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Composition, Structure and Function of the Corneal Stroma

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Abstract

No other tissue in the body depends more on the composition and organization of the extracellular matrix (ECM) for normal structure and function than the corneal stroma. The precise arrangement and orientation of collagen fibrils, lamellae and keratocytes that occurs during development and is needed in adults to maintain stromal function is dependent on the regulated interaction of multiple ECM components that contribute to attain the unique properties of the cornea: transparency, shape, mechanical strength, and avascularity. This review summarizes the contribution of different ECM components, their structure, regulation and function in modulating the properties of the corneal stroma. Fibril forming collagens (I, III, V), fibril associated collagens with interrupted triple helices (XII and XIV), network forming collagens (IV, VI and VIII) as well as small leucine-rich proteoglycans (SLRP) expressed in the stroma: decorin, biglycan, lumican, keratocan, and fibromodulin are some of the ECM components reviewed in this manuscript. There are spatial and temporal differences in the expression of these ECM components, as well as interactions among them that contribute to stromal function. Unique regions within the stroma like Bowman's layer and Descemet's layer are discussed. To define the complexity of corneal stroma composition and structure as well as the relationship to function is a daunting task. Our knowledge is expanding, and we expect that this review provides a comprehensive overview of current knowledge, definition of gaps and suggests future research directions.

Keywords

cornea; stroma; collagens; proteoglycans; collagen fibril; structure; composition

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1. Introduction

The cornea is the major refractive structure of the eye and transparency is its major attribute. In addition, the cornea provides mechanical stability and is a protective barrier for the eye. The cornea is avascular and is composed of three layers. The corneal epithelial layer is the most anterior region while the corneal endothelium is the posterior layer. Between these layers rests the corneal stroma that makes up approximately 90% of the corneal thickness. The stroma extends from the corneal epithelial basement membrane to the endothelial basement membrane. The corneal stroma is the focus of this review.

2. Corneal stroma

The corneal stroma has 3 distinct regions. Bowman's layer is the most anterior region providing an interface with the epithelial basement membrane. The stroma proper makes up the bulk of the corneal stroma. Descemet's Membrane is the most posterior region separating the stroma proper from the corneal endothelial layer. Each of these structures have unique structural, compositional and functional characteristics.

2.1 Bowman's layer

This is the most anterior region of the corneal stroma. It is often considered a separate corneal region; however, it can be considered a specialized region of the anterior stroma mediating interactions with the corneal epithelium. This smooth layer is approximately 15– 18 µm thick in humans as determined by live imaging and avoiding chemical tissue fixation (Kermani et al., 2008; Li et al., 1997). It is believed to have a mechanical role in maintaining corneal shape (Tong et al., 2019). Bowman's layer is present in humans, but not in all mammals. In humans, Bowman's layer thins with aging (Germundsson et al., 2013). This region is composed of a network of very small diameter collagen fibrils around 18 - 22 nm (Birk et al., 1986; Gordon et al., 1994; Linsenmayer et al., 1998). Bowman's layer is acellular and the network of thin collagen fibrils and their non-lamellar organization is distinct from that seen in the stroma proper. This interfacial ECM integrates the corneal epithelial basement membrane and attached epithelial cells with the corneal stroma proper. In addition to the collagen fibrillar networks, Bowman's layer contains anchoring complexes composed of collagen VII-containing anchoring fibrils and collagen IV-containing anchoring plaques. These complexes intertwine with the fibrillar network of Bowman's layer to anchor the basement membrane to the underlying stroma proper (Gipson et al., 1987; Tisdale et al., 1988). Species without a structurally distinct Bowman's layer may have some of the compositional properties characteristic of the region providing unique properties to this interfacial region and is an area requiring further investigation. It is well known that the absence of Bowman's layer, as seen following photorefractive keratectomy, does not seem to affect corneal function, and that once it is disrupted, it will not regenerate (Wilson, 2020; Wilson and Hong, 2000). However, in recent years, a technique for harvesting Bowman's layer from a cadaveric donor and transplantation into recipients with progressive corneal ectasia and significant anterior corneal scars has been reported with success (Tong et al., 2019).

The collagen composition in Bowman's layer is unique and differs from that of the corneal stroma proper both in collagen content and fibril structure. This was originally defined by analyses of avian corneas and is consistent in all species studied including human. In corneas reacted with antibodies directed against the triple helical domain of collagen V strong reactivity is observed in Bowman's layer with little to no reactivity in the stroma proper. However, after disruption of fibril structure there was strong reactivity for collagen V in the stroma proper as well as Bowman's layer. These results suggest differences in the collagen fibril organization in Bowman's layer and the stroma proper (Birk et al., 1986; Fitch et al., 1984; Gordon et al., 1994; Linsenmayer et al., 1998). A higher ratio of collagen V to collagen I is present during development at the stromal – epithelial interface due to higher Col5a1 expression by epithelial cells compared to keratocytes. These data indicate both epithelial and keratocyte contributions to Bowman's layer, a key interfacial matrix. The higher availability of collagen V is one explaination for the smaller collagen fibrils present in Bowman's layer (Gordon et al., 1994; Linsenmayer et al., 1998; Linsenmayer et al., 1993). However, the epithelial cells had high expression of the *Col5a1* gene, but not the Col5a2 gene. There are multiple collagen V isoforms with the $a1(V)_2a2(V)$ form being the predominant form in the stroma proper. However, the $a_1(V)_3$ isoform has been found in other tissues and organized into smaller fibrils organized as networks (Bonod-Bidaud et al., 2012; Chanut-Delalande et al., 2004). It is likely that increased *Col5a1* expression would favor epithelial homotrimer formation whereas the keratocytes would assemble the heterotrimer (Roulet et al., 2010). Therefore, differences in collagen V isoforms in Bowman's layer would determine its unique structure. However, this has not been demonstrated. It is expected that differences in collagen composition, fibril size and structure as well as fibril organization in Bowman's layer create functional differences between Bowman's layer and the corneal stroma proper.

2.2 Stroma proper

The stroma proper makes up \sim 90% of the corneal structure and provides unique properties necessary for function; including transparency, avascularity, as well as its mechanical properties necessary for strength, and the maintenance of shape. The stroma is composed of ECM molecules, water and a communicating network of neural crest derived keratocytes that synthesize the stromal extracellular matrix (Chen et al., 2015; Hassell and Birk, 2010; Linsenmayer et al., 1998; Massoudi et al., 2016; Quantock and Young, 2008). The function of the stroma proper relies on the tightly controlled assembly of collagen I into fibrils and higher ordered structures (Hassell and Birk, 2010; Linsenmayer et al., 1998; Maurice, 1957). The stroma proper contains homogeneous, small diameter collagen fibrils that are characteristic of the corneal stroma. The fibrils are highly organized with a rigid packing pattern. Interactions of different fibrillar collagens, fibril-associated collagens (FACIT), small leucine rich proteoglycans (SLRP) and glycoproteins have all been implicated in the regulation of corneal fibril structure and packing (Birk and Trelstad, 1984; Chen et al., 2015; Hassell and Birk, 2010; Linsenmayer et al., 1998; Mienaltowski and Birk, 2014; Quantock and Young, 2008). Corneal collagen fibrils are then organized as fibers that form lamellae. Adjacent lamellae are oriented $\sim 90^{\circ}$ from each other with an approximate orthogonal arrangement (Maurice, 1957; Meek and Knupp, 2015). Lamellae are structures of variable thickness, in humans typically of 0.5 to 250 μ m in width and up to 2.5 μ m in thickness

(Komai and Ushiki, 1991). Rigid control at all levels of hierarchal structure are essential for stromal function and dysfunction at any level may contribute to ocular pathologies. Alterations in hierarchical organization are hypothesized to be an important contributor to keratoconus. Alterations in lamellae organization have been demonstrated in X-ray scattering studies, and possible inter lamellae slippage proposed as the main etiology of corneal ectasias (Hayes et al., 2007). What causes or induces lamellar slippage is unknown, but oxidative stress is suspected in some subgroups of patients (Shinde et al., 2020).

The structure and composition of the stroma differs in the anterior and posterior stroma. The interfibrillar spacing is increased in the posterior stroma compared to the anterior stroma, (Freund et al., 1995) and in mouse corneas, extracellular matrix components are not homogeneously distributed e.g., lumican is localized mainly to the adult posterior stroma (Chakravarti et al., 2000). These structural differences translate to functional differences including in light scattering and propensity to swell (Freund et al., 1995; Kikkawa and Hirayama, 1970; Meek et al., 2003). There are differences in the refractive index between the anterior and posterior stroma with the anterior stroma having a higher refractive index (Patel et al., 1995).

Differences in interfibrillar spacing are more noticeable during corneal edema and in this clinical situation, increases in interfibrillar spacing are more significant in the posterior stroma compared to the anterior stroma (Meek et al., 2003; Patel et al., 1995). These differences in structure and function are noted in the propensity for corneal edema to occur first in the posterior stroma, a clinical sign known as Descemet folds (Freund et al., 1995; Kikkawa and Hirayama, 1970). The limbal area is a unique interfacial region of the stroma at the corneal and scleral junction. This region has a different organization of the fibrillar extracellular matrix distinct from the stroma proper and functions to integrate these 2 adjacent tissues. At the limbus, a variable circumcorneal annulus of collagen fibrils is present as revealed by synchroton X-ray diffraction. The scleral and corneal fibrils have different orientations, and bend at this annulus to run circumferentially at the limbus. It is hypothesized that unique mechanical properties in the limbal area may regulate corneal curvature and are essential to resist increased circumferential tension (Kamma-Lorger et al., 2010; Newton and Meek, 1998a, b).

Imaging of the stromal extracellular matrix and its hierarchical organization can be supplemented with new technologies or new uses of old technologies that provide new insight or make previously unaccessible studies accessible. Imaging approaches have been central to analyses of corneal structure since the pioneering work of Jakus (Jakus, 1954, 1956, 1962). Conventional transmission electron microscopy still plays a central role, however, a broadening of its use has enhanced the ability to analyze structure at different levels. Initially, a three-dimensional electron imaging study of the cornea was done by stacking serial electron microscopic images taken sequentially after tissue was removed using an ion beam in the microscope (Bushby et al., 2011). Currently, serial block face scanning electron microscopy allows for reconstruction of tissues and their individual elements at the ultrastuctural level. A serial, aligned, stack of images is obtained that can be reconstructed in three dimensions for analysis (Denk and Horstmann, 2004; Kremer et al., 2015). Additionally, tomography using transmission electron microscope can generate high

resolution three-dimensional images for analysis of three-dimensional structure (Kremer et al., 2015; Midgley and Dunin-Borkowski, 2009; Quantock et al., 2015). This technology can be used for determining molecular structures as well as the three-dimensional ultrastructure of organelles and macromolecular interactions such as fibril-SLRP relationships (Kremer et al., 2015; Midgley and Dunin-Borkowski, 2009). Recently, this technique was used to demonstrate endothelial projections into the stroma during development in mouse corneas (Feneck et al., 2020a). Light and confocal microscopy are central to the study of corneal structure and localization of matrix components. Second harmonic generation microscopy (SHG) is well suited to analyze structures built of fibrillar collagens in tendon, bone, blood vessels and cartilage (Zipfel et al., 2003). In the cornea, SHG imaging is a powerful approach in evaluating organization of collagen fibers and lamellae as well as fibrosis after wound healing in different species including mice and humans (Farid et al., 2008; Kivanany et al., 2018; Morishige et al., 2006). There are limitations, this approach can image fibril bundles, but in the cornea, stromal fibrils can not be detected due to their small size (Quantock et al., 2015). Synchrotron x-ray diffraction approaches provide another useful way to characterize the structure and organization of tissues at the nano level. X-ray diffraction was used originally to define the structure of collagen fibrils. This technique uses the scattering of a beam of X-rays to provide objective measurements. Wide-angle scattering provides data on molecules within fibrils while small-angle scattering provides data on fibrils within lamellae (Meek et al., 1991; Meek and Quantock, 2001; Quantock et al., 2015; Sayers et al., 1982). It has been applied in numerous studies addressing stromal function, aging, ocular pathologies, and to evaluate the function of different matrix components. For example, the effects of aging on interfibrillar spacing and fibril diameter in aging human corneas have been studied using this technique (Daxer et al., 1998). Corneal buttons obtained from patients with keratoconus, macular corneal dystrophy and Morquio syndrome also have been characterized (Fullwood et al., 1992; Palka et al., 2010; Rawe et al., 1997). In addition, mouse models deficient in mimecan and lumican have been studied to evaluate the function of theses matrix components in stromal structure and function (Beecher et al., 2005; Ouantock et al., 2001).

2.3 Descemet's membrane

This layer is an interfacial matrix integrating the posterior stroma with the corneal endothelial basement membrane. Descemet's membrane is formed in fetal life and the endothelial cells continuously add a material making the Descemet's membrane thicker with aging. It is an acellular extracellular matrix composed of hexagonal collagen VIII networks, as well as associated collagens IV and XII (Fitch et al., 1990; Hemmavanh et al., 2013; Ljubimov et al., 1996; Marchant et al., 2002; Sawada et al., 1990). It has not been characterized, but it is likely that the unique structural and compositional properties of Descemet's membrane are involved in the integration of the corneal endothelial basement membrane, and Descemet's membrane into the stroma (Cintron et al., 1988; Feneck et al., 2020a; Hemmavanh et al., 2013; Jeang et al., 2020). It has recently been demonstrated that these processes allow functional communication between the corneal endothelium and posterior stroma keratocytes (Jeang et al., 2020).

3. Cellular types in the corneal stroma

3.1 Keratocytes

The predominant cell type in the corneal stroma is the keratocyte. Keratocytes are a unique population of neural crest-derived cells that populate the developing corneal stroma and synthesize the stromal extracellular matrix components. Keratocytes are essential for the development of the stroma and for the maintenance of its unique properties (Hassell and Birk, 2010; Jester et al., 1994). During avian stromal development, neural crest cells migrate into a hyauronate-rich environment between the developing corneal epithelium and endothelium (Johnston et al., 1979; Linsenmayer et al., 1998; Trelstad and Coulombre, 1971). These neural crest derivatives differentiate into active keratocytes (keratoblasts), that proliferate in this space and synthesize components of the stromal matrix, i.e., collagens and keratan sulfate as well as dermatan sulfate proteoglycans that replace the hyaluronan/waterrich extracellular matrix with the densely packed collagen fibrillar extracellular matrix seen in adult corneas (Cintron et al., 1983; Funderburgh et al., 1986). A similar sequence of events occurs in all species, but a distinct primary stroma is nor presnt in all species, including human.

Keratocytes regulate and direct the deposition of collagen fibrils and organize lamellae during development (Birk and Trelstad, 1984; Young et al., 2014). Keratocytes define extracellular domains, during stromal extracellular matrix assembly, where the sequential steps in stromal collagen fibril assembly can be partitioned and regulated. This is the case in the stroma and an array of other connective tissues (Birk and Trelstad, 1986; Canty and Kadler, 2002; Ploetz et al., 1991). Fibril assembly begins in deep recesses or channels in the keratocyte surface (Birk and Trelstad, 1984). The extracellular channels form during secretion as specialized post-Golgi secretory compartments. The compartments then fuse with the keratocyte surface and because of slow membrane recycling due to the presence of newly assembled fibrils (protofibrils) the channels are transiently maintained. Threedimensional electron microscopy studies point to actin rich cytoplasmic protrusions in the keratocytes, named keratopodia, as regulators of cell-cell and cell-matrix interactions that regulate fibril deposition during stromal development (Young et al., 2014). The channels and/or keratopodia are reorganized and fibrils are deposited into a second domain where fibrils are collected into small fibers (Birk and Trelstad, 1984, 1986). As stromal matrix assembly continues the fibers are collected in a larger domain where lamellae assembly takes place. This hierarchy of compartments represents a series of spatially restricted sites where specific interactions of extracellular molecules involved in the regulation of stromal matrix assembly are compartmentalized. Keratocyte-directed matrix deposition seems to be the leading process of collagen and matrix deposition because the axes of the extensive network of keratocyte cell processes is well aligned with the alignment of stromal fibrils (Birk and Trelstad, 1984; Young et al., 2014). The fact that the dendritic keratocytes are organized into a communicating network throughout the stroma provides the means to coordinate the long-range assembly of the stromal hierarchal organization. In contrast, collagen deposition and organization in early development, in the acellular primary stroma in avian embryos, before keratocytes invade the primary stroma could be self-directed (Young et al., 2019).

Keratocytes are mitotically quiescent, exhibit a dendritic morphology with extensive intercellular contacts and gap junctions (Jester et al., 1994; Poole et al., 1993; Watsky, 1995). Keratocytes are organized as networks between the stromal lamellae with compact small cell bodies that minimize light scattering. There is no single specific marker that defines the keratocyte phenotype. However, panels of markers can be used to define the keratocyte phenotype and could include keratocan, (Liu et al., 2003; Liu et al., 1998), crystallins (Jester, 2008; Jester et al., 1995) and CD34 (Espana et al., 2004; Joseph et al., 2003; Toti et al., 2002) among others. When a scar forms during corneal wound healing, keratocyte dendritic morphology is lost and there is a down-regulation of keratocan, CD-34 and crystallin expression (Espana et al., 2003; Jester et al., 2012; Kawakita et al., 2005a; Toti et al., 2002). Fibroblasts can continue to activate and phenotypically transition into highly contractile myofibroblasts by developing muscle-like features, including formation of actin-myosin bundles (Hinz, 2016; Hinz and Lagares, 2020).

Keratocytes synthesize and store crystallins in their cytoplasm at high concentrations. This accumulation of crystallins within the keratocyte, is through to contribute to stromal transparency, in a manner similar to cells in the natural lens (Jester, 2008; Jester et al., 1999). Keratocytes occupy a significant volume of the stroma, up to 15%, (Huang and Meek, 1999) and the presence of crystallins in the keratocyte cytoplasm is believed to minimize light scattering. Crystallins also function to absorb UV-light in the lens and cornea, but they also may play a role in matching the refractive index of the cell cytoplasm to that of the surrounding extracellular matrix and decrease or eliminate scattering (Chen et al., 2013b). In the mammalian cornea, the most likely candidate crystallins are aldehyde dehydrogenases, particularly ALDH3A1. Members of the ALDH class 1 and ALDH3A1 are well conserved in mammals, showing ~90% homology in amino acid sequence among human, rabbit, mouse and rat (Chen et al., 2013b; Manzer et al., 2003). ALDH3A1 directly absorbs UV energy, and reduces damage to inner ocular tissues. Interestingly, ALDH3a1-deficient mice have normal clear and transparent corneas (Nees et al., 2002). Another mouse model with genetic mutations in the ALDH3a1 gene has no evident stromal changes (Downes et al., 1994). These results suggest further studies on the roles of corneal crystallins are required to fully elucidate their role(s) in corneal biology.

3.2 Stem cells

Adult stem cells are present in the corneal stroma and are located in the limbal stromal region (Chen et al., 2011b; Du et al., 2005; Kawakita et al., 2005b; Pinnamaneni and Funderburgh, 2012). Characteristic of stem cells, these cells can differentiate into different cell lineages when properly stimulated including chondrocytes and glial fibrillar acidic protein expressing cells (Du et al., 2005). These cells also can be expanded as keratocytes that are able to recreate stromal tissue under specific culture conditions (Du et al., 2005; Funderburgh et al., 2016). Mesenchymal "niche cells" previously described by Tseng's laboratory who isolated them from the limbal stroma with collagenase after removing an intact epithelial sheet seem to have similar characteristics (Chen et al., 2011b; Xie et al., 2012). Clinically, the existence of stromal "progenitor cells" was suspected decades ago

based on the analysis of sex-mismatched human full thickness corneal transplants, by fluorescence in situ hybridization of the sex-chromosomes, that showed host invasion and repopulation by keratocytes into the donor tissue. These finding suggested that keratocytes can replicate and that progenitor stromal cells exist in vivo (Wollensak and Green, 1999). Although the exact function of these cells is unknown, it is believed that, in vivo, adult corneal stromal stem cells provide a biological support system for maintenance of the epithelial stem cells in the limbal niche where both cell types interact (Dziasko and Daniels, 2016; Yamada et al., 2015). Stem cells isolated from limbal biopsies and expanded in vitro have shown promise in the regeneration of the corneal stroma following injury in mice (Basu

et al., 2014; Ghoubay et al., 2020). Clinically, the success of the technique of Simple Limbal Epithelial Transplantation where pieces of epithelial and stromal limbal tissue are transplanted to damaged corneas to restore functionality suggests that stromal stem cells are functional and have the potential for significant translational use (Sangwan et al., 2012).

3.3 Dendritic cells

Dendritic cells are a subset of phagocytic tissue-specific antigen-presenting cells that regulate the immune response (Davies et al., 2013; Ginhoux and Guilliams, 2016; Liddiard et al., 2011). Dendritic cells are considered the most efficient antigen presenting cells in processing and presenting exogenous antigens on both MHC I and MHC II molecules to T cells, and initiate the adaptive immune response. Dendritic cells are a heterogeneous population of bone-marrow-derived cells that are present in all tissues including the cornea (Hattori et al., 2016). Once dendritic cells phagocytose an antigen in the cornea, they traffic to the lymph node and present antigens to initiate an immune response (Banchereau and Steinman, 1998; Steinman, 2012). In the cornea, as in other organs, dendritic cells are key players in the pathogenesis of ocular allergy, (Liu et al., 2014; Saban, 2014) response to infection, (Hamrah et al., 2009; Hu et al., 2015) and even wound healing (Gao et al., 2011). Dendritic cells seem to be essential for dynamic and functional interaction with corneal nerves (Hamrah et al., 2016). The term neuroimmunology synapse or cross-talk is used to explain the interactions between the immune and nervous systems (Hamrah et al., 2016). A classic example of such interaction in the cornea is the increased infiltration of dendritic cells around the nerve fibers with subsequent damage of the sub-basal nerve plexus noted in diabetics (Leppin et al., 2014). Dendritic cells are required for proper epithelial wound healing in the cornea and depletion of dendritic cells is associated with decreased healing (Gao et al., 2011).

4. Extracellular matrix of the corneal stroma

The precise structural organization of the stroma is a requisite for corneal transparency. Corneal transparency relies on the regular packing of homogeneous, small diameter collagen fibrils (Hassell and Birk, 2010; Linsenmayer et al., 1998; Maurice, 1957). Fibril diameter varies based on species, fibril diameters range from 23–35 nm (Bard and Bansal, 1987; Meek and Leonard, 1993). The fibrils are regularly packed with equidistance spacing (Massoudi et al., 2016; Meek and Leonard, 1993). Finally, the fibrils are organized into layers or lamellae that are approximately perpendicular to one another (Birk and Trelstad, 1984; Linsenmayer et al., 1998). The structure and organization of collagen fibrils are the

most distinctive features of the corneal stroma. The complexity of the stromal hierarchical organization is clearly noted in the evolutionary changes observed between species. Species specific differences in stromal structure have been identified (Koudouna et al., 2018). The angle between parallel fibers that are rotated relative to each other is less than 90° angles in mammals, but over 100–200° in nonmamalian corneas. Second, the length of continuous lamellae varies with lamellae extending from limbus to limbus in nonmammalian corneas. Finally, an increased complexity of the corneal lamellae structure is observed from from reptiles to birds.

The predominant fibril-forming collagen type in the corneal stroma is collagen I. However, corneal stroma structure and extracellular matrix structure, in general, is not determined by the collagen type present. Collagen I is the predominant collagen in striated collagen fibrils that have a vast array of tissue-specific structures and organizations. A good example being the corneal stroma and the sclera, both composed predominantly of collagen I, but with markedly different fibril structures, organizations and hierarchal structure (Birk, 2011; Chakravarti et al., 2003; Komai and Ushiki, 1991; Meek and Fullwood, 2001). A likely explanation is that collagen fibrils in different tissues, at different developmental stages, or in response to injury have different macromolecular compositions that include other collagen types as well as non-collagenous components. Complex interactions with collagen I containing fibrils include networks of collagenous structures in the interfibrillar spaces and associated with cellular interfaces; non-fibrillar collagens and proteoglycans; networks of fibrillin; and a variety of glycoproteins. These additional macromolecules may vary widely in amount, however, invariably the tissue-specific composite structure of collagen fibrils is a major determinant of architecture and function. These stromal extracellular matrix components have a functional role in determining stromal structure, however, many have additional functions that are not fully defined. Work remains to fully elucidate the importance of the components in the structure and function of the cornea.

4.1 Collagens

4.1a Fibril-forming collagens—The structural unit of the corneal stroma is the collagen fibril. The fibril-forming collagen subfamily includes collagens I, II, III, V, and XI. These collagens have a uninterrupted triple helical domain of about 300 nm (Birk, 2011). Collagen I is most abundant protein in the corneal stroma and comprises the bulk of collagen fibrils. Collagens V and XI are quantitatively minor collagens found co-assembled with collagens I, II and III in different tissues (Birk, 2011; Smith and Birk, 2012). In the corneal stroma collagen V makes up 10-20% of the fibril-forming collagens (McLaughlin et al., 1989; Poschl and von der Mark, 1980; Tseng et al., 1982) and collagen XI may be present in trace amounts in development, as is the case in other collagen I containing tissues. The collagen V/XI subclass has been termed regulatory fibril-forming collagens (Birk, 2011; Chen et al., 2015; Smith and Birk, 2012). The regulatory fibril-forming collagens retain portions of the N-terminal propeptide and are involved in the regulation of fibril assembly (Fichard et al., 1995; Smith and Birk, 2012). The $\alpha 1(V)_2 \alpha 2(V)_1$ isoform of collagen V is present in the stroma proper. It is a quantitatively minor regulatory fibril-forming collagen and is the primary determinant responsible for control of collagen fibril diameter in the corneal stroma with diameters of \sim 25–35 nm, compared to fibril diameter in other tissues,

for example, the sclera, that has minimal collagen V content and contains collagen fibrils ranging from 25 – 250 nm (Komai and Ushiki, 1991).

The fibril-forming collagens are synthesized and secreted as procollagens. Procollagens contain a non-collagenous C-terminal propeptide and an N-terminal propeptide. The Npropeptide is composed of several non-collagenous domains and a short collagenous domain. The presence of the propeptides prevents premature assembly of collagen molecules into fibrils (Hulmes, 2002; Kadler, 2017). The initial assembly of collagen into fibrils is regulated by the processing of the propeptides and processing involves a number of enzymes. The C-propeptides are processed by BMP-1/tolloid proteinases or furin (Hopkins et al., 2007). The processing of the N-propeptides involves ADAMTS 2, 3 and 14 as well as BMP-1 (Colige et al., 2005; Hopkins et al., 2007). These processing enzymes have specificity for different collagen types (Kadler et al., 2007). In the corneal stroma, propeptide processing may be complete, i.e., collagen I, leaving a collagen molecule with one large central triple helical domain and terminal, short noncollagenous sequences termed the telopeptides. Processing also can be incomplete, i.e., in collagens V and XI, leaving a Ctelopeptide and a partially processed N-propeptide domain. The N terminal domains of collagens V and XI both have been implicated in the regulation of fibrillogenesis (Birk, 2011; Smith and Birk, 2012; Wenstrup et al., 2011). After processing of the propeptides, collagen molecules self-assemble to form striated fibrils with a periodicity of 67 nm. Within the fibril, the collagen molecules are arranged in longitudinally staggered arrays with a gap occurs between the ends of neighboring molecules. This generates a gap-overlap structure in all collagen fibrils with a D-periodic banding pattern (Fig. 1). This basic collagen fibril structure was worked out in simple well ordered tissues such as the rat tail tendon which is primarily collagen I with little proteoglycan content. Attempts have been made to correlate periodicity with the genetic collagen type without success (Eikenberry et al., 1980). However, tissue-specific difference in composition of collagens, e.g. heterotypic fibrils, and other matrix macromolecules such as proteoglycans can influence fibril structure. This is demonstrated in the stroma where the fibril periodicity is 65nm (Meek, 2009).

Collagen fibrils are heterotypic, assembled of 2 or more fibril-forming collagen types. The corneal stroma contains collagen I, the quantitatively major fibril-forming collagen, as well as minor amounts of collagens V and XI. These quantitatively minor regulatory fibril-forming collagens V and XI are characterized by a partial processing of the N-propeptide domain. The N-propeptides have a flexible, hinge domain between the triple helical domain and a short triple helical domain. The N-terminal domain is composed of variable and PARP domains. Processing involves specific cleavage of the PARP domain with retention of the hinge, COL2 and variable domains (Gregory et al., 2000; Hoffman et al., 2010; Linsenmayer et al., 1993). These regulatory fibril-forming collagens co-assemble with the major fibril-forming collagens to form a heterotypic fibril. The N-terminal domain of the regulatory fibril forming collagens cannot be integrated into the staggered packing of the helical domains. The hinge region (NC2) is flexible so that the rigid COL2 domain can project toward the fibril surface in the gap region and the variable domain is present in the gap and on the fibril surface (Fig. 2).

It is clear that interaction between fibrillar collagens act as key regulators of the collagen organization in the fibril, resulting in tissue-specific fibril differences. Absence of collagen V is lethal during development, but corneal stroma-specific deletion of collagen V expression in mouse models results in an abnormal matrix with abnormal large diameter fibrils, aberrant fibril structure, disorganized fibrils, corneal thinning due primarily to a reduced number of fibrils and loss of corneal transparency (Sun et al., 2011). Patients with classic Ehlers - Danlos syndrome, deficient in collagen V, present with limbus to limbus corneal thinning, (Segev et al., 2006) and to our knowledge there is no reported increased incidence of corneal ectasia or spontaneous corneal peroration in humans. A heterozygous mouse model for collagen V replicates corneal thinning suggesting a role for collagen V in corneal thickness (Segev et al., 2006). Figure 3 presents a model for regulated control of initial fibril assembly, diameter and fibril number via collagen V/I interactions. Collagen V acts as a nucleator associated with the keratocyte surface. It interacts with collagen I and initiates fibril assembly. Diameter is regulated by increasing or decreasing the number of nucleation sites to decrease and increase fibril diameter respectively. This assumes a constant expression of collagen I. This mechanism also determines the number of fibrils assembled. Since the collagen V is associated with the keratocyte surface it provides a mechanism whereby keratocytes can influence fibril deposition and organization.

Collagen II, a homotrimeric protein, and is the major fibril-forming collagen in cartilage and vitreous where it assembles fibrils with collagen XI as a nucleator. In the cornea, collagen II is found in the developing avian primary stroma (Chen et al., 1993; Linsenmayer et al., 1990). There are several alternatively spliced forms of collagen II and collagen IIA is expressed in a variety of developing tissues including mouse cornea (Cheah et al., 1991). Also, expression of collagen II can be induced in isolated rat keratocytes with dexamethasone and TGF- β 3 (Greene et al., 2016). The collagen II gene also undergoes alternative splicing to generate the α 3(XI) chain of collagen XI. So the possibility for miss identification in tissues exists. Overall, the specific function(s) of collagen II in developing tissues, including the corneal stroma, remain to be defined.

The presence and role of collagen III in the corneal stroma is controversial. Collagen III is widely distributed in multiple organs, including blood vessels, skin, uterus and bowel (Laurent et al., 1981; Pope et al., 1975). In humans, the vascular type of Ehlers-Danlos disease is secondary to a deficiency of collagen III (Kontusaari et al., 1990; Pope et al., 1975; Prockop and Kivirikko, 1984). In the cornea, the expression is contradictory. Some authors report no expression found in the adult human stroma, (White et al., 1997) while other found collagen III in human corneal tissue (Newsome et al., 1982). Collagen III was observed in the adult rabbit cornea and during development, as well as in Descemet's membrane, and it was suggested that collagen III is secreted by endothelial cells (Cintron et al., 1988). In bovine stroma, the expression of collagen III is present during development, but decreases with aging (Schmut, 1977). The decrease in expression with maturation is present in tissue culture models of bovine keratocytes where higher expression is found in cultures from younger tissue (Kane et al., 2009). In contrast, while the presence of collagen III in normal, uninjured corneal tissue is controversial, its presence during the injury response is much stronger. Collagen III gene expression is suggested as a marker of scarring in mouse injury models following trauma or induced stromal injury (Ghoubay et al., 2020;

Gupta et al., 2018; Marino et al., 2017; Shojaati et al., 2019). The processing of procollagen III is unique in that the N-propeptide is processes slowly compared to procollagen I (Fessler et al., 1981). The slow processing of the N-prppepide has been suggested to confer transient regulator properties similar to those seen with collagen V. Further analysis of the role(s) of collagen III in the normal stroma as well as in the injury response is needed.

4.1b Fibril-associated collagens with interrupted triple helices (FACIT)—

FACIT collagens do not form fibrils but interact with collagen fibrils (Fig. 4). In addition, these collagens interact with basement membranes and cell interfaces. FACIT collagens have been implicated in regulation of matrix organization and cell behavior (Birk, 2011; Chiquet et al., 2014; Gordon and Hahn, 2010; Linsenmayer et al., 1998). This group of collagens includes collagens IX, XII, XIV, XIX, XX, XXI, and XXII (Ricard-Blum, 2011). The two most studied FACITs expressed in the stroma are collagens XII and XIV. FACIT collagens are localized on the surface of the fibrils and in the interfibrillar space (Fig. 2). The changes in fibril properties afforded by these interactions generate diversity in the properties of stromal collagen fibrils, fibers and lamellae. Their function is not completely understood, but they are implicated in the regulation of tissue structure and function as well as cell organization(Birk, 2011; Chiquet et al., 2014; Gordon and Hahn, 2010; Izu et al., 2011; Sun et al., 2020). In addition, their expression is influenced by mechanical forces.(Birk, 2011; Kadler et al., 2007; Linsenmayer et al., 1998; Massoudi et al., 2016)

Collagen XII is expressed in the human, mouse, chicken and other corneal stromas (Font et al., 1996; Gordon et al., 1987; Marchant et al., 2002; Massoudi et al., 2012). This FACIT collagen has the highest stromal expression. It is a homotrimeric molecule composed of two collagenous domains, COL1-COL2, and three noncollagenous domains, NC1 to NC3 (Shaw and Olsen, 1991). Alternatively spliced variants at the NC1 and NC3 terminals are believed to confer tissue specific properties (Kania et al., 1999). Human stroma and sclera contain the long variant form as the predominant form of collagen XII (Wessel et al., 1997). Collagen XII is expressed in tissue regions of high mechanical stress, and its expression is upregulated by mechanical stimulation (Arai et al., 2008). Collagen XII plays a major role in establishing hierarchical organization of the stroma as demonstrated by collagen XII upregulation at times of fibril formation and organization and disruption of keratocyte and lamellar organization in a mouse model null for collagen XII (Sun et al., 2020). Figure 5 is a schematic illustrating how FACIT - fibril interactions regulate and stabilize lamellae formation. A lack of collagen XII expression in null mouse models is associated with disruption of stromal structure at the fibril, lamellar and tissue level (Sun et al., 2020). In human and mouse corneas, collagen XII is upregulated during stromal injury and is present in scarred stromas suggesting a role in stromal remodeling and regeneration (Massoudi et al., 2012). In addition, in zebrafish models of spinal injury, Wnt/ β -catenin signaling induces a specific axon regrowth permissive matrix with collagen XII in the lesion site, suggesting that recapitulation of collagen XII expression occurs with regeneration (Wehner et al., 2017). Collagen XII is overexpressed in the subepithelial area in patients with bullous keratopathy (Ljubimov et al., 1996). In keratoconus corneas, proteomic analysis demonstrated decreased collagen XII, as well as decreased proteoglycans and collagen I levels (Chaerkady et al., 2013).

Collagen XIV is a homotrimer that contains two collagen triple-helical domains (COL1 and COL2) and three non-collagenous domains (NC1, NC2, and NC3). The triple-helical domains interact with and adhere to the surface of fibrillar collagens (Ansorge et al., 2009; Birk, 2011; Gordon et al., 1996). The collagen XIV COL1 and NC1 domains interact with collagen I. The NC3 domain is a large amino terminal globular domain that extends away from the fibril into the interfibrillar space. The NC3 subdomain has structural homology to von Willebrand factor A domains and fibronectin type III repeats.

Collagen XIV is implicated in the regulation of corneal stromal compaction (Gordon et al., 1996) and promotes collagen gel contraction by fibroblasts in vitro (Nishiyama et al., 1994). In vivo studies of chicken tendon during embryogenesis and early post-hatching stages showed high collagen XIV expression during development that decreases during tissue maturation (Young et al., 2002). Similar findings were reported in mouse tendons and heart during development (Ansorge et al., 2009; Tao et al., 2012). These studies suggest that collagen XIV plays an important role during early development, but its expression, regulation and specific roles in adult tissue and during wound healing remain to be elucidated.

4.1c Network forming collagens—These collagens do not form fibrils, but rather form networks with different spatial localizations and functions within the corneal stroma. It is unlikely that the network-forming collagens have a direct influence on regulation of fibril assembly and organization. Rather they are involved in integrating cells and matrix structures and/or integration of different matrix structures such as basement membranes and the stroma. These collagens are differentially expressed in Bowman's layer, the stroma proper and Descemet's Membrane and play vital roles in stromal structure and function.

Collagen IV networks form the backbone of the corneal basement membrane. The collagen IV network also interacts with basement membrane proteoglycans and glycoproteins that determine its function (Khoshnoodi et al., 2008; Pozzi et al., 2017; Yurchenco, 2011). Interactions with the components of basement membranes are important in integrating epithelia and the supporting stroma. Collagen IV is present in the corneal epithelial and endothelial basement membranes (Kabosova et al., 2007; Medeiros et al., 2018; Saikia et al., 2018). Collagen IV also is present in Bowman's Layer as a part of the anchoring complex (Gipson et al., 1983; Gipson et al., 1987; Keene et al., 1987) and extends into Descemet's membrane (Fitch et al., 1990). However, for the purposes of this review we are excluding further discussion of the basement membranes.

Collagen VI is a ubiquitous component of connective tissues and is widely and abundantly expressed in the corneal stroma. It is found as an extensive network of beaded filaments associated with collagen fibrils and is often enriched in pericellular regions. In addition to beaded microfibrils, there are other tissue forms, i.e., hexagonal networks and broad banded structures (Bruns et al., 1986; Linsenmayer et al., 1986; von der Mark et al., 1984). Collagen VI binds a large number of extracellular molecules including: collagens I, II, IV, XIV, microfibril-associated glycoprotein (MAGP-1), perlecan, decorin, biglycan, hyaluronan, heparin and fibronectin as well as integrins and the cell-surface proteoglycan NG2 (Bonnemann, 2011; Cescon et al., 2015; Lamande and Bateman, 2018). Since collagen VI is

able to bind to multiple matrix and cell surface proteins it has the capacity to integrate the surrounding connective tissue with cells and organize the three-dimensional tissue architecture (Cescon et al., 2015; Lamande and Bateman, 2018). In addition, collagen VI may influence cell migration, differentiation and apoptosis/proliferation. It also promotes adhesion and spreading of keratocytes (Doane et al., 1996; Doane et al., 1992). This indicates a role(s) in the development of tissue-specific extracellular matrices, repair processes and in the maintenance of tissue homeostasis.

The best characterized form of collagen VI is a heterotrimer composed of $\alpha 1(VI)$, $\alpha 2(VI)$ and $\alpha 3(VI)$ chains (Chu et al., 1987; Kielty et al., 1990). This form is present in the corneal stroma (Takahashi et al., 1993). The collagen VI monomer has a short, 105 nm triple helical domain with flanking N- and C-terminal globular domains. The N–terminal domain is approximately twice the size of the C-terminal domain and is primarily derived from the $\alpha 3(VI)$ chain. In addition, alternative splicing of the $\alpha 3(VI)$ N–terminal domain introduces structural heterogeneity. There are multiple isoforms of collagen VI with 3 additional α chains, $\alpha 4(VI)$, $\alpha 5(VI)$, $\alpha 6(VI)$ able to form different combinations (Fitzgerald et al., 2008; Gara et al., 2008). These chains have high homology with the $\alpha 3(VI)$ chain and may form additional isoforms.

The assembly of collagen VI into beaded filaments begins intracellularly (Fig. 6). First, a dimer is formed via lateral, anti-parallel association of two monomers. The monomers are staggered by 30nm with the C-terminal domains interacting with the helical domains. This overlap generates a central 75nm helical domain flanked by a non-overlapped region with the N- and C-globular domains, each about 30 nm. These interactions are stabilized by disulfide bonds (Ball et al., 2003). This is followed by tetramer formation where two dimers align with the ends in register. Finally, tetramers are secreted and are the building blocks used to assemble beaded filaments. Extracellularly, tetramers associate end-to-end to form to thin, beaded filaments (3–10nm) with a periodicity of approximately 100nm. These beaded filaments laterally associate, forming beaded microfibrils (Baldock et al., 2003; Bruns et al., 1986; Furthmayr et al., 1983). In addition to beaded microfibrils, other collagen VI containing supramolecular structures are found in the ECM including hexagonal lattices; and broad banded fibrils with a 100nm periodicity. The broad banded fibrils represent continued lateral growth of beaded microfibrils and/or lateral association of preformed beaded microfibrils. In contrast, hexagonal lattices are formed via end-to-end interactions of tetramers in a non-linear fashion (Wiberg et al., 2002).

Comparable to fibrillar collagen, supramolecular assemblies of collagen VI are composite structures with other associated molecules modulating the functional properties of these assemblies. For example, biglycan interactions with tetramers induced hexagonal lattice formation rather than beaded microfibrils which was dependent on the glycosaminoglycan chains. In contrast, decorin, which binds to the same site, was less effective in inducing hexagonal lattice formation (Wiberg et al., 2002). The interaction of small leucine-rich proteoglycans with collagen VI influences the structure of the tissue aggregate and therefore its function. This provides a mechanism to assemble different collagen VI structures in adjacent regions or tissues with different functions.

Collagen VII is a large collagen that is assembled into anchoring fibrils (termed fibrils, but 'anchoring fibrils' are structurally distinct from 'collagen fibrils') that form networks tethering epithelial basement membranes to the underlying connective tissue (Burgeson and Christiano, 1997). As a homotrimer, the large central collagenous domain of collagen VII is flanked by N- and C-terminal non-collagenous domains (Bruckner-Tuderman et al., 1999). Unlike the fibril-forming collagens, the collagenous domain contains numerous interruptions that provide flexibility to this collagen. Collagen VII is secreted into the ECM where it forms antiparallel tail-to-tail dimers with a central C-terminal overlap and with the N-termini pointing outwards. There is a proteolytic processing of a portion of the NC2 domain that permits lateral association. Subsequently, the processed dimers aggregate laterally in a non-staggered manner into the anchoring fibrils (Fig. 7). Mature anchoring fibrils are stabilized by transglutaminase cross-links.

In the corneal stroma, anchoring fibrils extend from the epithelial basement membrane into Bowman's layer, thus integrating the corneal epithelium with the stroma. The NC1 domains of collagen VII at both ends of the anchoring fibrils bind to macromolecules in the basement membrane including collagen IV and laminin. This forms a network of loops that entrap collagen fibrils. It has been shown that collagen VII has poor affinity to most collagens, including collagen I (Brittingham et al., 2006). However, in the dermis, anchoring fibrils bind tightly to cross-striated collagen fibrils containing, among other types, collagen I. This indicates that there are binding determinants that exist only at the level of supramolecular aggregates and these sites are important for dermo-epidermal cohesion (Villone et al., 2008) and are compromised in patients with dystrophic epidermolysis bullosa, a severe heritable skin blistering disease (Bruckner-Tuderman, 2010). This bullous disorder of the skin and mucous membranes, is frequently associated with ocular complication. Eyelid ulcerations, chronic conjunctivitis, diffuse subepithelial corneal scarring, recurrent corneal ulcerations and sclerocornea are described in these patients (Destro et al., 1987; Sharkey et al., 1992).

Collagen VIII is a short chain collagen found as a major component in Descemet's membrane (Sawada et al., 1990; Shuttleworth, 1997). Descemet's membrane is composed of layers of hexagonal lattices (Jakus, 1956). These lattices contain collagen VIII (Sawada et al., 1990). Collagen VIII is a homo- or hetero-trimer of $\alpha 1$ (VIII) and $\alpha 2$ (VIII) chains and both homotrimers and the $\alpha 1$ (VIII) $_{2}\alpha 2$ (VIII) heterotrimer exist in tissues (Illidge et al., 1998, 2001). The collagen VIII monomer has a short central COL domain and is flanked by N- and C-terminal NC domains. The monomers form lattices in vitro comparable to those in tissues (Stephan et al., 2004). It was proposed that collagen VIII monomers form a tetrahedron through the interaction of 4 molecules. This structure serves as the building block that assembles into three-dimensional hexagonal lattices. The assembly of a layered hexagonal lattice could involve interaction of the N-terminal non-collagenous domains or anti-parallel interactions involving both helical and terminal domains (Fig. 8). Collagen VIII expression in Descemet's membrane has been the object of different studies due to its association with Fuchs endothelial dystrophy. Missense mutations in the gene encoding the α_2 (VIII) subunit of collagen VIII are associated with an early-onset form of Fuchs dystrophy (Biswas et al., 2001; Gottsch et al., 2005; Mok et al., 2009). In addition, two different mouse models with Col8a2 mutations, recapitulate some of the findings in

endothelial cells and Descemet's membrane found in humans (Jun et al., 2012; Meng et al., 2013).

4.2 Proteoglycans

Small leucine-rich proteoglycans (SLRP) consist of a protein core with a central leucine-rich repeat domain that is flanked by N- and C-terminal cysteine-rich domains. Covalently linked to the protein core are 1 or 2 glycosaminoglycan (GAG) chains. The GAGs are chondroitin sulfate/dermatan sulfate in the Class I SLRPs, keratan sulfate in the class II corneal SLRPs and class III osteoglycin. Class I SLRPs includes decorin and biglycan. Class II includes: fibromodulin, lumican, and keratocan. Six SLRPs are expressed in the stroma: decorin, biglycan, lumican, keratocan, fibromodulin, and osteoglycin. These proteoglycans act as tissue organizers, influence cell growth, modulate and tether growth-factors, bind water through their GAG chains maintaining stromal hydration, and regulate collagen fibrillogenesis. Decorin, biglycan and fibromodulin bind TGF-β, (Brown et al., 2002; Hildebrand et al., 1994) to reduce its bioavailability and compete with the signaling receptors to attenuate signal transduction (Droguett et al., 2006; Frikeche et al., 2016). The importance of the GAG chains covalently attached to the protein core to from a proteoglycan is evident in macular corneal dystrophy. In macular corneal dystrophy, mutations in the sulfotransferase 6 gene creates deficiencies in the sulfation of keratan sulfate GAG chains with unsulfated keratan sulfate proteoglycans being deposited in the stroma with subsequent stromal opacification (Akama et al., 2000; Lewis et al., 2019). Sulfation of keratan sulfate GAG chains is blocked in a mouse model deficient in the enzyme N-acetyl-glucosamine-6-O-sulfotransferase. These mice have transparent corneas. However, the stroma is thin compared to wild type controls with abnormal collagen fibril organization and packing with increased inter-fibrillar spacing (Hayashida et al., 2006). These data clearly illustrate the importance of GAG chains in stromal structure and function.

4.2a Decorin and Biglycan—Expression of both class I SLRPs is homogenous across the corneal stroma. Biglycan expression is low in the mature stroma while decorin expression is higher (Doane et al., 1996; Mohan et al., 2011; Rada et al., 1993; Zhang et al., 2009). Biglycan expression is increased during wound healing (Basu et al., 2014). Secreted biglycan interacts via its core protein or GAG chains with numerous components of the stromal extracellular matrix including collagens I, II, III and becomes integrated into the matrix (Douglas et al., 2006; Hunzelmann et al., 1996; Schonherr et al., 1995). These SLRPs play key roles in the regulation of stromal fibril structure and organization. The absence of decorin in mutant mice models results in a severe disruption of fibril structure and stromal structure (Zhang et al., 2009). In decorin null stromas biglycan was upregulated masking most of the decorin effect. This indicates a potentially modulatory role biglycan in the corneal stroma depending on development stage and/or in the injury response.

Two important decorin related processes are of translational relevance in the cornea. Autosomal-dominant congenital stromal corneal dystrophy, a rare human genetic disease is linked to mutations in decorin (Rodahl et al., 2006). The mutations result in a truncation of the decorin core altering the ability to bind collagen fibrils. This results in a disruption of

matrix organization and opacity (Bredrup et al., 2010; Chen et al., 2011a; Kamma-Lorger et al., 2016). A novel animal model that recapitulated this corneal dystrophy was generated in mutant mice. Corneal opacities were found with increased severity toward the posterior stroma. The architecture of the lamellae was disrupted with relatively normal lamellae separated by regions of abnormal fibril organization (Chen et al., 2011a). While the exact(s) mechanisms underlieing this congenital disorder are not fully understood abnormal decorin has a central role (Chen et al., 2013a; Mellgren et al., 2015). Second, studies indicate that decorin is an effective candidate for diminishing TGF-β bioavailability and therefore down-regulation of haze and corneal scarring. Through formation of complexes with TGF-β, decorin neutralizes TGF-β, and by competitive inhibition, decorin inhibits the binding of TGF-β to its receptor reducing scar formation (Harper et al., 1994; Zhang et al., 2018).

4.2b Lumican and keratocan—Lumican and keratocan are the predominant class II SLRPs in the corneal stroma. While not totally corneal-specific together these SLRPs are excellent biomarkers for the tissue. They are expressed homogeneously across the cornea stroma at birth, but the expression of lumican is restricted to the posterior stroma in the adult. The role of lumican in regulating stromal function has been studied in lumican null mouse models. In lumican deficient corneas, an initially clear cornea becomes cloudy, postnatally, with a majority of the light backscattering located in the posterior stroma where lumican expression is located in adult corneas (Chakravarti et al., 2000). This suggest a role for lumican in regulating corneal transparency in post-natal maturation (Chakravarti et al., 1998). In lumican deficient corneas, analysis of hierarchical structure shows that lamellar structure was disrupted across the stroma with disorganized fibrils, and altered fibril packing in the posterior stroma, indicating that lumican is a regulator of fibrillogenesis with changing expression patterns providing spatially restricted regulation. There are no well characterized human conditions associated with mutations in lumican. Mutant mice deficient for keratocan expression have transparent, but thin corneal stromas with a mild increase in collagen fibril diameter with no further abnormalities (Liu et al., 2003). In humans, mutations in the keratocan gene are associated with a flattened cornea in a rare condition known as cornea plana (Pellegata et al., 2000). The relative specificity of keratocan to corneal keratocytes has been useful for tissue-specific targeting for genetic manipulation of the corneal stroma (Sun et al., 2011; Zhang et al., 2017).

4.2c Fibromodulin—Fibromodulin is not considered to be a major corneal SLRP. Fibromodulin and lumican show 50% identity in primary sequence and bind the same site on collagen I (Kalamajski and Oldberg, 2009). In mouse models deficient in fibromodulin, lumican compensates for the absence of fibromodulin, suggesting that they can function as a coordinated pair. Fibromodulin is expressed in scleral tissue, but its expression in the corneal stroma of adult mice is weak (Chakravarti et al., 2003). However, during development, fibromodulin is found in the peripheral cornea and the posterior stroma. In adult corneas, stromal expression has regressed and is localized to the scleral and limbal stroma, with minimal posterior peripheral stroma expression (Chen et al., 2010). The data suggest a key role in regulation eye growth in emmetropization as well as corneal-stromal integration.

4.2d Osteoglycin—Osteoglycin also known as mimecan is a class III SLRP. Corneal development in osteoglycinnull mice appeared normal and changes in corneal clarity were not detected (Tasheva et al., 2002). There were minor effects on corneal collagen fibril diameter and interfibrillar spacing, observed in these mice. Immuno-localization of osteoglycin in the mouse cornea showed localization primarily to the epithelium and epithelial basement membrane with minor stromal localization. In the stroma, osteoglycin was primarily localized to the keratocytes (Chakravarti et al., 2006). Therefore, the stromal role of this SLRP is ambiguous.

4.2e SLRPs in regulation of stromal collagen fibrillogenesis—SLRPs are regulators of collagen fibril assembly. They have been shown to be critical in regulating linear and lateral growth of protofibrils into mature fibrils in the corneal stroma as well as other tissues (Chakravarti et al., 1998; Chakravarti et al., 2003; Chakravarti et al., 2006; Chen and Birk, 2013; Chen et al., 2010; Ezura et al., 2000; Mienaltowski and Birk, 2014; Zhang et al., 2009). Figure 9 presents a model illustrating SLRP and collagen fibril interactions in the regulation of stromal fibril growth. Mouse models deficient for decorin, biglycan, lumican, and keratocan have been particularly informative in the corneal stroma. Interestingly, null mice deficient in decorin or biglycan have a mild stromal phenotype. However, deficiency in both decorin and biglycan results in a severe phenotype. These compound null stromas have an increase in large diameter fibrils, a very heterogeneous diameter distribution, and irregular, fibril contours in both the anterior and the posterior stroma. Biglycan is up-regulated in the absence of decorin and it functionally compensate for the loss of the class I SLRP decorin in both in vivo and in vitro studies (Chen et al., 2015; Zhang et al., 2009). Lumican-null mice demonstrate a progressive corneal opacity with age. This opacity results from irregularly packed, and large diameter fibrils with irregular contours in the posterior stroma. The altered collagen fibril properties seen in the absence of decorin and lumican are related to a dysfunctional stromal regulation of lateral fibril growth. Since stromal transparency requires a homogeneous population of small diameter fibrils, the observed abnormal fibril phenotypes results in increased light scattering and opacity(Chakravarti et al., 2000; Song et al., 2003).

Keratocan or fibromodulin null mice do not have changes in stromal fibril structure. Keratocan null-mice have thinner corneal stromas and narrower cornea-iris angles suggesting an involvement in stromal hydration and shape during development (Liu et al., 2003). Fibromodulin is expressed in a narrow window during stromal development. The data suggests that it contributes to cornea-sclera integration (Chen et al., 2010). Interestingly, a deficiency of lumican in the stroma alters expression of both keratocan and fibromodulin (Shao et al., 2011). Additionally, SLRP expression can be altered by the presence or absence of other class members. Moreover, regulatory interactions across classes also have been demonstrated by an increased severity of the corneal stromal fibril structural phenotype in the absence of both biglycan and lumican, compared to either one alone (Chen et al., 2014). This is evidence of inter-class cooperation in the regulation of fibril growth. While decorin and lumican appear to be the major SLRPs regulating stromal lateral fibril growth, others SLRPs have the ability to modulate their effects. Defining the network of regulatory SLRP

interactions is essential to elucidate the roles in development, maintenance and regeneration of tissue-specific structures and functions.

The mechanisms regulating linear fibril growth within the corneal stroma are less understood. Prior to compaction of the stroma the newly formed protofibrils may be spaced so that the frequency of end to end interaction is inhibited. Ex vivo studies demonstrated that when end to end interaction of fibrils are increased linear fibril growth results (Graham et al., 2000). It has been suggested that the end-to-end interactions increase in development as the charge densities of GAG chains on stromal SLRPs increase that would induce order to the inter-fibrillar environment. In addition, the tapered ends of stromal protofibrils may have binding properties that stabilize the ends, with the normal turnover of SLRPs and/or other bound molecules providing increased opportunities for controlled interactions.

4.3 Fibrillin/elastic fiber associated macromolecules

Elastic fibers are extracellular macromolecules that allow tissue deformability and recoil (Kielty et al., 2002). Elastic fibers are complex structures composed of numerous molecules. Simplified, an elastic fiber consists of an elastin core surrounded associated with fibrillin microfibrils (Hanlon et al., 2015; Kielty et al., 2002). Although there is no clear evidence of elastic fibers in the adult stroma, (Bruns et al., 1987; Carlson and Waring, 1988; Hanlon et al., 2015) microfibrillar structures are present in the stroma of some species, (Feneck et al., 2020b; Hanlon et al., 2015) and recently elastin tissue expression has been demonstrated in human Descemet's membrane (Lewis et al., 2019; Mohammed et al., 2018). Microfibrils are found widely distributed in the entire stroma as orthogonal arrays of parallel bundles in different species, including young and adult organisms (Bruns et al., 1987; Carlson and Waring, 1988; Hanlon et al., 2015). Transmission electron microscopy has shown 10-15 nm microfibrils arranged in quasi-parallel bundles within or between orthogonally arranged stromal collagen lamellae and some structures crossing Descemet's membrane are suspected to be of elastic origin (Bruns et al., 1987; Carlson and Waring, 1988; Mohammed et al., 2018). In the family of the microfibrils, fibrillin 1 is the most common of the 3 proteins (Jensen et al., 2012). Marfan syndrome is an autosomal dominant disease of connective tissue in humans caused by mutations in the fibrillin 1 gene encoding the fibrillin-1 protein and it is characterized by a thinner cornea (Sultan et al., 2002). Studies in a mouse model deficient in fibrillin 1, that recapitulates Marfan's syndrome, concluded that the function of this elastic tissue is to provide the cornea with mechanical strength/elastic recoil, and maintain corneal curvature (White et al., 2017). Fibrillin 1 binds different extracellular matrix proteins including decorin, collagen VI and latent transforming growth factor- β binding protein (Kielty et al., 2002). By binding latent transforming growth factor- β binding protein, fibrillin-1 may have a mechanotransduction role and affect transforming growth factor- β signaling (Buscemi et al., 2011; Robertson et al., 2015). A fibrillin 1 deficient mouse model is accompanied by a thinner cornea with decreased collagen I production, abnormalities in transforming growth factor- β as well as decreased decorin content in the cornea (Feneck et al., 2020b). While the fibrillin microfibrils have not been observed in the human cornea this deserves further evaluation to address its potential presence in an alternative structural form and their role in pathological conditions like keratoconus.

4.4 Stromal glycoproteins

4.4a Fibronectin—Fibronectin is a well-studied large and structurally ubiquitous complex glycoprotein that binds to (Hsia and Schwarzbauer, 2005)multiple matrix structures, various proteoglycans, and growth factors. Fibronectin occurs in two principal forms, the soluble plasma fibronectin circulating in the blood and the cellular fibronectin, which polymerizes into insoluble fibers in the matrix of tissues (Pankov and Yamada, 2002; Zollinger and Smith, 2017). Fibronectin fibril assembly involves interactions between its RGD sequence and corresponding binding sites within cell surface receptors such as integrins (Labat-Robert, 2012; Singh et al., 2010; Zollinger and Smith, 2017). Fibronectin is also essential to the process of collagen matrix deposition and is highly expressed in the corneal stroma during wound healing since fibronectin forms a temporary scaffold in the early stages of injury (Barker and Engler, 2017; Kadler et al., 2008). During wound healing, an early provisional matrix matures in later phases, the early provisional fibrin-rich matrix, is replaced primarily by fibronectin and proteoglycans (Barker and Engler, 2017; Kadler et al., 2008). Inhibition of fibronectin matrix assembly inhibited deposition of collagens I and III (McDonald et al., 1982). Fibronectin repeats form a promiscuous binding domain that interacts with multiple growth factors: platelet-derived growth factor, vascular endothelial growth factor, and some of the transforming growth factor- β family (Martino and Hubbell, 2010; Zhu and Clark, 2014). Fibronectin recruits and stores latent transforming growth factor- β binding protein and therefore regulates transforming growth factor- β . The extra domain A fibronectin variant is expressed in embryos, but only during wound healing in adults (Ffrench-Constant et al., 1989). Due to its pro-fibrotic effect, extracellular availability, and high expression in fibrosis, this alternatively spliced variant is proposed as an antifibrotic target (Walraven and Hinz, 2018). Keratocytes are known to express fibronectin during homeostasis (Jester et al., 1994). Fibronectin is upregulated in the stroma during wound healing in different injury models including stromal or epithelial debridement (Basu et al., 2014; Fujikawa et al., 1984; Nickeleit et al., 1996; Tervo et al., 1991).

4.4b Matricellular proteins—This is a group of secreted glycoproteins that facilitate cellular control over their surrounding extracellular matrix and influence structure and function in multiple tissues. The matricellular family includes among others: thrombospondins 1 and 2, SPARC (secreted protein, acidic and rich in cysteine), and osteopontin (Murphy-Ullrich and Sage, 2014).

Thrombospondins comprise a family of extracellular, multidomain, calcium-binding glycoproteins. The family consists of thrombospondins 1 to 5. Thrombospondin 5 is also known as COMP. Thrombospondins interact with cell surfaces, growth factors, cytokines, and other components of the extracellular matrix. Thrombospondin-1 (TSP-1) is a large (450 kDa) trimeric extracellular glycoprotein released by platelets, and epithelial and mesenchymal cells in response to wound healing, angiogenesis, tumor cell migration, and platelet aggregation. It is abundant in platelet granules, and its expression is increased dramatically during the woundhealing process. Absence of TSP-1 leads to prolonged inflammation, delayed wound healing, and delayed scab loss (Agah et al., 2002).

In the human and bovine cornea, TSP-1 localizes to the epithelial basement membrane and posterior Descemet's membrane. No stromal or keratocyte expression is reported (Hiscott et al., 1997). In murine corneas, minimal expression is found on epithelial and endothelial cells with no keratocyte expression (Matsuba et al., 2011). However, TSP-1 expression increases significantly 48 hours after creating a full thickness corneal laceration. TSP-1 expression in the wound increases daily and peaks by day 14, and upregulation in expression is present in the entire wound from epithelium to endothelium. In a TSP-1 deficient mouse model, stromal, as well as endothelial healing, are severely impaired. TSP-1 deficient corneas rapidly become opaque after an incision wound and never appeared to heal after a 1 month follow-up (Blanco-Mezquita et al., 2013). TSP-1 is believed to act by activation of TGF- β during wound healing. TSP-1 binds to the latent complex and converts latent TGF- β to its biologically active form through a non-proteolytic mechanism. These data suggest that TSP is a potent physiologic regulator of TGF- β activation (Schultz-Cherry and Murphy-Ullrich, 1993). The expression and role of Thrombospondins 2–5 in the stroma are mostly unknown (Armstrong et al., 2003; Si et al., 2003).

SPARC is a 32 kDa calcium-binding matricellular protein also known as osteonectin or basement membrane protein 40. Initially found in bone, expression of SPARC in adult tissues is frequently associated with excessive deposition of collagen (Bradshaw, 2009). A lack of SPARC expression has been shown to diminish mature collagen accumulation in the matrix of many connective tissues (Murphy-Ullrich and Sage, 2014; Rosset and Bradshaw, 2016). For example, SPARC-null mice have decreased total collagen I content in bone, and other tissues (Bradshaw, 2009; Murphy-Ullrich and Sage, 2014). The increased in SPARC during wound healing and pathological fibrosis is a topic of interest. In the corneal stroma, SPARC is upregulated during the response to injury and during stimulation of cultured corneal fibroblasts with TGF- β (Berryhill et al., 2003). A potential role for *SPARC* in the etiology of corneal ectasias has been explored (De Bonis et al., 2011).

Osteopontin (OPN) is a matrix and structural glycophosphoprotein that is abundantly expressed in tissues during inflammation and repair. OPN has different functions, including in matrix remodeling and repair, inflammatory response, cell death, and survival (Giachelli and Steitz, 2000; Icer and Gezmen-Karadag, 2018; Liaw et al., 1998). In a mouse model deficient in OPN, healing of a corneal incision injury was delayed, with fewer myofibroblasts and decreased TGF- β 1 expression, as well as a higher incidence of corneal perforation (Miyazaki et al., 2008).

4.4c Tenascins are a family of large oligomeric extracellular matrix glycoproteins that consists of 4 members: tenascin C, R, X, and W (Hsia and Schwarzbauer, 2005; Midwood et al., 2016). They have similar structures, but their expression patterns vary in different tissues. Tenascin-C knock out mouse models have a normal phenotype, but an impaired response to stress and injury (Mackie and Tucker, 1999). There is no expression of tenascin C in the normal adult uninjured cornea (Maseruka et al., 1997). However, tenascin C expression is upregulated following corneal injury and in scarred corneas (Maseruka et al., 1997). During healing of a perforating injury wound model, only weak induction of tenascin-C was seen in corneas from wild type mice, and healing in tenascin-C null mice was indistinguishable from that of wild type mice. In a sutured wound model, fibronectin

expression was absent in the tenacin-C knockout model, but not in wild type wounds. Tenascin-C seemed to regulate the expression of fibronectin or its retention in the extracellular matrix (Matsuda et al., 1999). More work is needed to explore the roles of tenascins in the corneal stroma during development and in pathological conditions.

6. Summary

The stroma has unique properties: transparency, tissue strength, avascularity and precise curvature. Early in corneal development, the precise temporal and spatial regulation of stromal extracellular matrix assembly, determining the structural and functional properties of the stroma, is dependent on cell-matrix and matrix-matrix interactions. Therefore, the keratocytes and the extracellular matrix molecules they secrete are critical determinants of stromal properties. The major structural building blocks of the stroma are the collagen fibrils. These fibrils are tissue specific to the stroma, and with a distinct hierarchal organization that define stromal structure, and therefore, function. The regulation of collagen fibrillogenesis and stromal hierarchical organization in the cornea involves interactions of fibril-forming collagens I and V. However, these regulatory interactions are fine-tuned by interactions with fibril-associated molecules including; FACIT collagens, and SLRPs (decorin, lumican, keratocan, and biglycan) that regulate lateral association of collagen molecules during fibril growth and regulate hierarchical organization. Superimposed of this are other extracellular matrix networks that add critical elements to the development and maintenance of stromal structure and function. For instance, collagen VII form a network of anchoring fibrils that integrate the epithelial basement membrane with the stroma; collagen VIII assembles a hexagonal lattice network in Descemet's membrane and serves as an interfacial matrix connecting the posterior stroma with the endothelium; and collagen VI networks bind to cells and numerous matrix molecules to integrate the different cell and matrix components within the stroma proper. In addition, there are networks of elastin associated molecules, e.g. fibrillins that may contribute to the mechanical properties of the stroma. In addition, fibronectin and matricellular proteins that are present in the stroma may have structural roles or be involved in mediating matrix interaction; they have major role(s) influencing cell behavior and biosynthetic profiles. These and other components of the stromal extracellular matrix have poorly defined roles that might regulate stromal function and may be essential for wound repair and in the pathogenesis of stromal diseases. Future research in this area will continue to expand our understanding of the roles of different matrix components, cells and cytokines in the regulation of stromal structure and function during development and in pathological conditions. The purpose of this review was to summarize our current knowledge and spark enthusiasm for the understanding of the regulation of matrix components essential for the function of this unique tissue.

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Highlights

- The unique stromal structure and function is regulated by different extracellular matrix components.
- Different structures within the stroma, including Bowman's and Descemet's layers, have unique ECM composition and function.
- Not only collagens are essential for regulation of fibril formation, other ECM components like Small Leucine Rich Proteoglycans regulate fibrillogenesis and have other functions including modulation of the availability of growth factors and stromal hydration.
- Regulation of ECM components play a major role in wound healing

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Collagen I Fibril Assembly

Fig. 1. Fibril-Forming Collagens: Fibrils.

Collagen I is the major stromal protein. This fibril-forming collagen is synthesized as procollagen. Procollagens have a central collagen (COL) domain with flanking N-and C-terminal propeptides. Extracellularly, the propeptides are processed and the resulting collagen molecules assemble to form striated fibrils. The collagen I molecule is approximately 300 nm in length and 1.5 nm in diameter. During fibril assembly, the collagen molecules are staggered N to C and this staggered pattern of collagen molecules gives rise to a 67nm repeat. An electron micrograph of a negative stained fibril is shown at the bottom of the panel. This fibril has the characteristic alternating light/dark pattern representing the gap (dark) and overlap (light) regions of the fibril.

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Fig. 2. Corneal Stroma Heterotypic Fibrils.

Corneal stromal collagen fibrils are heterotypic, co-assembled from quantitatively a major fibril forming collagen, e.g., collagen I and regulatory fibril-forming collagen, e.g., collagen V. Regulatory fibril-forming collagens have a partially processed N-terminal propeptide, retaining a non-collagenous domain that must be in/on the gap region/fibril surface. This is the major regulatory domain.

Stromal Fibril Assembly



Fig. 3. Heterotypic Collagen I/V Interactions Regulate Initial Fibril Assembly.

Stromal fibril assembly involves a sequence of regulatory interactions. (A) Initially, collagen V interacts with collagen I to nucleate collagen assembly into fibrils at the keratocyte surface. This results in the regulated assembly of immature, small diameter, short fibrils termed protofibrils. This initial step in fibril assembly is cell-directed involving interactions with organizers at the keratocyte surface, e.g., integrins and syndecans either directly or through intermediate interactions, e.g. fibronectin (indicated by shaded blue region). This permits kertocyte control over the initial assembly steps and allows for positioning of newly assembled fibrils into the stromal matrix. (B) In the absence of collagen V regulation of collagen I assembly and positioning of assembled fibrils is lost. This results in formation of fewer, larger and heterogenoeus fibril diameters, structurally abberent fibrils as well as disrupted fibril organization. This unregulated assembly is not consistent with stromal transparency.



Fig. 4. FACIT Collagens.

Collagens XII and XIV are fibril-associated in the stroma. Their domain structures are illustrated. All FACITs have alternativly spliced variants and collagen XII can have glycosaminoglycan chains covalently attached. The FACIT collagens have 2–3 collagen (COL) domains and 3–4 non-collagenous (NC) domains. Characteristic of this collagen type is a large N-terminal NC domain that projects into the inter-fibrillar space. The FACIT collagens all associate with the surface of collagen fibrils and this is illustrated, including N-truncated isoforms due to alternative splicing in collagen XII. Collagen XII is capable of non-fibrillar interactions (not shown), it is not known if this is true for collagen XIV.



Lamellar Assembly & Stroma Stabilization

Fig. 5. FACIT Regulation of Stromal Hierarchal Assembly.

FACIT collagens bind to fibril surfaces. In addition, they can interact with cells and a number of other matrix components. These properties are required for integration of different stromal components. FACIT collagens XII and XIV are associated with stromal fibrils. These interactions, along with SLRPs (see Fig. 9) can stabilize fibril diameter and spacing. In the absence of collagen XII, stromal lamellae fail to develop properly and there is a general disorganization of lammelar and stromal architecture. This indicates a critical role in integration of the fibrillar components necessary for stable lamellae formation. There is also evidence that collagen XII is enriched at cell and basement membrane interfaces (not shown) and may facilitate cell-matrix integration.



Fig. 6. Collagen VI.

Collagen VI forms networks of beaded filaments in the corneal stroma. (**A**) Collagen VI monomers have a C-terminal non-collagenous (NC) domain, a central triple helical domain and an N-terminal NC domain. Intracellularly, monomers assemble N-C to form dimmers. Tetramers are assembled from two dimmers aligned in register. (**B**) The tetramers are secreted, and extracellularly they form the building blocks of 3 different collagen VI Assemblies. These include beaded filaments, broad banded fibrils and hexagonal lattices form via end-to-end interactions of tetramers and varying degrees of lateral association.



Collagen VII Assembly

Fig. 7. Collagen VII.

Collagen VII forms a network of anchoring fibrils that adhere to the epithelial basement membrane and form loops entrapping the collagen fibrils in Bowman's layer. This integrates the epithelial basement membrane with the underlying stroma. Collagen VII has a long central triple-helical collagenous (COL) domain containing numerous interruptions conferring flexibility to the domain. The COL domain is flanked by non-collagenous N-(NC-1) and C-terminal (NC-2) domains. Two monomers interact to form an anti-parallel dimer with a central C-terminal overlap and the NC-1 domains pointing out. Processing occurs, with a cleavage of the NC-2 propeptide and covalent stabilization of the dimer. At this point, a non-staggered lateral association of dimers occurs that produces anchoring fibrils.



Fig. 8. Collagen VIII Forms Hexagonal Lattices In Descemet's. Membrane.

Collagen VIII is a short chain collagen with a central collagenous (COL) domain and flanking N- and C-terminal non-collagenous (NC) domains. The C-terminal NC domains of 4 collagen VIII molecules interact to form tetrahedrons. Tetrahedrons assemble further to form hexagonal lattices. A planar hexagonal lattice is illustrated. In Descemet's membrane continued assembly, involving interactions of the N-terminal NC domains or anti-parallel interactions involving both helical and terminal domains (not shown) generates the layered hexagonal lattice characteristic of Descemet's membrane (not shown).

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Fig 9. SLRPs Regulate Lateral Fibril Growth.

SLRPs regulate linear and lateral stromal collagen fibril growth by binding to fibril surfaces. (A) Newly assembled stromal fibrils (protofibrils) are deposited into the matrix where they are stabilized via interactions with SLRPs. After deposition into the stromal matrix, protofibrils mature by a process of fibril growth. Bound SLRPs mediate and controlled fibrillar interactions resulting in coordinated growth of mature stromal fibrils. In the stroma there is a a tissue-specific regulation of lateral fibril growth. Diameter and packing are rigidly regulated for corneal transparency. (B) In most tissues there is a robust lateral growth resulting in heterogeneous populations of large diameter fibrils this is blocked in the stroma. Changes in fibril stabilization necessary for growth can result from processing, turnover, and/or displacement of SLRPs. SLRPs affect fibril diameter and spacing in the corneal stroma. When SLRPs are absent, as in null mice or in gene mutations in human patients, fibril structure, organization and spacing are impacted, compromising transparency. Also, the block to lateral fibril growth is lost in the stroma when SLPR expression is altered.