A Primer of Collagen Biology: Synthesis, Degradation, Subtypes, and Role in Dupuytren's Disease

17

Susan Emeigh Hart

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S.E. Hart

Intrexon Corporation, Germantown, MD, USA e-mail: SHart@intrexon.com

17.1 Introduction

Historically, investigations into the pathogenesis of Dupuytren's disease have focused on the roles of genetic and epigenetic factors (such as growth factors, trauma, concurrent medications and/or disease states) and their influence on the cellular components of the subcutaneous tissues (fibroblasts and myofibroblasts) (reviewed in Cordova et al. 2005; Al-Qattan 2006; Rayan 2007) The collagen matrix (the primary constituent of the cords found in late stage Dupuytren's contracture) has been considered merely a biomarker of the cellular processes, with little importance as a therapeutic target (except as an inert structure whose disruption or removal will result in symptomatic relief to the patient).

However, more recent investigations into the genomics and proteomics of cells and tissues isolated from surgically excised Dupuytren's tissue have revealed significant overlap with the patterns of gene and protein expression in normal wound healing. These findings suggest that the abnormalities in Dupuytren's disease may represent an aberrant or exaggerated wound healing response in affected patients, a process which is largely mediated through the interaction of the fibroblast with the extracellular matrix, specifically via attachments to collagen fibers. The genomic and proteomic changes detected at the cellular level, coupled with structural differences in collagen components of Dupuytren's tissue compared to those in normal palmar fascia, indicate an additional contribution to the pathogenesis of this disease from an upset in the normal balance of extracellular matrix remodeling.

Thus, the collagen matrix continues to represent a key therapeutic target in Dupuytren's disease, both as

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Classification	Types	Tissue distribution	General functions	
Fibril forming	I, II, III, V, XI,	Skin, bone, tendon, blood vessels, cornea (I, III)	Primary structural components of	
	XXIV, XXVII	Reticular fibers (III)	extracellular matrix (ECM)	
		Associated with Type I (V) or Type II (XI)		
		Cartilage, intervertebral disk, vitreous (II)		
		Developing/embryonic tissues (XXIV, XXVII)		
Network	IV, VIII, X	Widespread, all basement membranes (IV)	Adhesion	
		Descement's membrane, endothelial cells (VIII)	Occlusion	
		Hypertrophic cartilage (X)	Source of matricryptins (IV, VIII) ^b	
Anchoring fibrils	VII	Dermal–epidermal junctions (skin, oral mucosa, genitourinary tract)	Anchoring	
FACIT	IX, XII, XIV, XIX, XX, XXI, XXII	Widespread, esp. corneal epithelium (XX)	Integration, stabilization, and structural regulation of ECM	
		Associated w. Type I (XII, XIV) or Type II (IX)	Signal transduction	
		Skeletal muscle (XIX)		
		Cornea and vitreous (IX)		
		Blood vessel wall (XXI)		
Transmembrane	XIII, XVII, XXIII,	Hemidesmosomes (XVII)	Cell-cell/cell-matrix adhesion	
(MACIT)	XXV	Neuromuscular junction (XIII)	Regulation of embryonic development	
Beaded filament (microfibrillar)	VI , XXVIII	Widespread in connective tissues, especially adipose and synovial membranes (VI)	Integration	
		Peripheral nerves (XXVIII)	Myelination (XXVIII)	
		Associated with Type VI in blood vessels (VI)		
Endostatin	XV, XVI, XVIII	Associated with basement membranes (widespread),	Antiangiogenic	
producing (multiplexins ^a)		but especially blood vessels, skeletal muscle (XV), and eye (XVIII)	Source of matricryptins ^b	
Unknown	XXVI	Testis and ovary (during development), elastic fibers	Unknown	

 Table 17.1
 Functional/structural classification and tissue distribution of collagen subtypes

Information from the following sources: van der rest and Garrone (1991); Prockop and Kivirikko (1995); Kuo et al. (1997); Zeichen et al. (1999); Ortega and Werb (2002); Gelse et al. (2003); Ricard-Blum and Ruggerio (2005); Khoshnoodi et al. (2006); Veit et al. (2006); Shoulders and Raines (2009)

FACIT Fibril Associated Collagens with Interrupted Triple Helices, MACIT Membrane Associated Collagens with Interrupted Triple Helices

^aMultiplexin indicates collagen with multiple triple-helix domains and interruptions

^bMatricryptin indicates C-terminal fragment with growth factor or other pharmacologic effect derived by proteolytic cleavage from the parent collagen molecule

a structural and as a functional component. An understanding of its structure, biology, regulation, and potential roles in Dupuytren's disease are important to development of novel approaches in modulating the disease via this target.

17.2 Collagens: Structurally and Functionally Diverse Proteins with Common Features

Collagens are an extremely structurally and functionally diverse group of proteins that are defined as such based on the following common features:

- Somewhere within the molecule, one or more triplehelical motifs consisting of three polypeptide chains (McAlinden et al. 2003; Khoshnoodi et al. 2006)
- The presence of multiple Gly-X-Y repeats (with X and Y usually being proline or hydroxyproline), which permit the formation of the helical structures (van der Rest and Garrone 1991; Ricard-Blum and Ruggerio 2005)
- A high content (up to 50% of the proline residues) of hydroxyproline, required for stabilization of the triple helix (Gelse et al. 2003; Shoulders and Raines 2009)

To date, 28 different types of collagen (the products of 34 distinct genes) have been identified; these have been



classified, based on their structural and/or functional similarity, into eight different classes (reviewed in van der Rest and Garrone 1991; Prockop and Kivirikko 1995; Gelse et al. 2003; Ricard-Blum and Ruggerio 2005; Khoshnoodi et al. 2006). An overview of collagen classification and tissue distribution is presented in Table 17.1.

The fibrillar collagens are the most abundant class of collagens and are the best characterized; all of them consist almost exclusively of triple-helical collagen composed of Gly-X-Y repeats which is deposited in the extracellular space in the form of overlapping fibrils. Type I is the primary structural component of the extracellular matrix in most tissues. In fibrils, it is usually found as a complex protein in combination with Type V collagen, which serves as a nucleus for fibril formation. Type III collagen fibrils are also referred to as reticulin; this collagen type is found in healing wounds, embryonic connective tissues, and as a primary structural component in tissues such as skin, lung, and blood vessels where greater elasticity is needed (reviewed in Prockop and Kivirikko 1995; Ricard-Blum and Ruggerio 2005; Kadler et al. 2008; Shoulders and Raines 2009). An increase in the content of Type III relative to Type I collagen compared to the normal palmar fascia is considered a hallmark feature of Dupuytren's disease tissue, regardless of the stage of the disease (Hanyu et al. 1984; Melling et al. 1999, 2000).

Other collagens can be found within Dupuytren's tissue or associated with adjacent structures, although they have not been implicated in the pathogenesis of this condition. These include Type IV (a primary component of epidermal and vascular basement membranes as well as perineural structures), Type VI (an important component of synovial membranes and blood vessel basement membranes), and Type VII (plays a role in anchoring the epidermis to the dermis).

17.3 Collagen Remodeling: Process and Controls

The components of the extracellular matrix are in a constant state of flux, with the changes in the composition and quantity of the matrix collagen dictated by environmental stimuli and stage of development. In order for new collagen to be deposited, the existing collagen must be removed; these two processes occur simultaneously in a balanced fashion in normal tissues so that there is no net change in either the quantity or composition of the extracellular matrix present (Fig. 17.1). Disruption of the dynamic balance between these two processes can occur in response to physiologic need but also occurs in a number of pathologic conditions, including Dupuytren's disease (Mansell and Bailey 2004; Stetler-Stevenson 1996).



Fig. 17.2 Key control points in collagen synthesis. The rate of collagen deposition is determined by the sum of the following processes: (1) the rate of COL gene expression and translocation of collagen monomers into the endoplasmic reticulum (ER), (2) aggregation of monomers into trimers via their C propeptides, which initiates triple-helix formation. Heat shock protein 47 (Hsp47) is required to prevent "tangling" of the monomers and to slow helix formation to allow for (3) hydroxylation of proline and lysine residues by prolyl-hydroxylase (P-OH'ase) and lysyl hydroxylase (L-OH'ase) and formation of intramolecular cross-links by these hydroxy amino acids, stabilizing the triple helix, (4) translocation into the Golgi apparatus and aggregation into

Of the two processes involved in collagen remodeling, the process of collagen deposition is more complex and thus can be regulated at multiple levels. In contrast, collagen degradation is primarily regulated by controlling the quantity and activity of collagen digesting enzymes.

17.3.1 Collagen Deposition

The transformation of labile newly synthesized collagen polypeptides into the stable collagen fibrils present within the extracellular matrix is a slow and complex process. The rate and effectiveness of collagen deposifibril "stacks" (speed of translocation depends on speed and effectiveness of triple-helix formation), (5) deposition of stacks into the extracellular space via the formation of "fibripositors" and cleavage of the N- and C-terminal propeptides by N- and C-terminal propeptidases (represented by scissors), (6) overlapping aggregation of collagen tripeptides into fibrils, enhanced by the presence of β_1 integrins ($\alpha\beta$) on the cell surface, and (7) stabilization of the collagen fibrils by intermolecular cross-links through the action of lysyl oxidase (L-oxidase) (Figure adapted from material in Kadler et al. 1996; Persikov and Brodsky 2002; Canty and Kadler 2005; Khoshnoodi et al. 2006; Kadler et al. 2008)

tion (the net result of synthesis and fibrillogenesis) is thus governed at many levels (as depicted in Fig. 17.2). These are described specifically as they relate to the fibrillar collagens in the following sections.

As with all proteins, the rate of collagen deposition can be regulated by up- or downregulation of the *COL* genes responsible for the synthesis of the collagen α chains. These are synthesized directly into the endoplasmic reticulum to undergo the posttranslational modifications needed for both the formation and stabilization of triple-helical procollagen. Assembly of collagen trimers from the monomeric α chains occurs due to the interaction of the C-NC domains located near the C termini of these molecules (Khoshnoodi et al. 2006).

Once trimerization is complete, triple-helix formation commences in a C to N direction; formation and stabilization of the helix requires conversion of proline residues located in the -Y position of the Gly-X-Y collagen motif to hydroxyproline through the action of prolyl-4hydroxylase and its essential cofactor, ascorbic acid (vitamin C). Further stabilization of the triple helix results from the action of lysyl hydroxylase which generates hydroxylysine from lysine residues within the collagen molecule; the hydroxylysine residues provide sites for the addition of glucose and galactose molecules to the procollagen molecules and are also critical to extracellular cross-linking of collagen fibrils. These modifications serve to increase the thermal stability of the collagen molecules (Prockop and Kivirikko 1995; Persikov and Brodsky 2002; Canty and Kadler 2005).

Additional stabilization of the forming procollagen triple helices results from their association with the molecular chaperone heat shock protein 47 (Hsp47). This protein becomes associated with the newly synthesized collagen α chains, facilitating trimerization; it also is critical to the correct formation of the procollagen triple helix by preventing premature and incorrect "folding" of the procollagen monomers as well as preventing their thermal denaturation until the necessary posttranslational modifications of proline and lysine are complete and triple-helix formation can take place. Additionally, Hsp47 assists with the translocation of the completed procollagen trimers into the Golgi apparatus for transportation to the extracellular space (Prockop and Kivirikko 1995; Canty and Kadler 2005).

Within the Golgi apparatus, the procollagen trimers are aligned into stacks and are transported to the cell membrane of the fibroblasts in specialized elongated vacuoles; these fuse with the plasma membrane surface to form specialized structures known as "fibripositors" in which the lumen of the vacuole is contiguous with the extracellular space but is still somewhat protected from the extracellular environment (Canty et al. 2004). The process known as "fibrillogenesis" is initiated; this requires cleavage of the C- and N-terminal propeptides by the appropriate peptidases, assembly of the cleaved collagen triple helices into fibrils, and stabilization of the forming fibrils by cross-linking the individual triple-helical collagen monomers through their hydroxylysine residues by the activity of extracellular lysyl oxidase. The confinement of these processes within the fibripositor not only protects the labile collagen monomers from degradation until stable fibrils can be formed but also directs the placement

of the forming collagen fibrils where they are needed, along the lines of force (Gelse et al. 2003; Canty and Kadler 2005; Canty et al. 2006).

Once the propeptides are cleaved, collagen monomers can self-assemble into fibrils at neutral pH, but the speed and effectiveness of fibrillogenesis as well as the thermal and enzymatic stability of the resulting fibrils are enhanced when this process is assisted (Prockop and Kivirikko 1995). Cell surface β_1 integrins (primarily α_{2} and α_{3}) can bind to collagen fibrils and assist in fibrillogenesis by keeping the monomers in close proximity with each other (facilitating cross-linking) as well as with Type V collagen fibrils (which serve as a nucleus for the formation of mature Type I collagen fibrils) and cell surface bound fibronectin (which assists in fibril assembly and protects newly formed fibrils from degradation) (Wenstrup et al. 2004; Kadler et al. 2008). Fibrillogenesis is also potentiated by the action of the matricellular protein periostin, which also plays a role in determining the ultimate diameter and orientation of newly laid collagen fibrils (Norris et al. 2007).

Additional stabilization of the collagen fibrils occurs once fibrillogenesis is complete. Covalent modification of the maturing fibrils (lysyl oxidase mediated cross-linking, along with enzymatic and nonenzymatic glycation), association with matrix proteins and small leucine-rich proteoglycans (such as periostin, decorin, and the FACIT collagens), increased fibril length and/ or diameter, and increased mechanical tension all serve to increase the resistance of the collagen fibrils to enzymatic and thermal degradation (Canty and Kadler 2005; Minond et al. 2006; Norris et al. 2007; Hamilton 2008; Perumal et al. 2008; Flynn et al. 2010; Kalamajski and Oldberg 2010).

17.3.2 Collagen Degradation

17.3.2.1 Collagenases

The collagen triple helix, once stabilized by intra- and intermolecular cross-linking, is remarkably resistant to degradation, as the labile peptide bonds are buried within the interior of the collagen molecule. For an enzyme to effectively initiate degradation of an intact triple-helical collagen molecule, it must possess the ability to identify and bind to "weaker" sites on the molecule, locally unwind the triple helix, and successfully cleave one or more strands of the triple helix. A collagenase is defined as an enzyme which can effectively perform all three of these activities (Lauer-Fields et al. 2002).

Enzyme designation	Common name(s)	Substrate(s)	Function(s)
MMP-1	Collagenase 1	Fibrillar collagens (Type III preferred)	Extracellular cleavage (physiologic and pathologic)
	Interstitial collagenase	Collagens VI, VII, X, IX	Wound healing
	Fibroblast collagenase	Gelatin	
	Synovial collagenase		
MMP-2	Gelatinase A	Gelatin (preferred)	Pericellular collagenolysis (phagocytosis)
		Fibrillar collagens	Inflammation
		Collagens IV, V, VII, X, XI	Activates proMMPs (8, 9, 13)
MMP-3	Stromelysin 1	Gelatin (preferred)	Activates most proMMPs
		Collagens III, IV, V, VII, IX, X, XI	
MMP-7	Matrilysin 1	Gelatin (preferred)	Activates many proMMPs
		Collagens I and V	
MMP-8	Collagenase 2	Fibrillar collagens (Type I preferred)	Inflammation
	Neutrophil collagenase		Wound healing
MMP-9	Gelatinase B	Gelatin	Inflammation
		Collagen I(?)	Pathologic remodeling
		Collagens IV, V, VII, X, XI	
MMP-10	Stromelysin 2	Gelatin (preferred)	Activates many proMMPs
		Collagens I, III, IV, V, IX, X	Wound healing
MMP-12	Metalloelastase	Gelatin	Basement membrane remodeling
		Collagens I, IV	
MMP-13	Collagenase 3	Gelatin	Cartilage and bone remodeling
		Fibrillar collagens (Type II preferred)	Wound healing
		Collagens VI, IX, X, XIV	
MMP-14	MT1-MMP ^a	Fibrillar collagens	Activates proMMPs (2, 8, 13)
		Gelatin	Pericellular collagenolysis (phagocytosis)
			Fibroblast migration
MMP-15	MT2-MMP ^a	Gelatins	Activates proMMP-2
		Collagen III	
MMP-16	MT3-MMP ^a	Fibrillar collagens	Activates proMMP-2

Table 17.2	Mammalian (collagenases	and their	substrates
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Information from the following sources: Everts et al. (1996); Stetler-Stevenson (1996); Sternlicht and Werb (2001); Lauer-Fields et al. (2002); Visse and Nagase (2003); Gutiérrez-Fernández et al. (2007); Barbolina and Stack (2008); Sabeh et al. (2009); Minond et al. (2006); Nagase et al. (2006); Pasternak and Aspenberg (2009)

^aMT-MMP indicates membrane-associated (transmembrane) MMP. These are not secreted but remain associated with the cell membrane and are activated intracellularly by furin-mediated cleavage

Mammalian collagenases fall into two enzyme classes: the zinc-dependent metalloproteinases (represented by a subset of the 23 known mammalian matrix metalloproteinases, or MMPs) and the cysteine proteases (represented by cathepsins K and L). Of the two classes, the MMPs are the primary enzymes responsible for both physiologic and pathologic remodeling of extracellular matrix collagen (Lauer-Fields et al. 2002; Pasternak and Aspenberg 2009); cathepsins primarily function as lysosomal proteases but do play a role in extracellular collagenolysis in bone and cartilage remodeling (Turk et al. 2001; Daley et al. 2007). The MMPs that can act as collagenases and/or have been

shown to have a role in collagen remodeling are listed in Table 17.2.

Cleavage of fibrillar collagens by MMPs occurs in the same fashion, regardless of the enzyme involved, as all of them recognize a single site on the collagen molecule (Gly₇₇₅-Ile/Leu₇₇₆ on the alpha chain). Cleavage at this site results in the generation of two fragments of approximately one-fourth and three-fourths the length of the original fibril (Lauer-Fields et al. 2002; Nagase et al. 2006). The resultant cleavage fragments are known as gelatin and are rapidly cleared from the site of their formation, either by additional proteolysis (in addition to the gelatinolytic MMPs, a number of nonspecific proteases can digest gelatin), by denaturation (gelatin is thermically unstable at physiologic temperatures), and by phagocytosis, a process that is mediated in part by the β_1 integrin-mediated interaction of collagen fibrils with the fibroblast cell surface (Evanson et al. 1968; Fesus et al. 1981; Everts et al. 1996; Arora et al. 2000; Leikina et al. 2002; Stultz 2002).

17.3.2.2 Control of Collagen Degradation

Control of collagen degradation depends on tight regulation of the activity of the MMPs as well as temporal and spatial limitation of these enzymes. There are four levels at which these enzymes are regulated:

Transcription

Only a few of the MMPs (notably MMP-2 and MMP-14) are constitutively expressed, and then only at low levels and in a few tissues. As a general rule, up- and downregulation of the genes responsible for MMP synthesis is required for these enzymes; additional regulation occurs via stabilization of the transcripts (Sternlicht and Werb 2001; Ra and Parks 2007).

Activation of Inactive Enzyme

With the exception of the matrix metalloproteinases (MT-MMPs) which are activated intracellularly, most MMPs are synthesized and secreted as inactive zymogens as the result of a direct internal interaction between a cysteine on the polypeptide and the zinc bound to the catalytic site of the molecule. Disruption of this interaction (resulting in the generation of catalytically active enzyme) requires proteolytic cleavage of the proMMP. While this most commonly results from interaction with another MMP, nonspecific proteases (such as plasmin) can activate the membrane-bound MMPs; additionally, chemical disruption of the cysteine-Zn⁺² interaction by strong oxidizing conditions, metal ions, or disulfides can also lead to MMP activation and autocatalysis of the prodomain (Somerville et al. 2003; Visse and Nagase 2003; Ra and Parks 2007).

Compartmentalization

Inactive forms of MMPs 8, 9, and 12 are retained within the secretory granules of inflammatory cells such as neutrophils and macrophages until released upon stimulation of the cell (Sternlicht and Werb 2001). MMPs that are freely secreted into the extracellular space are generally held close to the surface of the secreting fibroblast via interactions with cell surface proteins such as integrins or membrane-bound MMPs; these interactions are critical to the activity and substrate specificity of each MMP (Ra and Parks 2007).

Inactivation of Active Enzymes

Temporal and spatial regulation of MMP activity results primarily from their inhibition due to interaction with one of the four small glycoproteins known as tissue inhibitors of metalloproteinases (TIMPs). Like MMPs, these are not constitutive proteins but are regulated in response to physiologic need (the exception is TIMP-3, which is present in an inactive complex with the carbohydrate moieties of the interstitial matrix and is released in active form during matrix degradation), with the relative balance between the levels of MMP and TIMP determining the net activity of matrix degradation. All MMPs are subject to inactivation by all of the TIMPs, with a few exceptions; TIMP-1 is not effective at inactivating the MT-MMPs, and TIMP-2 actually enhances the activation of proMMP-2 by MMP-14 (MT1-MMP) by facilitating the interaction between these two proteins (Baker et al. 2002; Visse and Nagase 2003). Any MMP that escapes local inactivation by TIMPS and/or enters the systemic circulation is rapidly inactivated by interaction with the nonspecific protease inhibitor α_2 -macroglobulin which is ubiquitously present in the serum and interstitial fluid, and to a lesser extent by the cell-surface-associated protein reversin-inducing cysteine-rich protein (RECK), which is widely distributed in many tissues (Cawston and Mercer 1986; Baker et al. 2002).

17.4 Roles of Collagen in Dupuytren's Disease

17.4.1 Structural Role of Collagen (Imbalance in Collagen Remodeling)

The hallmark feature of Dupuytren's contracture is the localized deposition of excess and abnormal collagen within the palmar fascia, which suggests that the normal balance of collagen remodeling has been locally perturbed in these patients. A number of studies evaluating genomic and proteomic differences in the diseased palmar fascia (cords, nodules, and/or fibroblasts) from Dupuytren's patients compared to either unaffected fascial components or palmar fascia from unaffected individuals clearly indicate the presence of a shift in this balance in favor of net collagen deposition. These studies are summarized in Table 17.3.

In addition, a number of structural and biochemical abnormalities have been identified in the collagen comprising the Dupuytren's cords that indicate an increase in the stability of the matrix to enzymatic and/ or thermal degradation, which would further tip the balance by decreasing collagen degradation even when collagen degrading enzymes are present in abundance. Increased thermal and enzymatic stability of collagen fibrils resulting from increased cross-linking of collagen due to increased hydroxylysine and/or hydroxyproline and the presence of abnormal collagen cross-links (Brickley-Parsons et al. 1981; Notbohm et al. 1995) or resulting from increased or altered collagen glycation (Brickley-Parsons et al. 1981; Hanyu et al. 1984; Melling et al. 1999) has been described in Dupuytren's disease tissue. The collagen fibrils are also larger in diameter in Dupuytren's disease tissue and are more closely packed in larger fascicles with thicker fascicular sheaths (Mansell and Bailey 2004), which prevents ready access to the labile portions of the individual collagen monomers by collagenases (Perumal et al. 2008). These structural changes in Dupuytren's collagen also result in increased stiffness (decreased elasticity) in the fibrils relative to normal tissue, which renders them more effective in their role as signal transducers to fibroblasts (detailed in the following section) (Melling et al. 2000; Shoulders and Raines 2009).

17.4.2 Functional Role of Collagen (Mechanotransduction and Fibroblast Responses to Force)

More recent studies investigating the pathophysiology of Dupuytren's disease have revealed the significant degree of overlap in its morphology and biology with several phases of wound healing. Features common to the two processes include the transition of fibroblasts to myofibroblasts, generation of tension by myofibroblasts, increased deposition of Type III collagen and fibronectin, the key role of TGF- β , and upregulation of collagen remodeling resulting in shortening of the existing collagen fibrils, which causes contraction (Brickley-Parsons et al. 1981; Tomasek et al. 2002; Rayan 2007). The key difference between these two

Fibroblasts are in constant contact with their external environment and monitor the degree of static and dynamic force present through cell surface β_1 integrins $(\alpha_2, \alpha_5 \text{ and/or } \alpha_{11})$ and the Type I collagen fibrils present in the extracellular matrix. Any increase in the degree of tension present in the matrix is transmitted to the intracellular cytoskeleton; this transmission of force results in alteration of gene expression which occurs either indirectly via the release and nuclear translocation of preformed transcription factors, or directly, resulting from mechanical deformation of the nuclear DNA due to its physical association with the cytoskeletal elements that cross the nuclear membrane (Fig. 17.3) (Chiquet et al. 2003, 2007; Wang et al. 2007, 2009). The alteration of mechanical force on resting fibroblasts is the primary stimulus for the initiation of wound healing and also for physiologic remodeling to ensure that the quantity and quality of the extracellular matrix is adequate to the load.

It has been shown that the morphologic changes common to both wound healing and the early stages of Dupuytren's disease can be induced in cultured fibroblasts (normal or derived from Dupuytren's disease tissue) or granulation tissue explants by subjecting them to mechanical tension; these include proliferation, transition to myofibroblasts, secretion of TGF-B and other cytokines, generation of contractile force in myofibroblasts, increased fibroblast motility, and increased thickness and stiffness of collagen fibrils (Alman et al. 1996, Hinz et al. 2001; Tomasek et al. 2002; Balestrini and Billiar 2009; Roeder et al. 2009). In addition, many of the same genomic and proteomic differences in the diseased palmar fascia (cords, nodules, and/or fibroblasts) from Dupuytren's patients compared to either unaffected fascial components or palmar fascia from unaffected individuals can be induced in cultured fibroblasts by subjecting them to mechanical force or have been identified as being differentially expressed in tissues under stress (Table 17.3). Conversely, decreased mechanical tension on myofibroblasts results in their disappearance via apoptosis, seen in the resolution phase of wound healing and also in the late stages of Dupuytren's disease (Fluck et al. 1998; Grinnell et al. 1999; Gabbiani 2003).

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Table

	Function	Effect on collagen remodeling	Direction of char	nge in:
Gene or motein			Dupuytren's	Fibroblasts under tension
ADAMTS-2	N-terminal propeptidase	T Collagen deposition	Ţ	←
ADAMTS-3	N-terminal propeptidase	↑ Collagen deposition	Ť	←
ADAMTS-14	N-terminal propeptidase	↑ Collagen deposition	$\downarrow\downarrow$	←
COLIAI	Collagen I alpha1 chain	↑ Collagen deposition	\downarrow	¢
COLIA2	Collagen I alpha2 chain	↑ Collagen deposition	↓	¢
COL3A1	Collagen III alpha1 chain	↑ Collagen deposition	¢	←
COL5AI	Collagen V alpha1 chain	\uparrow Collagen deposition	¢	
COL5A2	Collagen V alpha2 chain	↑ Collagen deposition	¢	
Integrin β_1	Signal transduction from collagen; facilitates fibrillogenesis	\uparrow Collagen deposition	¢	←
Fibronectin	Facilitates fibrillogenesis	\uparrow Collagen deposition	←	←
Hsp47	Intracellular collagen stabilization and triple-helix formation	\uparrow Collagen deposition	←	←
Lysyl oxidase-2	Extracellular collagen cross-linking (enhances fibrillogenesis and fibril	\uparrow Collagen deposition	$\downarrow\downarrow$	←
	stability/stiffness)	↓ Collagen degradation		
MMP-1	Collagenase	↑ Collagen degradation	¢	$\stackrel{\rightarrow}{\rightarrow}$
MMP-2	Gelatinase; pericellular collagenase	\uparrow Collagen degradation ("local" remodeling)	††	←
MMP-3	Activates proMMPs	↑ Collagen degradation	\Rightarrow	←
MMP-7	Activates proMMPs	↑ Collagen degradation	←	
MMP-8	Collagenase	↑ Collagen degradation	\rightarrow	
MMP-13	Collagenase	↑ Collagen degradation	¢	←
MMP-14	Collagenase (membrane-associated); activates proMMPs	\uparrow Collagen degradation ("local" remodeling)	↑ (nodule)	
			\leftarrow (cord)	
Periostin	Enhances fibrillogenesis; stabilizes extracellular collagen fibrils	1 Collagen deposition 1 collagen degradation	↓	←
TIMP-1	Inhibits MMPs (except 14)	1 Collagen degradation	111	
TIMP-2	Allows activation of MMP-2 by MMP-14; inactivates MMPs	↑ Collagen degradation (via MMP-2); ↓ collagen degradation	\rightarrow	↑,↓, or no change
TIMP-3	Inhibits all MMPs	↓ Collagen degradation	\rightarrow	
TIMP-4	Inhibits all MMPs	↓ Collagen degradation	$\uparrow\uparrow\uparrow$	
Information from et al. (2007); Ham Unless specified, g	the following sources: Lambert et al. (1992, 2001); Wilde et al. (2003); Qi uilton (2008); Rehman et al. (2008); Kaneko et al. (2009); Vi et al. (2009); gene or protein changes are in the same direction in both nodules and cord.	an et al. (2004); Lee et al. (2006); Webb et al. (200 Ziegler et al. (2010) s from Dupuytren's disease patients)6); Johnston et al.	(2007); Merryman

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Fig. 17.3 Fibroblast and matrix responses to mechanical forces. Fibroblast responses to mechanical forces are mediated through β , integrin interaction with collagen fibrils in the extracellular matrix and the actin cytoskeleton. (a) No signaling occurs in the absence of tension on the collagen matrix or the actin cytoskeleton; note normal orientation of the integrin molecules (depicted as perpendicular to the collagen fibrils) that link the collagen matrix to the actin cytoskeleton. (b) Increased tension on the collagen matrix is transmitted to the actin cytoskeleton due to altered orientation of the cell surface integrins, resulting in the release of transcription factors and rapid changes in gene/protein expression. Effects may also be mediated due to direct cytoskeletal coupling of the cell membrane to the chromosomal DNA through the nuclear membrane; deformation of DNA by transferred tension results in direct alteration of gene transcription. NOTE: a decrease in the elasticity of either the collagen matrix or the actin cytoskeleton increases the intensity of the signal (Figure adapted from material in Chiquet et al. 2003, 2007; Wang et al. 2007, 2009)

17.5 Conclusions

Collagen has been described as "an unstable molecule that can form stable tissues." This property results from the careful shepherding of the unstable precursor through a highly complex process as well as close regulation over the processes that initiate its degradation, so that the quantity and quality of this essential structural component is balanced to the physical requirements of each tissue. Either as the primary structural component of the Dupuytren's cord or as the primary functional mediator of the pathophysiologic processes that underlie this disease, it remains an important target for therapeutic intervention, and a basic understanding of its biology is critical to therapeutic success.

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