals in vertebrates (I–XXVIII) (Table 1). A novel epidermal

collagen has been called collagen XXIX (Söderhäll et al. 2007), but the COL29A1 gene was shown to be identical to the COL6A5 gene, and the $\alpha 1$ (XXIX) chain corresponds to the $\alpha 5$ (VI) chain (Gara et al. 2008). The common structural feature of collagens is the presence of a triple helix that can range from most of their structure (96% for collagen I) to less than 10% (collagen XII). As described in the following discussion, the diversity of the collagen family is further increased by the existence of several α chains, several molecular isoforms and supramolecular structures for a single collagen type, and the use of alternative promoters and alternative splicing.

The criteria to name a protein collagen are not well defined and other proteins containing one triple-helical domain (Table 2) are not numbered with a Roman numeral so far and do not belong to the collagen family *sensu stricto*. Some of them, containing a recognition domain contiguous with a collagen-like triple-helical

Editors: Richard Hynes and Kenneth Yamada

Additional Perspectives on Extracellular Matrix Biology available at www.cshperspectives.org

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Cite this article as *Cold Spring Harb Perspect Biol* 2011;3:a004978

S. Ricard-Blum

Table 1. The collagen family.

Collagen type	α Chains	Molecular species
Collagen I	$\alpha 1(I)$, $\alpha 2(I)$	$[\alpha 1(I)]_2$, $\alpha 2(I)$ $[\alpha 1(I)]_3$
Collagen II	$\alpha 1(II)$	$[\alpha 1(II)]_3$
Collagen III	$\alpha 1(III)$	$[\alpha 1(III)]_3$
Collagen IV	$\alpha 1(IV)$, $\alpha 2(IV)$, $\alpha 3(IV)$, $\alpha 4(IV)$, $\alpha 5(IV)$, $\alpha 6(IV)$	$[\alpha 1(IV)]_2$, $\alpha 2(IV)$ $\alpha 3(IV)$, $\alpha 4(IV)$, $\alpha 5(IV)$ $[\alpha 5(IV)]_2$, $\alpha 6(IV)$
Collagen V	$\alpha 1(V)$, $\alpha 2(V)$, $\alpha 3(V)$, $\alpha 4(V)^a$	$[\alpha 1(V)]_2$, $\alpha 2(V)$ $[\alpha 1(V)]_3$ $[\alpha 1(V)]_2\alpha 4(V)$ $\alpha 1(XI)\alpha 1(V)\alpha 3(XI)$
Collagen VI	$\alpha 1(VI)$, $\alpha 2(VI)$, $\alpha 3(VI)$, $\alpha 4(VI)^b$, $\alpha 5(VI)^c$, $\alpha 6(V)$	
Collagen VII	$\alpha 1(VII)$	$[\alpha 1(VII)]_3$
Collagen VIII	$\alpha 1(VIII)$	$[\alpha 1(VIII)]_2$, $\alpha 2(VIII)$ $\alpha 1(VIII)$, $[\alpha 2(VIII)]_2$ $[\alpha 1(VIII)]_3$ $[\alpha 2(VIII)]_3$
Collagen IX ^e	$\alpha 1(IX)$, $\alpha 2(IX)$, $\alpha 3(IX)$	$[\alpha 1(IX)$, $\alpha 2(IX)$, $\alpha 3(IX)]$
Collagen X	$\alpha 1(X)$	$[\alpha 1(X)]_3$
Collagen XI	$\alpha 1(XI)$, $\alpha 2(XI)$, $\alpha 3(XI)^d$	$\alpha 1(XI)\alpha 2(XI)\alpha 3(XI)$ $\alpha 1(XI)\alpha 1(V)\alpha 3(XI)$
Collagen XII ^e	$\alpha 1(XII)$	$[\alpha 1(XII)]_3$
Collagen XIII	$\alpha 1(XIII)$	$[\alpha 1(XIII)]_3$
Collagen XIV ^e	$\alpha 1(XIV)$	$[\alpha 1(XIV)]_3$
Collagen XV	$\alpha 1(XV)$	$[\alpha 1(XV)]_3$
Collagen XVI ^e	$\alpha 1(XVI)$	$[\alpha 1(XVI)]_3$
Collagen XVII	$\alpha 1(XVII)$	$[\alpha 1(XVII)]_3$
Collagen XVIII	$\alpha 1(XVIII)$	$[\alpha 1(XVIII)]_3$
Collagen XIX ^e	$\alpha 1(XIX)$	$[\alpha 1(XIX)]_3$
Collagen XX ^e	$\alpha 1(XX)$	$[\alpha 1(XX)]_3$
Collagen XXI ^e	$\alpha 1(XXI)$	$[\alpha 1(XXI)]_3$
Collagen XXII ^e	$\alpha 1(XXII)$	$[\alpha 1(XXII)]_3$
Collagen XXIII	$\alpha 1(XXIII)$	$[\alpha 1(XXIII)]_3$
Collagen XXIV	$\alpha 1(XXIV)$	$[\alpha 1(XXIV)]_3$
Collagen XXV	$\alpha 1(XXV)$	$[\alpha 1(XXV)]_3$
Collagen XXVI	$\alpha 1(XXVI)$	$[\alpha 1(XXVI)]_3$
Collagen XXVII	$\alpha 1(XXVII)$	$[\alpha 1(XXVII)]_3$
Collagen XXVIII	$\alpha 1(XXVIII)$	$[\alpha 1(XXVIII)]_3$

Individual α chains, molecular species, and supramolecular assemblies of collagen types.^aThe $\alpha 4(V)$ chain is solely synthesized by Schwann cells.^bThe $\alpha 4(VI)$ chain does not exist in humans.^cThe $\alpha 5(VI)$ has been designated as $\alpha 1(XXIX)$.^dThe $\alpha 3(XI)$ chain has the same sequence as the $\alpha 1(II)$ chain but differs in its posttranslational processing and cross-linking.^eFACIT, Fibril-Associated Collagens with Interrupted Triple helices.

Collagens

Table 2. Proteins containing a collagen-like domain.

Protein name	Domain composition	Cellular component
Complement C1q (subcomponent subunits A, B, C)	Collagen-like domain C1q domain	Secreted
Adiponectin	Collagen-like domain C1q domain	Secreted
Mannose-binding protein C	Collagen-like domain C-type lectin Cystein-rich domain	Secreted
Ficolins 1, 2, and 3	Collagen-like domain Fibrinogen-like domain	Secreted
Acetylcholinesterase collagenic tail peptide (collagen Q)	Collagen-like domain Proline-rich attachment domain domain	Secreted
Pulmonary surfactant-associated proteins A1 and A2	Collagen-like domain C-type lectin	Secreted Extracellular matrix
Pulmonary surfactant-associated protein D	Collagen-like domain C-type lectin	Secreted Extracellular matrix
Ectodysplasin A	Collagen-like domain Signal-anchor for type II membrane protein Cytoplasmic	Single-pass type II membrane protein
Macrophage receptor (MARCO)	SRCR Collagen-like domain Signal-anchor for type II membrane protein Cytoplasmic	Single-pass type II membrane protein
Gliomedin	Pro-rich domain Olfactomedin-like domain Collagen-like domain Signal-anchor for type II membrane protein	Single-pass type II membrane protein
EMI domain-containing protein 1	EMI domain Collagen-like domain	Secreted Extracellular matrix
Emilin-1	EMI domain Collagen-like domain C1q domain	Secreted Extracellular matrix
Emilin-2	EMI domain Collagen-like domain C1q domain	Secreted Extracellular matrix

The names are those indicated for human proteins in the UniProtKB database (<http://www.uniprot.org/>, release 2010_08 - Jul 13, 2010).

S. Ricard-Blum

domain, are called soluble defense collagens (Fraser and Tenner 2008), and gliomedin is recognized as a membrane collagen (Maertens et al. 2007).

Beyond Collagen Types: Increased Molecular Diversity of the Collagen Family

Collagens consist of three polypeptide chains, called α chains, numbered with Arabic numerals. Beyond the existence of 28 collagen types, further diversity occurs in the collagen family because of the existence of several molecular isoforms for the same collagen type (e.g., collagens IV and VI) and of hybrid isoforms comprised of α chains belonging to two different collagen types (type V/XI molecules) (Table 1). Indeed collagen XI is comprised of three α chains assembled into a heterotrimer (Table 1), but the α (XI) chain forms type V/XI hybrid collagen molecules by assembling with the α 1(V) chain in vitreous (Mayne et al. 1993) and cartilage (Wu et al. 2009) (Table 1). There is an increase in α 1(V) and a decrease in α 2(XI) during postnatal maturation of cartilage (Wu et al. 2009).

The use of two alternative promoters gives different forms of α 1(IX) and α (XVIII) chains, and alternative splicing contributes to the existence of several isoforms of α 1(II), α 2(VI), α 3(VI), α 1(VII), α 1(XII), α 1(XIII), α 1(XIV), α 1(XIX), α 1(XXV), and α 1(XXVIII) chains. Splicing events are sometimes specific to a tissue and/or a developmental stage, and splicing variants modulate collagen functions. Several collagens (IX, XII, XIV, XV, XVIII) carry glycosaminoglycan chains (chondroitin sulfate and/or heparan sulfate chains) and are considered also as proteoglycans.

Additional levels of functional diversity are due (1) to the proteolytic cleavage of several collagen types to release bioactive fragments displaying biological activities of their own, and (2) to the exposure of functional cryptic sites because of conformational changes induced in collagens by interactions with extracellular proteins or glycosaminoglycans, multimerization, denaturation, or mechanical forces (Ricard-Blum and Ballut 2011). Membrane collagens

exist in two different forms, a transmembrane form and a soluble one, released by shedding, that regulates cell behavior (Franzke et al. 2005).

THE STRUCTURAL ORGANIZATION OF COLLAGENS

A Common Structural Motif: The Triple Helix

Collagen α chains vary in size from 662 up to 3152 amino acids for the human α 1(X) and α 3(VI) chains respectively (Ricard-Blum et al. 2000; Gordon and Hahn 2010). The three α chains can be either identical to form homotrimers (e.g., collagen II) (Table 1) or different to form heterotrimers (e.g., collagen IX) (Table 1). The three α chains of fibril-forming collagens are three left-handed polyproline II helices twisted in a right-handed triple helix with a one-residue stagger between adjacent α chains. The triple helix is stabilized by the presence of glycine as every third residue, a high content of proline and hydroxyproline, interchain hydrogen bonds, and electrostatic interactions (Persikov et al. 2005), involving lysine and aspartate (Fallas et al. 2009). The triple-helical sequences are comprised of Gly-X-Y repeats, X and Y being frequently proline and 4-hydroxyproline, respectively. Location of 3-hydroxyproline residues, which could participate in the formation of supramolecular assemblies, have been identified in collagens I, II, III, and V/XI (Weiss et al. 2010). The triple helix is rod-shaped, but it can be flexible because of the presence of Gly-X-Y imperfections (one to three amino acid residues) and interruptions (up to 21–26 interruptions in the collagen IV chains, Khoshnoodi et al. 2008). These interruptions are associated at the molecular level with local regions of considerable plasticity and flexibility and molecular recognition (Bella et al. 2006).

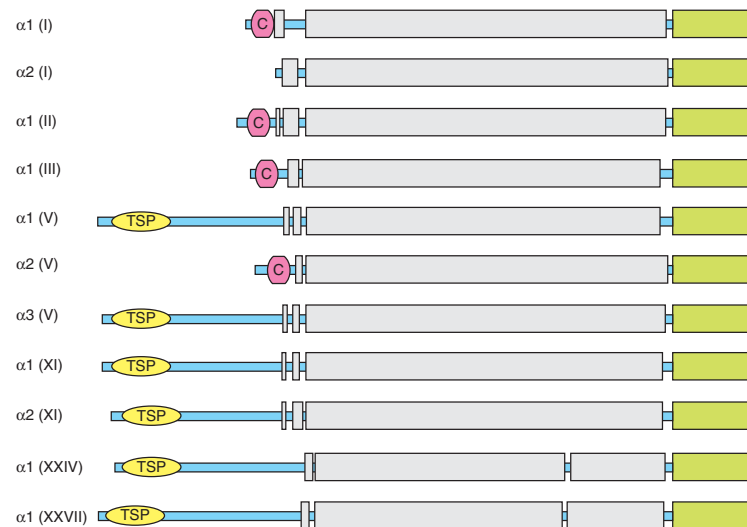
Collagens are Multidomain Proteins

Fibrillar collagens contain one major triple-helical domain. In contrast, collagens belonging to the fibril-associated collagens with interrupted triple-helices (FACIT), the multiplexins and

the membrane collagen subfamilies contain several triple-helical domains (Fig. 1). The discovery of collagen IX, the first FACIT, was a major breakthrough in the collagen field showing that triple-helical, collagenous domains could be interspersed among non-collagenous (NC)

domains (Shaw and Olsen 1991) and that collagens were multidomain proteins (Fig. 1). The non-collagenous domains participate in structural assembly and confer biological activities to collagens. They are frequently repeated within the same collagen molecule and are also

Fibril-forming collagens



Fibril-associated collagens with interrupted triple helices

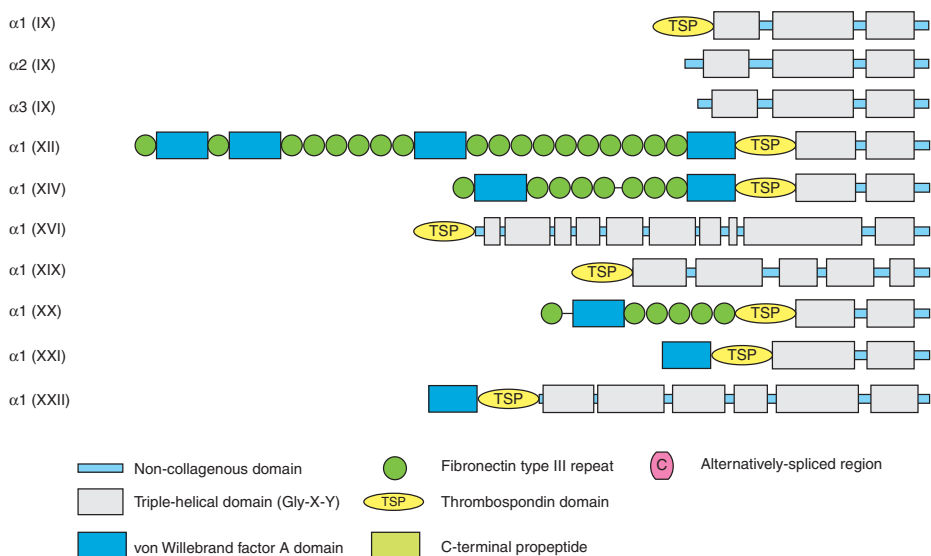


Figure 1. Structural organization of collagens. Domain composition and supramolecular assemblies of collagens. COL, Collagenous, triple-helical, domains; NC, Non-collagenous, nontriple-helical, domains. They are numbered from the carboxy- to the amino-terminus, except for collagen VII. (Figure continued on following page.)

S. Ricard-Blum

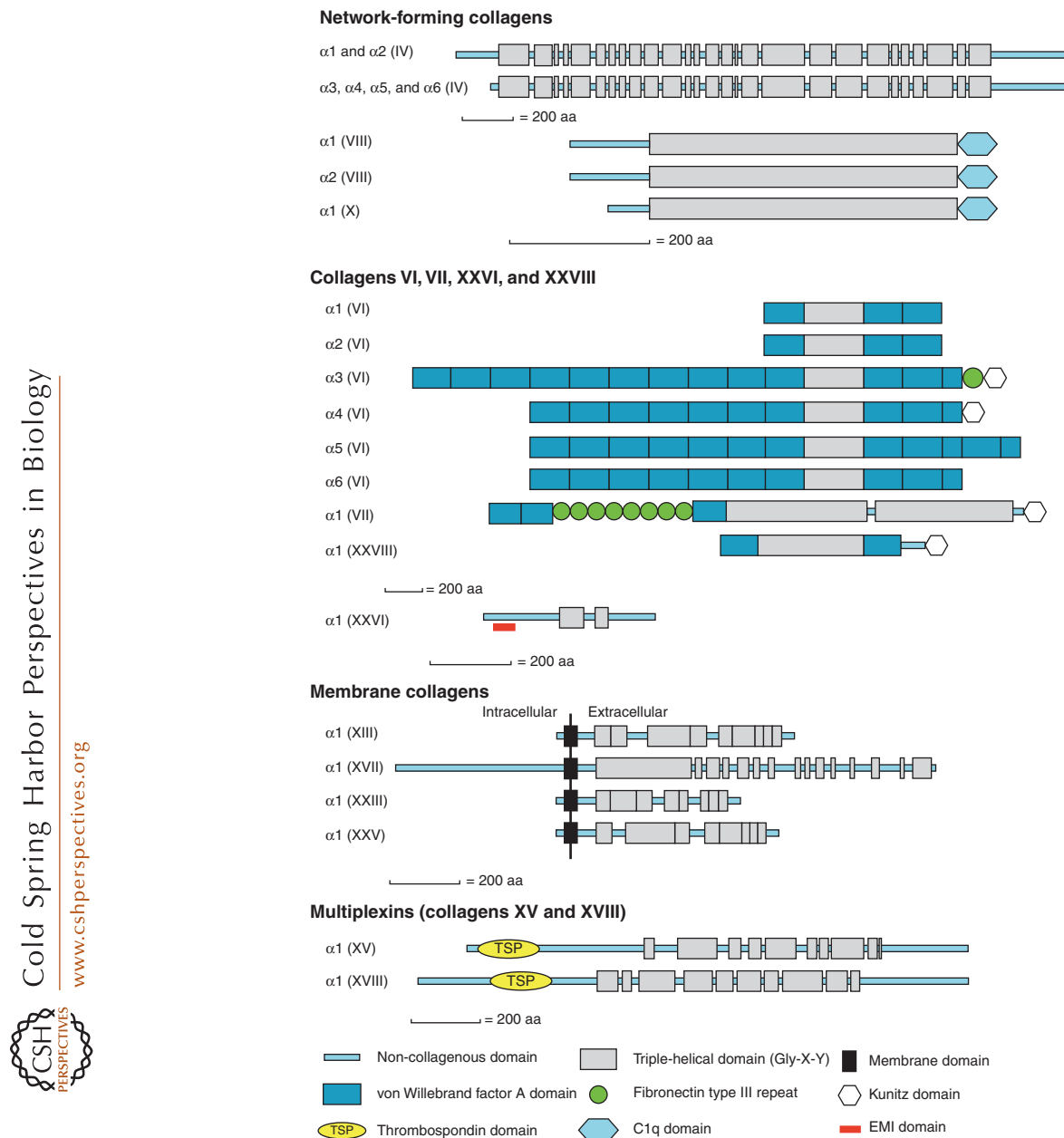


Figure 1. Continued.

found in other extracellular proteins. Fibronectin III, Kunitz, thrombospondin-1, and von Willebrand domains are the most abundant in collagens (Fig. 1). The von Willebrand domain that participates in protein-protein interactions is found in collagens VI, VII, XII, XIV, XX, XXI,

XXII, and XXVIII (Fig. 1). The role of the Kunitz domain that is cleaved during the maturation of collagens VI or VII is not yet elucidated. Collagen XXVIII closely resembles collagen VI by having a triple-helical domain flanked by von Willebrand domains at the amino-terminus

and a Kunitz domain at the carboxy-terminus, but its tissue distribution is more restricted than collagen VI (Veit et al. 2006). The four membrane collagens (Table 1) are single-pass type II membrane proteins comprising a cytoplasmic domain, a transmembrane domain, and several triple-helical domains located in the extracellular matrix (Franzke et al. 2005).

The Trimerization Domains

Folding of the triple helix requires trimerization domains that ensure the proper selection and alignment of collagen α chains, and allows the triple helix to fold in a zipper-like fashion (Khosnoodi et al. 2006). The formation of the triple-helix is initiated from the carboxyl terminus for fibrillar collagens and from the amino terminus for membrane collagens (Khosnoodi et al. 2006). The trimerization domains of collagens IV, VIII, and X that assemble into networks are their non-collagenous carboxy-terminal domains. The carboxy-terminal trimeric NC1 domains of the homotrimers $[\alpha 1(\text{VIII})]_3$ and $[\alpha 1(\text{X})]_3$ are comprised of a ten-stranded β sandwich, and expose three strips of aromatic residues that seem to participate in their supramolecular assembly (Bogin et al. 2002, Kvensakul et al. 2003) (PDB ID: 1O91). The trimerization domain of collagen XVIII, a member of the multiplexin subfamily, spans the first 54 residues of the non-collagenous carboxy-terminal (NC1) domain. Each chain has four β -strands, one α -helix, and a short 3_{10} helix (Boudko et al. 2009) (PDB ID: 3HON and 3HSH). This domain is smaller than the trimerization domain of fibrillar collagens (~250 residues) and shows high trimerization potential at picomolar concentrations (Boudko et al. 2009). The trimerization domain of collagen XV, the other multiplexin, has been modeled by homology. The trimerization of collagens IX and XIX (FACITs) is governed by their NC2 domain (Fig. 1), the second non-collagenous domain starting from the carboxyl terminus (Boudko et al. 2008, Boudko et al. 2010). The C1 subdomain located at the carboxyl terminus of $\alpha 1$, $\alpha 2$ and $\alpha 3$ chains of collagen VI is sufficient to promote chain

recognition and trimeric assembly (Khosnoodi et al. 2006).

SUPRAMOLECULAR ASSEMBLIES OF COLLAGENS

When visualized by electron microscopy after rotary shadowing, collagen molecules are visualized as rods varying in length from approximately 75 nm for collagen XII to 425 nm for collagen VII (Ricard-Blum et al. 2000). The molecular structure of collagen XV extracted from tissue has an unusual shape, most molecules being found in a knot/figure-of-eight/prezel configuration (Myers et al. 2007), although recombinant collagen XV appears elongated in rotary shadowing (Hurskainen et al. 2010). Kinks caused by the presence of non-collagenous domains are observed in electron microscopy of nonfibrillar collagen preparations. Non-collagenous domains can also be characterized by electron microscopy after rotary shadowing (e.g., the trimeric carboxy-terminal NC1 domain of collagen XVIII, Sasaki et al. [1998]).

Fibril-Forming Collagens

Collagens can be subdivided into subfamilies based on their supramolecular assemblies: fibrils, beaded filaments, anchoring fibrils, and networks (Fig. 2). Most collagen fibrils are comprised of several collagen types and are called heterotypic. Collagen fibrils are made of collagens II, XI, and IX or of collagens II and III (Wu et al. 2010) in cartilage, of collagens I and III in skin, and of collagens I and V in cornea (Bruckner et al. 2010). Furthermore, collagen fibrils can be considered as macromolecular alloys of collagens and non-collagenous proteins or proteoglycans. Indeed, small leucine-rich proteoglycans regulate fibrillogenesis, as do collagens V and XIV (Wenstrup et al. 2004; Ansoerge et al. 2009), and could also influence collagen cross-linking (Kalamajski and Oldberg 2010). Fibronectin and integrins could act as organizers, and collagens V and XI as nucleators for fibrillogenesis of collagens I and II (Kadler et al. 2008). Collagen fibrillogenesis has been

S. Ricard-Blum

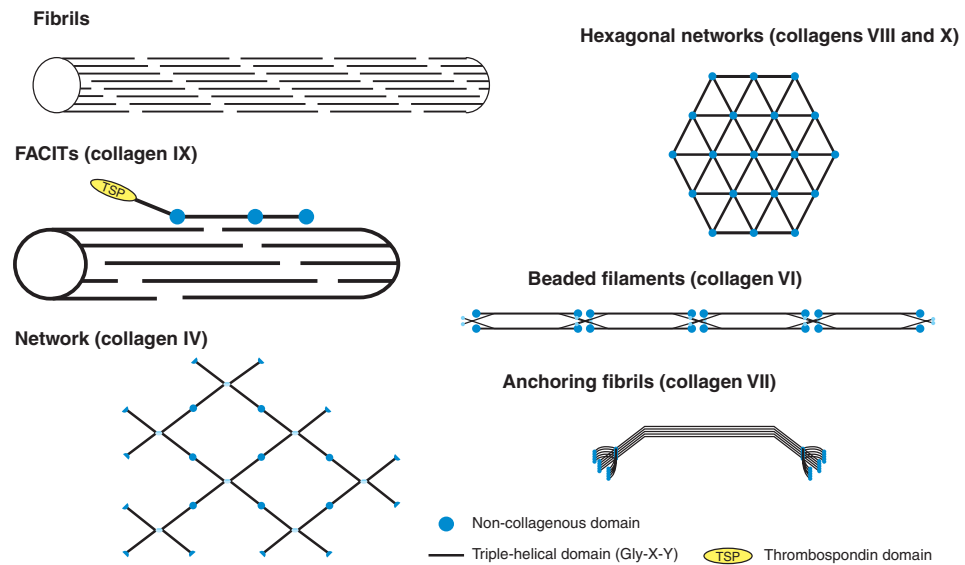


Figure 2. Supramolecular assemblies formed by collagens.

extensively studied in tendons, but the site of the initial steps of fibrillogenesis is not clearly defined so far. They may take place in extracellular compartments where fibril intermediates are assembled and mature fibrils grow through a fusion process of intermediates (Zhang et al. 2005), or they may occur intracellularly, in Golgi-to-membrane carriers containing 28-nm-diameter fibrils that are targeted to plasma membrane protrusions called fibripositors (Canty et al. 2004). The two models have been discussed (Banos et al. 2008).

Collagen fibrils show a banding pattern with a periodicity (D) of 64–67 nm (Brückner 2010), and collagen molecules are D-staggered within the fibrils. Collagen fibrils range in diameter from approximately 15 nm up to 500 nm or more depending on the tissue (Kadler et al. 2007; Brückner 2010). Collagen XXVII forms thin nonstriated fibrils (10 nm in diameter) that are distinct from the classical collagen fibrils (Plumb et al. 2007). The microfibrillar structure of collagen I fibrils has been investigated in situ by X-ray diffraction of rat tail tendons (Orgel et al. 2006). Collagen I forms supertwisted microfibrils of five molecules that interdigitate with neighboring microfibrils, leading to the quasi-hexagonal packing of collagen molecules

(Orgel et al. 2006). In contrast, cartilage fibrils are made of a core of four microfibrils (two of collagen II and two of collagen XI) surrounded by a ring of ten microfibrils, each microfibril containing five collagen molecules in cross-section (Holmes and Kadler 2006).

Fibril-Associated Collagens

The FACITs do not form fibrils by themselves, but they are associated to the surface of collagen fibrils. Collagen IX is covalently linked to the surface of cartilage collagen fibrils mostly composed of collagen II (Olsen 1997), and collagens XII and XIV are associated to collagen I-containing fibrils. Collagen XV is associated with collagen fibrils in very close proximity to the basement membrane and forms a bridge linking large, banded fibrils, likely fibrils containing collagens I and III (Amenta et al. 2005).

Network-Forming Collagens

Collagen IV forms a network in which four molecules assemble via their amino-terminal 7S domain to form tetramers, and two molecules assemble via their carboxy-terminal NC1 domain to form NC1 dimers. Because the NC1

domains are trimeric, the NC1 dimer is a hexamer. The three-dimensional structure of the hexameric form of the NC1 domain that plays a major role in collagen IV assembly and in the stabilization of the collagen $[\alpha 1(\text{IV})]_2\alpha 2(\text{IV})$ network has been determined (Sundaramoorthy et al. [2002], PDB ID: 1M3D, Than et al. [2002], PDB ID: 1LI1). It was hypothesized that collagen IV was stabilized via a covalent Met-Lys cross-link (Than et al. 2002), but studies of a crystal structure of the NC1 domain (PDB ID: 1T60, 1T61) at a higher resolution failed to confirm its existence (Vanacore et al. 2004). A combination of trypsin digestion and mass spectrometry analysis has led to the identification of a S-hydroxylysyl-methionine connecting Met93 and Hyl211 as the covalent cross-link that stabilizes the NC1 hexamer of the $[\alpha 1(\text{IV})]_2\alpha 2(\text{IV})$ network (Vanacore et al. 2005). Other collagen IV networks result from the assembly of the two molecular isoforms $[\alpha 1(\text{IV})]_2\alpha 2(\text{IV})$ and $[\alpha 5(\text{IV})]_2\alpha 6(\text{IV})$, and from the assembly of $\alpha 3(\text{IV})\alpha 4(\text{IV})\alpha 5(\text{IV})$ with itself (Borza et al. 2001). Collagens VIII and X form hexagonal networks in Descemet's membrane and in hypertrophic cartilage, respectively. Collagen VI forms beaded filaments and collagen VII assembles into anchoring fibrils connecting the epidermis to the dermis (Ricard-Blum et al. 2000; Gordon and Hahn 2010; Fig. 2).

Some collagens participate in distinct molecular assemblies. Collagen XVI is a component of microfibrils containing fibrillin-1 in skin, whereas it is incorporated into thin, weakly banded fibrils containing collagens II and XI in cartilage (Kassner et al. 2003). Collagen XII, a fibril-associated collagen, has been reported to be associated with basement membranes in zebra fish (Bader et al. 2009). Supramolecular assemblies of several collagens are able to interact as shown for the anchoring fibrils that are tightly attached to striated collagen fibrils (Villone et al. 2008).

COLLAGEN BIOSYNTHESIS

Collagen biosynthesis has been extensively studied for fibril-forming collagens that are synthesized as procollagen molecules comprised

of an amino-terminal propeptide followed by a short, nonhelical, N-telopeptide, a central triple helix, a C-telopeptide and a carboxy-terminal propeptide. Individual pro α chains are submitted to numerous posttranslational modifications (hydroxylation of proline and lysine residues, glycosylation of lysine and hydroxylysine residues, sulfation of tyrosine residues, Myllyharju and Kivirikko 2004) that are stopped by the formation of the triple helix. The heat shock protein 47 (HSP47) binds to procollagen in the endoplasmic reticulum and is a specific molecular chaperone of procollagen (Sauk et al. 2005). The stabilization of procollagen triple helix at body temperature requires the binding of more than 20 HSP47 molecules per triple helix (Makareeva and Leikin 2007). It has been recently suggested that intracellular Secreted Protein Acidic and Rich in Cysteine (SPARC) might be a collagen chaperone because it binds to the triple-helical domain of procollagens and its absence leads to defects in collagen deposition in tissues (Martinek et al. 2007).

Both propeptides of procollagens are cleaved during the maturation process (Green-span 2005). The N-propeptide is cleaved by procollagen N-proteinases belonging to the A Disintegrin And Metalloproteinase with Thrombospondin motifs (ADAMTS) family, except the N-propeptide of the pro $\alpha 1(\text{V})$ chain that is cleaved by the procollagen C-proteinase also termed Bone Morphogenetic Protein-1 (BMP-1) (Hopkins et al. 2007). BMP-1 cleaves the carboxy-terminal propeptide of procollagens, except the carboxy-terminal propeptide of the pro $\alpha 1(\text{V})$ chain, that is processed by furin. The telopeptides contain the sites where cross-linking occurs. This process is initiated by the oxidative deamination of lysyl and hydroxylslyl residues catalyzed by the enzymes of the lysyl oxidase family (Mäki 2009).

COVALENT CROSS-LINKING OF COLLAGENS

Collagen is considered as an elastic protein with a resilience of $\sim 90\%$. Collagen fibrils are thus able to deform reversibly and their mechanical

S. Ricard-Blum

properties can be investigated by force spectroscopy (Gutsmann et al. 2004). The mechanical properties of fibril-forming collagens I, II, III, V, and XI are dependent on covalent cross-links including (1) Disulfide bonds (in collagens III, IV, VI, VII, and XVI); (2) the N^ε(γ-glutamyl)lysine isopeptide, the formation of which is catalyzed by transglutaminase-2 in collagens I, III, V/XI, and VII (Esposito and Caputo 2005); (3) reducible and mature cross-links produced *via* the lysyl oxidase pathway; and (4) advanced glycation end products (Avery and Bailey 2006). Furthermore, a hydroxylysine-methionine cross-link involving a sulfilimine (-S=N-) bond has been identified in collagen IV (Vanacore et al. 2009).

Lysyl-mediated cross-linking involves lysine, hydroxylysine, and histidine residues, and occurs at the intramolecular and intermolecular levels between collagen molecules belonging either to the same type or to different

types (I/II, I/III, I/V, II/III, II/IX, II/XI, and V/XI) (Eyre et al. 2005; Wu et al. 2009, 2010). Cross-linking is tissue-specific rather than collagen-specific. Reducible, bifunctional, cross-links (aldimines and keto-imines) are formed in newly synthesized collagens, and they spontaneously mature into nonreducible trifunctional cross-links, pyridinoline and deoxypyridinoline in bone and cartilage, pyrrole cross-links in bone, and histidinohydroxylysinonorleucine in skin (Eyre and Wu 2005; Robins 2007) (Fig. 3). Another mature cross-link, an arginyl ketoimine adduct called arginine because of the contribution of one arginine residue, has been identified in cartilage (Eyre et al. 2010) (Fig. 3). Cross-link maturation provides added resistance to shear stress. Pyridinoline and deoxypyridinoline are used as urinary markers of bone resorption in patients with bone diseases such as osteoporosis (Saito and Marumo 2010).

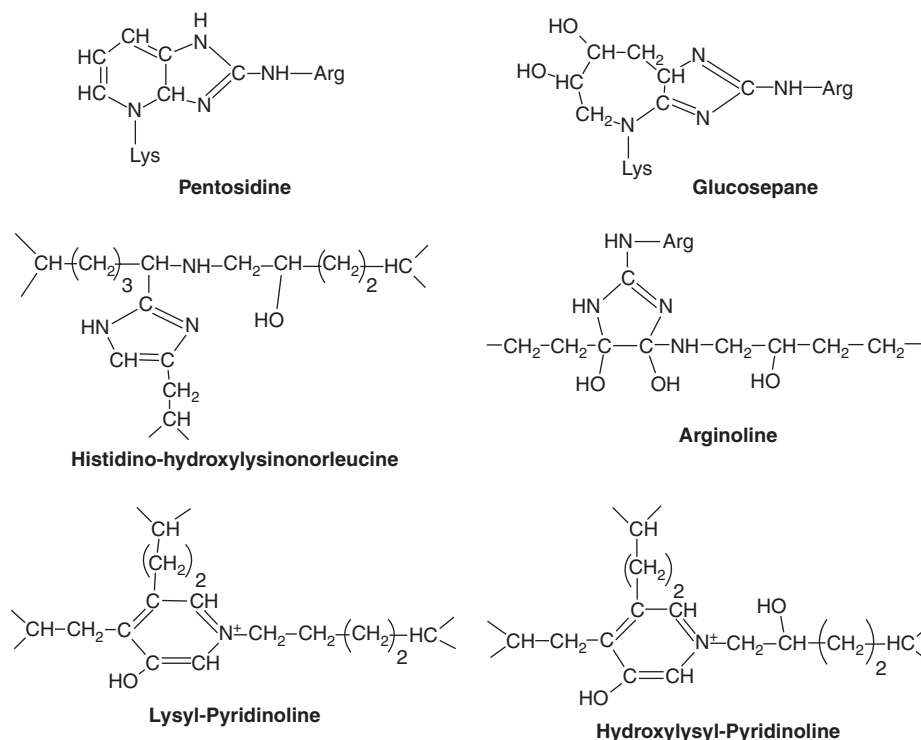


Figure 3. Collagen cross-links. Lysyl-mediated mature cross-links: arginine, deoxypyridinoline, pyridinoline, and histidinohydroxylysinonorleucine. Advanced glycation endproducts: glucosepane and pentosidine.

Collagens are long-lived proteins that are modified by glycation (Avery and Bailey 2006). Glycation increases with age and several advanced glycation endproducts act as cross-links that contribute to the progressive insolubilization and to the increased stiffness of collagens in aged tissues. Two lysine-arginine cross-links, pentosidine (a fluorescent product formed from ribose), and glucosepane (a nonfluorescent product formed from glucose) have been identified in collagens. Glucosepane, the most abundant cross-link in senescent skin collagen, is able to cross-link one in five collagen molecules in the skin of the elderly (Sjöberg and Bulterijs 2009).

COLLAGEN DEGRADATION

Matrix metalloproteinases (MMPs) are zinc-dependent endopeptidases belonging to the metzincin superfamily. They participate in physiological (development and tissue repair) and pathological (tumorigenesis and metastasis) processes. Fibril-forming collagens I, II, and III are cleaved by MMP-1 (interstitial collagenase), MMP-8 (neutrophil collagenase), MMP-13 (collagenase 3) that generate three-quarter and one-quarter sized fragments, and by membrane-anchored MMP-14. MMP-2 is also able to cleave collagen I (Klein and Bischoff 2010). Collagen II is a preferential substrate of MMP-13, whereas collagens I and III are preferentially cleaved by MMP-1 and MMP-8 (Klein and Bischoff 2010). Denatured collagens and collagen IV are degraded by MMP-2 and MMP-9 (also known as 72-kDa and 92-kDa gelatinases respectively). In contrast to the $[\alpha 1(I)]_2\alpha 2(I)$ heterotrimer of collagen I, the $[\alpha 2(I)]_3$ homotrimer is not degraded by mammalian collagenases. This is because of resistance of the homotrimer to local triple helix unwinding by MMP-1 because it has higher triple helix stability near the MMP cleavage site (Han et al. 2010). MMPs also contribute to the release of bioactive fragments or matricryptins such as endostatin and tumstatin from full-length collagens (Ricard-Blum and Ballut 2011). Another group of enzymes, collectively called sheddases (Murphy 2009) releases the

ectodomain of membrane collagens as soluble forms.

COLLAGEN RECEPTORS

Collagens are deposited in the extracellular matrix, but they participate in cell-matrix interactions via several receptor families (Heino et al. 2007, 2009; Humphries et al. 2006; Leitinger and Hohenester 2007). They are ligands of integrins, cell-adhesion receptors that lack intrinsic kinase activities. Collagens bind to integrins containing a $\beta 1$ subunit combined with one of the four subunits containing an αA domain ($\alpha 1$, $\alpha 2$, $\alpha 10$, and $\alpha 11$) via GFOGER-like sequences, O being hydroxyproline (Humphries et al. 2006; Heino et al. 2007). There are other recognition sequences in collagens such as KGD in the ectodomain of collagen XVII, which is recognized by $\alpha 5\beta 1$ and $\alpha v\beta 1$ integrins but not by the “classical” collagen receptors (Heino et al. 2007). Several bioactive fragments resulting from the proteolytic cleavage of collagens are ligands of $\alpha v\beta 3$, $\alpha v\beta 5$, $\alpha 3\beta 1$, and $\alpha 5\beta 1$ integrins (Ricard-Blum and Ballut 2011).

Collagens I–III are also ligands of the dimeric discoidin receptors DDR1 and DDR2 that possess tyrosine kinase activities (Leitinger and Hohenester 2007). The major DDR2-binding site in collagens I–III is a GVMGFO motif (Heino et al. 2009). The crystal structure of a triple-helical collagen peptide bound to the discoidin domain (DS) of DDR2 has provided insight into the mechanism of DDR activation that may involve structural changes of DDR2 surface loops induced by collagen binding (Carafoli et al. 2009) (PDB ID: 2WUH). The activation may result from the simultaneous binding of both DS domains in the dimer to a single collagen triple helix, or DS domains may bind collagen independently (Carafoli et al. 2009). The soluble extracellular domains of DDR1 and DDR2 regulate collagen deposition in the extracellular matrix by inhibiting fibrillogenesis (Flynn et al. 2010). DDR2 affects mechanical properties of collagen I fibers by reducing their persistence length and their Young's modulus (Sivakumar and Agarwal 2010).

S. Ricard-Blum

Collagens bind to glycoprotein VI (GPVI), a member of the paired immunoglobulin-like receptor family, on platelets (Heino et al. 2007), and to the inhibitory leukocyte-associated immunoglobulin-like receptor-1 (LAIR-1, Leb- bink et al. 2006). Both receptors recognize the GPO motif in collagens. Ligands of LAIR-1 are fibrillar collagens I, II, and III, and membrane collagens XIII, XVII, and XXIII. Collagens I and III are functional ligands of LAIR-1 and inhibit immune cell activation in vitro. LAIR-1 binds multiple sites on collagens II and III (Leb- bink et al. 2009). LAIR-1 and LAIR-2 are high affinity receptors for collagens I and III. They bind to them with higher affinity than GPVI (Lebbink et al. 2006, Lebbink et al. 2008), but three LAIR-1 amino acids central to collagen binding are conserved in GPVI (Brondijk et al. 2010). Fibril-forming collagens and collagen IV are also ligands of Endo180 (urokinase-type plasminogen activator associated protein), a member of the macrophage mannose-receptor family that mediates collagen internalization (Leitinger and Hohenester 2007; Heino et al. 2009). The identification of collagen sequences that bind to receptors has benefited from the Toolkits (overlapping synthetic trimeric pep- tides encompassing the entire triple-helical domain of human collagens II and III) devel- oped by Farndale et al. (2008).

FUNCTIONS OF COLLAGENS

Fibrillar collagens are the most abundant colla- gens in vertebrates where they play a structural role by contributing to the molecular archi- tecture, shape, and mechanical properties of tissues such as the tensile strength in skin and the resistance to traction in ligaments (Kadler 1995, Ricard-Blum et al. 2000). Several colla- gens, once referred to as “minor” collagens, are crucial for tissue integrity despite the fact that they are present in very small amounts. Collagen IX comprises 1% of collagen in adult articular cartilage (Martel-Pelletier et al. 2008) and collagen VII, crucial for skin integrity, con- stitutes only about 0.001% of total collagens in skin (Bruckner-Tuderman et al. 1987). Excess collagen is deposited in the extracellular matrix

during fibrosis and fibrillogenesis is a new tar- get to limit fibrosis by blocking telopeptide- mediated interactions of collagen molecules (Chung et al. 2008). Collagens are no longer restricted to a triple helix, banded fibrils or to a structural and scaffold role. As stated by Hynes (2009) for the extracellular matrix, collagens are not “just pretty fibrils.” Collagens interact with cells through several receptors, and their roles in the regulation of cell growth, differentiation, and migration through the binding of their receptors is well documented.

Some collagen types with a restricted tissue distribution exert specific biological functions. Collagen VII is a component of anchoring fibrils, and participates in dermal-epidermal adhesion. Collagen X, expressed in hypertro- phic cartilage, plays a role in endochondral ossi- fication and contributes to the establishment of a hematopoietic niche at the chondro-osseous junction (Sweeney et al. 2010). Collagen XXII is present only at tissue junctions such as the myotendinous junction in skeletal and heart muscle (Koch et al. 2004). An association be- tween COL22A1 and the level of serum cre- atinine, the most important biomarker for a quick assessment of kidney function, has been detected in a meta-analysis of genome-wide data. This association may reflect the biological relationship between muscle mass formation and creatinine levels (Pattaro et al. 2010). Colla- gen XXIV is a marker of osteoblast differentia- tion and bone formation (Matsuo et al. 2008), and collagen XXVII appears to be restricted mainly to cartilage into adulthood. It is associ- ated with cartilage calcification and could play a role in the transition of cartilage to bone during skeletogenesis (Hjorten et al. 2007). Its involve- ment in skeletogenesis has been confirmed in zebra fish where it plays a role in vertebral min- eralization and postembryonic axial growth (Christiansen et al. 2009). The $\alpha 5(VI)$ chain is not expressed in the outer epidermis of patients with atopic dermatitis, a chronic inflammatory skin disorder and a manifestation of allergic disease, suggesting that it contributes to the integrity and function of the epidermis (Söder- häll et al. 2007). The association of COL6A5/ COL29A1 with atopy has been confirmed at

the genetic level (Castro-Giner et al. 2009). The gene coding for the $\alpha 1$ chain of collagen XVIII has also been identified as a new potential candidate gene for atopy (Castro-Giner et al. 2009).

The four membrane collagens seem to fulfill different functions. Collagen XIII affects bone formation and may have a function in coupling the regulation of bone mass to mechanical use (Ylönen et al. 2005). Collagen XVII is a major structural component of the hemidesmosome (Has and Kern 2010), whereas collagen XXIII is associated with prostate cancer recurrence and distant metastases (Banyard et al. 2007). However, membrane collagens XIII, XVII (Sepänen et al. 2006), and XXV (Hashimoto et al. 2002) are expressed in neurons, or neuronal structures, and collagen XXVIII is predominantly expressed in neuronal tissue (Veit et al. 2006). New roles of collagens have been found in the development of the vertebrate nervous system, when collagen IV plays a role at the neuromuscular junction as a presynaptic organizer (Fox et al. 2007, 2008). Collagen XIX is expressed by central neurons, and is necessary for the formation of hippocampal synapses (Su et al. 2010). Several collagens (IV, VI, XVIII, and XXV) are deposited in the brains of patients with Alzheimer's disease where they bind to the amyloid β peptide. Furthermore, there is genetic evidence of association between the COL25A1 gene and risk for Alzheimer's disease (Forsell et al. 2010). Collagen VI seems to protect neurons against A β toxicity (Cheng et al. 2009).

MATRICRYPTINS OF COLLAGENS

Bioactive fragments released by proteolytic cleavage of collagens regulate a number of physiological and pathological processes such as development, angiogenesis, tumor growth and metastasis, and tissue repair (Nyberg et al. 2005; Ricard-Blum and Ballut 2011). These fragments, called matricryptins, increase the functional diversity of collagens because most of them possess biological activities that are different from their parent molecule. A single collagen type can give rise to several matricryptins (collagen IV) (Table 3). Most collagen matricryptins are derived from basement membrane collagens (collagens IV, VIII, and XVIII) (Table 3) or located in the basement membrane zone (collagens XV and XIX) and show antiangiogenic and antitumoral properties (Nyberg et al. 2005, Ricard-Blum and Ballut 2011). Endostatin, the carboxy-terminal fragment of collagen XVIII, and tumstatin, the carboxy-terminal domain of the $\alpha 3(\text{IV})$ chain, have been extensively studied. The extracellular domains of membrane collagens released by shedding because of furin-like proprotein convertases (collagens XIII, XXIII, XXV), or ADAM-9 and ADAM-10 (collagen XVII) (Franzke et al. 2009) show paracrine activities and might be considered as matricryptins (Table 3). Matricryptins are potential drugs and Endostar, a derivative of endostatin, has been approved in 2005 in China for the treatment of nonsmall cell lung cancer in conjunction with chemotherapy (Ling et al. 2007).

Table 3. Major matricryptins of collagens.

Collagens	Collagen α chain	Matricryptins	Domain
Collagen IV	$\alpha 1(\text{IV})$ chain	Arresten	NC1
	$\alpha 2(\text{IV})$ chain	Canstatin	NC1
	$\alpha 3(\text{IV})$ chain	Tumstatin	NC1
	$\alpha 4(\text{IV})$ chain	Tetrastatins 1-3	
	$\alpha 5(\text{IV})$ chain	Pentastatins 1-3	
	$\alpha 6(\text{IV})$ chain	NC1 $\alpha 6(\text{IV})$	NC1
		Hexastatins 1-2	
Collagen VIII	$\alpha 1(\text{VIII})$ chain	Vastatin	NC1
Collagen XV	$\alpha 1(\text{XV})$ chain	Restin	NC1
Collagen XVIII	$\alpha 1(\text{XVIII})$ chain	Endostatin	NC1
Collagen XIX	$\alpha 1(\text{XIX})$ chain		NC1

S. Ricard-Blum

**GENETIC AND ACQUIRED DISEASES
OF COLLAGENS**

Several autoimmune disorders involve auto-antibodies directed against collagens. Collagen VII is the autoantigen of epidermolysis bullosa acquisita (Ishii et al. 2010), and collagen XVII

is the major autoantigen of the skin blistering disease bullous pemphigoid (Franzke et al. 2005). The NC1 domain of the $\alpha 3(\text{IV})$ chain contains the epitopes recognized by the anti-glomerular basement membrane antibodies found in patients with Goodpasture syndrome characterized by glomerulonephritis and lung

Table 4. Genetic diseases because of mutations in collagen genes.

Gene	Disease	References, databases
COL1A1	Osteogenesis imperfecta	Marini et al. (2007)
COL1A2	Ehlers–Danlos syndrome	Dalgleish (1997, 1998) www.le.ac.uk/genetics/collagen Bodian and Klein (2009) http://collagen.stanford.edu/
COL2A1	Spondyloepiphyseal dysplasia Spondyloepimetaphyseal dysplasia, Achondrogenesis, hypochondrogenesis Kniest dysplasia, Stickler syndrome	Bodian and Klein (2009) http://collagen.stanford.edu/
COL3A1	Ehlers–Danlos syndrome	Dalgleish (1997, 1998) www.le.ac.uk/genetics/collagen Bodian and Klein (2009) http://collagen.stanford.edu/
COL4A1	Familial porencephaly Hereditary angiopathy with nephropathy, aneurysms and muscle cramps syndrome	Van Agtmael and Bruckner-Tuderman (2010)
COL4A3	Alport syndrome	Van Agtmael and Bruckner-Tuderman (2010)
COL4A4	Benign familial haematuria	
COL4A5	Alport syndrome	Bateman et al. (2009), Van Agtmael and Bruckner-Tuderman (2010)
COL4A6	Leiomyomatosis	
COL5A1	Ehlers–Danlos syndrome	Callewaert et al. (2008)
COL5A2		
COL6A1	Bethlem myopathy	Lampe and Bushby (2005)
COL6A2	Ullrich congenital muscular dystrophy	
COL6A3		
COL7A1	Dystrophic epidermolysis bullosa	Fine (2010)
COL8A2	Corneal endothelial dystrophies	Bateman et al. (2009)
COL9A1	Multiple epiphyseal dysplasia	Carter and Raggio (2009)
COL9A2		
COL9A3	Multiple epiphyseal dysplasia Autosomal recessive Stickler syndrome	Carter and Raggio (2009)
COL10A1	Schmid metaphyseal chondrodysplasia	Grant (2007)
COL11A1	Stickler syndrome Marshall syndrome	Carter and Raggio (2009)
COL11A2	Stickler syndrome Marshall syndrome Otospondylomegal epiphyseal dysplasia Deafness	Carter and Raggio (2009)
COL17A1	Junctional epidermolysis bullosa-other	Has and Kern (2010)
COL18A1	Knobloch syndrome	Nicolae and Olsen (2010)

hemorrhage (Khoshnoodi et al. 2008). Bronchiolitis obliterans syndrome, the most common cause of lung transplant failure, is associated with a strong cellular immune response to collagen V (Burlingham et al. 2007).

Many disorders are caused by mutations in the genes coding for collagen α chains (Table 4) (Lampe and Bushby 2005; Callewaert et al. 2008; Bateman et al. 2009; Carter and Raggio 2009; Fine 2010). Mutations of collagen I, II, and III genes are catalogued in the human collagen mutation database (Dalglish 1997, 1998) and in the COLdb database that links genetic data to molecular function in fibrillar collagens (Bodian and Klein 2009). Regions rich in osteogenesis imperfecta lethal mutations align with collagen binding sites for integrins and proteoglycans in the helical domain of type I collagen (Marini et al. 2007). The mutations affect the extracellular matrix by decreasing the amount of secreted collagen(s), impairing molecular and supramolecular assembly through the secretion of a mutant collagen, or by inducing endoplasmic reticulum stress and the unfolded protein response (Bateman et al. 2009).

CONCLUDING REMARKS

During the last 40 years, the collagen field has evolved from collagen chemistry to cell therapy as recounted by Michael Grant (2007). Twenty-eight collagen types have been identified and characterized at the molecular level. Their functions have been determined either through direct assays or from the generation of knockout mice and the knowledge of defects occurring in tissues of patients with genetic diseases because of mutation(s) in genes coding for collagens. Cell therapy gives promising results for recessive dystrophic epidermolysis bullosa (Kern et al. 2009; Conget et al. 2010), and osteogenesis imperfecta (Niyibizi and Li 2009). To understand how collagens work in a concerted fashion with their extracellular and cell-surface partners, a global, integrative approach is needed. Ligand-binding sites, functional domains and mutations have been mapped on the collagen I fibril that appears to

be composed of cell interaction domains and matrix interaction domains (Sweeney et al. 2008). Defining the structures and functions of collagen domains along the collagen fibril will provide new insights into collagen fibril functions, and into their possible modulation, specifically in fibroproliferative diseases where collagen fibrillogenesis is a new target to limit fibrosis (Chung et al. 2008). The binding force between collagen and other proteins can be calculated by atomic microscopy, and these measurements, in addition to kinetics, affinity and thermodynamics data, could be used to hierarchize interactions participating in biological processes. Interaction data on collagens and other extracellular biomolecules are stored in a database called MatrixDB (<http://matrixdb.ibcp.fr>) (Chautard et al. 2009). These data can be used to build extracellular interaction networks of a molecule, a tissue or a disease and to make functional hypothesis. New tools to identify binding partners of a protein (protein and glycosaminoglycan arrays probed by surface plasmon resonance imaging (Faye et al. 2009, 2010), and a proteomics workflow to isolate complexes associated with integrin adhesion receptors (Humphries et al. 2009), will be helpful in deciphering the functions of collagens at the systems biology level.

ACKNOWLEDGMENTS

Romain Salza (UMR 5086 CNRS-University Lyon 1, France) is gratefully acknowledged for drawing the figures of the manuscript, and David J. Hulmes (UMR 5086 CNRS - University Lyon 1, France) for his critical reading of the manuscript and his suggestions.

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S. Ricard-Blum

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S. Ricard-Blum

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Cold Spring Harb Perspect Biol 2011; doi: 10.1101/cshperspect.a004978 originally published online December 15, 2010

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