The Role of Extracellular Matrix Quality in Pulmonary Fibrosis

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We discuss and argue that the altered quality of the individual ECM proteins contributes to the progression of PF and may also lead to the increased quantity of lung proteins. Thus, both quantity and quality appear to be of utmost importance.

\section*{Key Words}
Chronic lung disease · Extracellular matrix · Fibrosis · Idiopathic pulmonary fibrosis · Lung biochemistry · Protein biomarkers · Protein function · Protein structure

\section*{Abstract}
This review discusses the role of extracellular matrix (ECM) quality in the pathogenesis of pulmonary fibrosis (PF). In PF, the highly ordered structure of collagens and elastin within the ECM of the lung is severely disrupted and lacks its original tissue quality. Discussions about the ECM have focused on the role of protein quantity in relation to the progression of PF, while the importance of lung ECM quality, defined by the levels of ECM protein modifications and by the protein distribution in lung tissue, has not been properly addressed. The quality and function of proteins may be altered by different post-translational modifications (PTMs), such as cross-linking, proteolytic cleavage, citrullination, misfolding and glycosylation. This paper is the first to review key data from the literature related to the lung ECM at the molecular level, relate these to changes observed at a macroscopic level and evaluate which PTMs most likely contribute to PF. This paper also reviews the role of novel neo-epitope-specific biomarkers in the early diagnosis and prognosis of fibrotic disorders.

\section*{Introduction}
Substantial changes in the normal distribution of various extracellular matrix (ECM) proteins are observed in a number of diseases \cite{1}. The function of the ECM was originally thought to be exclusively structural, but it is now commonly acknowledged that its role stretches beyond structural changes and may include regulatory properties \cite{1}. There are several indications that even a few changes in the complex distribution of ECM proteins can trigger severe damage of tissue \cite{2–9}. In addition to changes in their distribution, proteins in the ECM may also be altered on a quantitative scale and at the molecular level, involving modifications to their chemical structure or to their natural degradation and rebuilding process. Examples of potential relationships between abnormal ECM protein structures or processes and tissue...
damage are the elevated levels of collagen cross-linking enzymes seen in pulmonary fibrosis (PF) [2] and the increased proteolytic cleavage and cross-linking of elastin [10, 11].

In this review, we focus mainly on the function, quantity and distribution of collagens and elastin, which constitute the majority of ECM proteins in lung tissue [12–14], during the progression of PF. The lung ECM has not been investigated to the same extent as the ECM in other tissues such as bone and cartilage [1], and some lessons may be learned from those studies. PF occurs during the progression of idiopathic PF (IPF) [15], which is a lung disorder with one of the highest mortality rates. ECM quality and quantity in lung disorders with a focus on IPF will be discussed, along with the most important post-translational modifications (PTMs) of proteins in the lung ECM (mainly cross-linking and proteolysis) and the processes leading to IPF.

**Idiopathic PF**

IPF is the most common idiopathic interstitial pneumonia and has one of the worst prognoses of all pulmonary diseases [16, 17]. Patients with IPF have a median survival of 2.5–3.5 years after diagnosis [16, 18]. Even in aggressive cancer types, except for lung and pancreatic cancer, the survival rates after diagnosis are higher than for IPF [15]. IPF was earlier considered a progressive inflammatory related disease in which fibroblast proliferation and extracellular remodelling leads to scar formation or fibrosis of the lungs [15]. This theory has now been replaced with the chronic epithelial lesion paradigm that posits that there is a continuous damage to the epithelium together with insufficient repair and hyperplasia. This is followed by an epithelial-mesenchymal transition during which epithelial cells undergo a transition to a mesenchymal phenotype leading to fibroblast and myofibroblast phenotypes [19]. This may initiate the deposition of excessive amounts of ECM material in the lungs. Several growth factors may have active roles in the initiation of PF. These include, among others: TGF-β [20], CTGF [21], ET-1 [22], TNF-α [23], PDGF [24] and Wnt [25]. A wider description of their role is not included here as the focus is on lung ECM proteins. The specific process responsible for the failure in epithelial repair that leads to excessive deposition of ECM proteins remains unknown.

The main clinical challenges for IPF is that the disease is diagnosed relatively late, and there are currently no prognostic markers or even simple serological markers that can be used to identify patients who are fast progressors and thus in most need of intervention. Therefore, more focus directed towards the progression of IPF is needed.

**ECM of the Lung**

The ECM is a 3-dimensional network that maintains the structure of tissues and organs by encapsulating cells and defining their microenvironment [9]. It consists of a highly organized, complex network of arranged proteins. Soluble factors such as cytokines and growth factors may adhere to the network and cells may migrate into it. Previously the ECM was thought to only maintain structural properties, but its role in various diseases has been reviewed [1] and it is now also considered a central regulator of cell and tissue behaviour via transmembrane signalling [26, 27]. In this section, we list some of the main structural properties of the ECM.

Two types of structural ECM exist: (1) the basement membrane interacts with the epithelium and endothelium and consists mainly of type IV collagen, laminin, entactin/nidogen and heparin sulphate proteoglycans [28]; (2) the interstitial matrix constitutes the bulk of the ECM. Elastin and several types of collagens contribute, together with fibronectin, to the mechanical strength of the tissue [26].

While the basic composition and characteristics of the basement membrane and interstitial matrix are similar in different tissues, the variations in ECM components, for example in the expression of protein isoforms, PTMs and the ratio between individual matrix proteins, contribute to the differentiation of ECM organization and structure throughout the body. This ensures tissue specificity [29–31].

The lung ECM includes several structural proteins. These are mainly collagens, elastin, proteoglycans, fibronectin and laminin.

Several studies have linked the levels of lung ECM protein fragments of, for example, elastin and collagen type I, III, IV, V and VI to lung disorders such as chronic obstructive pulmonary disease (COPD) and IPF [32–35]. The collagen superfamily contains at least 27 collagen types and accounts for approximately 20% of the dry weight of the lung ECM [14]. Cross-linking is the final step in the biosynthesis of collagen and it is essential for the physical and mechanical properties of collagen fibrils. Cross-linking is an enzymatic process that is performed...
mainly by the enzymes lysyl oxidase (LOX) and transglutaminase (TG) [36–40]. The large number of cross-links contributes to the characteristically high tensile strength and minimal extensibility of collagens.

Elastin provides elasticity and resilience to many tissues and organs including the lung, skin, aorta, ligaments, tendons and cartilage and is therefore considered critical for their long-term functions [41]. The precursor of elastin, known as tropoelastin, is secreted from fibroblasts, smooth muscle cells, chondrocytes or endothelial cells before it is degraded to elastin [42]. The formation of covalent lysyl-derived desmosine cross-links by LOX further stabilizes the formed elastin fibres [43]. Elastic fibres are designed to maintain their elastic function for a lifetime and, once formed, are mostly only degraded by a few specialized proteases. Elastin is mainly degraded by matrix metalloproteinases (MMPs) and serine and cysteine proteases including neutrophil elastase (NE) [4, 44–47]. It accounts for more than 30% of the dry weight of the lung [12, 13] and is therefore the most representative protein of the lung ECM. Elastin is predominant in the pleura, alveolar septa and walls of the blood vessels and airways covering the thin, highly branched respiratory tree. Its ability to extend and contract enables alveolar expansion and recoil during breathing [48].

Hyaluronic acid (HA) is a non-sulphated glycosaminoglycan. Li et al. [49] demonstrated how overexpression of HA synthase 2 (HAS2) could induce PF. Deletion of HAS2 also inhibited the development of PF. HA may therefore contribute to the initiation of PF.

Integrins are essential for ECM remodelling as they transduce signals from the interior of the cells to the ECM and vice versa. Integrin regulation of TGF-β can lead to several fibrotic diseases including IPF [50].

Other molecules comprising the lung ECM may include fibrinogen, which is a glycoprotein. Laminin is the most abundant glycoprotein in the lung ECM basement membrane and is often associated with entactin [5]. Proteoglycans are also found in the integral membrane of lung cells or the lung ECM [5].

**PTMs in the Lung ECM**

PTMs are modifications of proteins that are non-DNA coded but are a consequence of the physiological or pathological state of a cell/tissue. PTMs of proteins are also known as neo-epitopes [31]. PTMs expand the chemical opportunities of a protein further than is possible with the 20 amino acid monomers alone. PTMs also enable regulation of a protein in its current state and location and provide the opportunity to monitor the state of a cell or tissue as PTM-specific biomarkers have proven previously [30]. They are often embedded in the non-globular regions of a protein [51, 52]. The focus is directed here towards the PTMs relevant for the organization of the ECM, mainly proteolytic cleavage and cross-linking. We will present examples from different diseases arising from ECM disorders and discuss PTMs that are of importance in lung disorders/fibrosis, especially IPF. A more extensive description of all of the PTMs observed in various diseases has been presented previously [29, 30]. Some PTMs discussed here have previously been identified and utilized as biomarkers for measuring pathological activity [31, 53]. This includes proteolytic cleavage, citrullination, cross-linking and glycosylation. The lung requires a large airway and epithelial surface area to function optimally, and this area is therefore constantly exposed to external factors that could affect the regulation of PTMs towards proteins of the lung ECM.

**Glycosylation**

Glycosylation is a common PTM. A well-known example of how glycosylation has been applied in diagnostics is the glycosylation of haemoglobin A1c [54] used to evaluate diabetes [55]. This example shows how a disease-specific PTM may enable a more precise diagnosis than measurements on intact molecules. Hyperglycosylation is also present in pulmonary diseases such as chronic bronchitis and cystic fibrosis, where it affects the airway’s innate immunity and promotes the attachment of pathogens [56, 57].

**Proteolytic Cleavage**

Among the most pathologically relevant PTMs in the lung are proteolytic cleavage of collagen and elastin by MMPs [8, 34, 36, 44, 46, 58–62] and NE [61, 63, 64]. The role of this modification in lung diseases was examined by analysing how MMP-induced elastin and collagen neo-epitopes are related to lung tissue degradation [33, 34]. This can be coupled to the properties of matrikines. Matrikines are ECM protein fragments that can regulate cell activity, which has been demonstrated by the anti-elastin autoimmunity induced by elastin matrikines in emphysema [65, 66]. The fragments were able to stimulate an immune response in tissues, with upregulation of cytokines leading to an increase in protease expression, which results in progressive destruction of the lung ECM [66]. Proteolytic cleavages may therefore have structural as well as regulative purposes in the lung ECM.
Cross-Linking

Cross-linking strongly affects the mechanical properties of the ECM, such as viscoelasticity and stiffness, which may enhance the mechanical strength of the tissue [67]. This is relevant as both the stiffness and the topology of the ECM regulate the growth, remodelling, differentiation, migration and phenotypes of a wide variety of cells and tissues [68–70].

LOX is a Cu-proenzyme that is essential for the stabilization of the lung ECM, inducing cross-linking of elastin and collagens in particular. The formation of these lysine-derived cross-links in connective tissue may constitute an essential defence against the proteolysis of elastin and collagen performed by non-specific proteases. LOX has the highest affinity for collagens precipitated in the form of fibrils and for clustered forms of elastin [71]. The number of cross-links per collagen molecule has been shown to be elevated in fibrotic tissue compared to the healthy state [72]. LOX has been pointed out as a main contributor to the increase in cross-linking in several diseases including PF [73]. This was demonstrated by a dramatic increase in LOX activity during the development of PF [73]. The distribution of LOX is tissue specific [74, 75]. LOX levels may also have an effect on the expression levels of ECM proteins such as elastin, where an increase in LOX induces an increase in elastin synthesis [76]. The LOX family consists of 9 members, among which LOX-like-2 (LOXL2) is the most expressed [38]. LOXL2 has been found to be over-expressed in lung tissue samples from IPF patients, especially in tissues with activated fibroblasts, reactive pneumocytes and vasculature in fibroblast foci [77].

Another ECM cross-linking enzyme is TG, which catalyses Ca2+-dependent acyl-transfer reactions between the γ-carboxamide group of specific glutamine residues and primary amines (e.g. the ε-amino group of lysine residues). This results in the formation of an Nε(γ-glutamyl) lysine cross-link [78]. The TG family includes 8 catalytic TG and 1 non-catalytic relative that lack TG activity [79]. The members of the TG family differ in tissue expression and function, and TG2 in particular has received increasing attention among fibrotic disorders. TG2, also known as tissueTG or tTG, is vital for the maturation of the lung ECM [80] and plays a role in the development of PF [39, 81].

Oxidation

Considering the high diffusion of oxygen gases and oxygen tension in the lung, oxidation of ECM proteins is an important PTM in pulmonary disorders. Thus, reactive oxygen species (ROS) may play a role in the progression of PF. This is demonstrated by the correlation of ROS levels with low pulmonary function in IPF patients and low ROS levels in controls [82]. These oxidative compounds may disturb the fine balance between oxidants and anti-oxidants in the lungs. It is the leucocytes that are responsible for the oxidase production in the lungs [83]. The high presence of oxidizing compounds in the lungs of IPF patients may not solely originate from smoking as oxidized proteins levels (new carbonyl groups) are also increased in the lungs of non-smoking IPF patients [84]. A temporary increase in anti-oxidant synthesis has been observed in bronchoalveolar lavage fluid from IPF patients as a means of compensation for the high oxidative stress [85]. However, local decreases in anti-oxidants have still been reported in fibrotic regions of the human lung, suggesting a predominance of oxidants in fibrotic regions [86]. Furthermore, the regulation of MMPs and their inhibitors may be changed by oxidative groups affecting lung ECM remodelling [87], and the apoptosis of cells may be enhanced by oxidative modifications of the Fas receptor [88].

Citrullination

A relevant PTM is the citrullination of arginine into citrulline. Arginine deamination removes its positive charge at a neutral pH, altering the isoelectric point of a protein [89, 90]. This results in a more open structure, which makes proteins more vulnerable to proteolysis [91] or may affect cell signalling of the proteins [92, 93]. Citrullinated proteins have also been found to have a less organized structure and to be a more favourable substrate for TG [94]. Citrullination has been previously linked to fibrosis as studies have shown an increase in citrullinated protein in liver fibrosis [95].

Protein (Mis)Folding

PTMs can be more complex than the examples of modifications discussed above. Especially the mechanisms leading to proper protein folding may be disturbed in the disordered distribution of ECM proteins during the progression of lung pathologies. The proteostasis network has been defined as a complex system that includes chaperones, protein disulphide isomerases, degradation components and multiple signalling networks that control both the composition and the concentration of its components in response to the cellular genome and the local environment to maintain proteome health/quality [96]. Disturbances in the proteostatic processes can induce a loss of protein function and/or aggregation of the...
misfolded proteins [97]. This also occurs in pulmonary
diseases where proteostasis may play a significant role
[96]. Furthermore, recommendations from the National
Heart, Lung and Blood Institute include a greater focus
on the improvement of biomarkers directed against the
proteostatic changes in pulmonary diseases [98].

Table 1 lists some of the consequences of uncontrolled
proteolytic cleavage, oxidation, citrullination, cross-link-
ing and glycosylation. These include, among others, fi-
brosis and various pulmonary disorders. These examples
emphasize how PTMs may play a significant role in the
progression of fibrotic diseases, particularly in the lung.

### Biochemical Markers in the Diagnosis and Prognosis
of Lung Diseases

As a consequence of ECM remodelling, protease-de-
derived fragments of proteins are deposited locally in patho-
logically affected tissues and released into the blood/urine
where they may be detected as serological biochemical
markers [1]. Several novel specific biomarkers have been
developed for the detection of such neo-epitopes and have
been proven successful for the assessment of fibrotic dis-
eases [31–34, 53, 99–101]. Table 2 includes novel sero-
logical biomarkers that are relevant in fibrosis, including
a broad range of biomarkers assessing certain ECM pro-
tein fragments that originate after specific PTM process-
ing. These biomarkers are often unaffected by the total
amount of proteins (quantity) but are very specific to-
wards neo-epitopes elevated in fibrotic diseases [33]. Bio-
markers specific for MMP-derived collagen fragments
have been shown to have diagnostic value in COPD and
IPF patients and are able to distinguish between two dis-
eases with low and high levels of fibrosis, respectively
[33]. In other studies, biomarkers specific for elastin frag-
ments were able to quantify elastin fragments in serum of
COPD and IPF patients and showed that the level of
MMP-degraded fragments of elastin was raised in dis-
eased patients compared to controls [33, 34]. This illus-
trates how MMP-derived fragments of ECM proteins are
relevant in pulmonary disorders/fibrosis.

### Protein Quantity in the Progression of PF

**Protease/Protease Inhibitor Imbalance**

The precise event that causes the onset of PF is still not
fully understood. The focus has generally been directed
towards quantification of proteins such as elastin and col-
lagens or cells such as neutrophils and macrophages
which are known to be important for the lung milieu [1,
The quantity of structural proteins is important in the pathology of PF; however, the amounts of proteases and protease inhibitors are just as relevant \([64, 103]\). Localized degradation of structural proteins in the lung ECM is often coupled with a confined increase in protease activity \([1]\). Within healthy lungs, there is a balance between ECM formation and degradation in order to obtain proper tissue remodelling. This tissue balance is not limited to a steady production of ECM proteins. A fragile balance between ECM-degrading enzymes and their inhibitors exists in the human lung \([64]\). A disturbance in the protease-anti-protease ratio may be induced by external factors such as smoking. Some studies indicate that this imbalance may progress into lung disorders such as COPD or IPF if the balance tips towards the proteases or the anti-proteases, respectively \([64, 104–106]\).

### Angiogenesis

The role of protease/protease inhibitor imbalance as the main initiator of IPF is, however, considered outdated. The protease/protease inhibitor discussion has been replaced with other theories including the role of the imbalance in the angiogenic/angiostatic ratio. Angiogenic growth factors in the lung may upregulate the expression of ECM components and thus disturb ECM remodelling \([107]\). The role of angiogenesis in the progression of IPF has been reviewed in recent years \([108]\). It has, however, not been confirmed whether an increase or a decrease in angiogenesis initiates IPF.

### Protein Quality in the Progression of PF

Although many studies have indicated that the progression of PF is initiated primarily by a change in the quantity of ECM proteins and cells in the lung, so far no conclusive evidence has been provided of whether it is the quantity or the quality of the proteins, or both, that is responsible for the progression of PF. The quality of ECM proteins may be defined by the levels of modifications such as proteolytic cleavage, cross-linking and their distribution in lung tissue.

To obtain a deeper insight into the progression of PF, it is useful to focus not only on quantitative/visual observations (such as fibroblast foci and cell and protein quantities) but also on factors at the molecular level, including analysis of PTMs, which may cause only minor chemical changes but can also contribute to the progression of PF.

### Table 2. Selected state-of-the-art serological biomarkers assessing the quantity and degradation of proteins

<table>
<thead>
<tr>
<th>Biomarker</th>
<th>Protein</th>
<th>Disease with altered concentrations</th>
<th>References</th>
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<tbody>
<tr>
<td><strong>Intact protein biomarker</strong></td>
<td></td>
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<tr>
<td>MMP-7</td>
<td>MMP-7</td>
<td>IPF</td>
<td>127, 133</td>
</tr>
<tr>
<td><strong>Biomarkers ECM processes</strong></td>
<td></td>
<td>Diseases with altered neo-epitope concentrations</td>
<td>References</td>
</tr>
<tr>
<td>C1M</td>
<td>MMP-mediated type I collagen degradation</td>
<td>Liver fibrosis</td>
<td>134</td>
</tr>
<tr>
<td>C3M</td>
<td>MMP-mediated type III collagen degradation</td>
<td>IPF, COPD</td>
<td>135</td>
</tr>
<tr>
<td>C4M</td>
<td>MMP-mediated type IV collagen degradation</td>
<td>COPD</td>
<td>35</td>
</tr>
<tr>
<td>C5M</td>
<td>MMP-mediated type V collagen degradation</td>
<td>IPF, COPD</td>
<td>136</td>
</tr>
<tr>
<td>C6M</td>
<td>MMP-mediated type VI collagen degradation</td>
<td>IPF, COPD</td>
<td>137</td>
</tr>
<tr>
<td>P1NP</td>
<td>Type I collagen formation in tissues other than bone</td>
<td>Liver fibrosis</td>
<td>138</td>
</tr>
<tr>
<td>P4NP 7S</td>
<td>Type IV collagen formation</td>
<td>Liver fibrosis</td>
<td>139</td>
</tr>
<tr>
<td>P5CP</td>
<td>Type V collagen formation</td>
<td>Liver fibrosis</td>
<td>140</td>
</tr>
<tr>
<td>P11NP</td>
<td>Type III collagen formation</td>
<td>Liver fibrosis</td>
<td>141</td>
</tr>
<tr>
<td>VICM</td>
<td>MMP-mediated citrullinated vimentin degradation</td>
<td>Liver fibrosis</td>
<td>95</td>
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<tr>
<td>ELM</td>
<td>MMP-mediated elastin degradation</td>
<td>IPF, COPD</td>
<td>142</td>
</tr>
<tr>
<td>BGM</td>
<td>MMP-mediated biglycan degradation</td>
<td>Liver fibrosis</td>
<td>143</td>
</tr>
<tr>
<td>HA</td>
<td>Hyaluronic acid</td>
<td>Liver fibrosis</td>
<td>141</td>
</tr>
<tr>
<td>MCV</td>
<td>Mutated citrullinated vimentin</td>
<td>Rheumatoid arthritis</td>
<td>144</td>
</tr>
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</table>
**ECM Quality in Non-Lung Tissues**

Few studies have focused on the role of the ECM quality during lung disease progression. Nevertheless, the effects of changes in ECM quality have been explored in other diseases such as osteoporosis, where the ECM of the bones is changed in terms of both quantity and quality [109–111]. In osteoporosis, the effect of non-enzymatic cross-linking of collagen on bone toughness and ECM quality in particular has been investigated [110]. It is known that many cancer types metastasize to bone [112]. When the bone microenvironment is invaded by cancer cells, the secretion of ECM proteins with specific neo-epitopes increases. These changes have been utilized for the development of a biochemical marker to detect locally high bone turnover by osteoclasts [101].

**Anti-Oxidants May Stop the Progression of Fibrosis**

Knowledge of oxidative reactants as markers for PF has been valuable in various clinical studies that have included anti-oxidants as a possible drug in PF treatment. Different anti-oxidants have been administrated to bleomycin- and asbestos-treated mice, followed by a reduction in PF. This includes anti-oxidants such as catalase [113] and carnosine [114]. In humans, administration of the anti-oxidant glutathione has resulted in a higher anti-oxidant-to-oxidant ratio in the lungs [115]. As an example of the importance of anti-oxidants in PF, even the known anti-fibrotic agent pirfenidone possesses some anti-oxidative effects [116]. The administration of anti-oxidants together with other known anti-fibrotic compounds has shown that anti-oxidants may enhance the effect of anti-fibrotic compounds with regard to important PF parameters such as forced vital capacity [117]. Anti-oxidants may therefore play a key role in future PF treatment.

**Cross-Linking Prevents Proper Remodelling**

The role of enzymatic cross-links was earlier thought to be purely structural. Studies have, however, described other roles for these enzymes in the creation and maintenance of the pathologic microenvironment of cancer and fibrotic diseases [77]. One study showed that LOX and LOXL2 activity and expression correlate with the disorders observed in the microenvironment of tissues leading to cancer and fibrosis [77]. This is supported by other studies showing an increase in the number of cross-links per collagen molecule in fibrotic tissues [72]. It is speculated that this increase in cross-links contributes to the accumulation of collagens by reducing collagen digestibility [3, 118, 119]. LOXL2 levels have been mostly investigated in fibrotic lung tissues from patients with IPF [77], although LOX is often described as the main contributor to the increase in cross-linking in PF [2, 73]. This is due to the higher LOXL expression in healthy tissues compared to LOXL2 [77].

Upregulation of LOXL2 mRNA as well as an increase in collagen cross-links has been associated with worsening of the lung tumour grade [77]. Therefore, a monoclonal antibody towards LOXL2 (AB0023) was developed which proved successful at inhibiting LOXL2 activity [77]. AB0023-treated mice in a primary tumour model experienced a significant decrease in the number of cross-linked collagens and a reduction in tumour volume compared to vehicle-treated mice. This not only links the ECM molecular environment to pathological states but also demonstrates the potential to exploit changes in the quality of the ECM to halt the progression of tumours. In this study, it was shown that the lung tissue of bleomycin-treated rats experienced a significant increase in LOXL2 and cross-linked collagens. The addition of AB0023 with bleomycin successfully reduced the amount of cross-linked collagen and fibrosis in lung tissue compared to the combination of vehicle and bleomycin. Besides preventing fibrosis, the addition of AB0023 after bleomycin injection showed that inhibition of LOXL2 could reverse established PF.

TG, especially TG2, is another type of enzymes capable of cross-linking ECM proteins into high molecular mass products with a high resistance against proteases [78, 80]. Studies have shown that the quality – that is, the order/distribution – of ECM proteins is also affected by the amount of TG, and that higher levels of this enzyme are detected during fibrosis [40]. TG is active at an earlier fibrosis stage than LOX [39, 40, 81]. As has been seen with LOX, inhibition of TG can also prevent ECM tissue remodelling [120].

These studies demonstrated how inhibition of an enzyme responsible for lung ECM quality could directly prevent and even reverse lung ECM remodelling and thus fibrosis. Other studies have also demonstrated that elastic fibres were present in the same quantity in lung ECM that was damaged and then repaired as compared to non-damaged lung ECM, but the distribution was still disordered after the repair process [102, 121].

**Protease-Derived ECM Fragments as Ameliorators**

To date, there are no approved efficacious therapies against fibrosis [122–124] but studies suggest that protease-derived ECM protein fragments may have potential therapeutic functions [1, 125]. The C-terminus of collagen XVIII contains a 20-kDa internal fragment named endostatin. Studies have determined the concentration of
endostatin in serum and/or bronchoalveolar lavage fluid from patients with IPF or systemic sclerosis-associated PF to be 2–20 times higher than in controls [125]. E4 is a fragment from the C-terminus of human endostatin with the addition of an amide modification at its C-terminus. Yamaguchi et al. [125] tested the anti-fibrotic properties of the endostatin-derived peptide E4 against PF ex vivo and in vivo. E4 was administrated either concomitantly or 3 days after bleomycin in rat lungs [125]. It was shown that E4 could not only prevent PF but also ameliorate it in vivo. This was demonstrated by immunohistochemistry and by a decreased concentration of collagen in the lung tissue. Furthermore, the secretion of LOX from normal adult human lung fibroblasts stimulated with TGF-β and in mouse lung injected with bleomycin was examined. A reduction in LOX concentration upon the addition of E4 was observed in all cases.

The study also showed an association between the increase in collagen and LOX concentrations and PF [125]. The correlation between the quantity of collagen and the amount of a cross-linking enzyme could indicate that the cross-linking prevented proteases from degrading the collagen molecules. The quantity of ECM proteins was previously thought to be the main initiator of PF as an...
increase in collagen levels was observed in lung tissues from patients with PF [103, 126] despite an increase in lung protease concentrations [127].

Additional studies have shown that the progression of bleomycin-induced PF in rats is halted by the administration of pepsin-digested porcine urinary bladder matrix [6], whereas fibrosis could not be halted by the injection of non-digested porcine urinary bladder matrix. Such data indicates that two matrix materials that are microscopically the same, but not on a molecular level, result in two different outcomes in the pathogenesis of PF.

The E4 and porcine urinary bladder matrix studies illustrated how the lung ECM has not only structural functions but also an endocrine function, proving its active role in tissue remodelling. These endocrine properties may also produce negative outcomes. Elastin-derived peptides may induce anti-elastin autoimmunity in emphysema [66]. These fragments are able to stimulate an immune response in tissue where cytokines are upregulated, resulting in the upregulation of proteases leading to progressive destruction of the lung ECM. ECM-derived peptides may therefore not always possess therapeutic properties.

Figure 1 illustrates the consequences of changes in the lung ECM at the molecular level, which include cross-linking, proteolysis and citrullination of lung ECM proteins. All of these changes in lung ECM quality may reduce lung function. It is important to consider that many of these PTMs are essential for proper ECM protein distribution in the lung. It is mainly when the PTMs are overexpressed or absent that the quality is altered.

**Conclusion**

We have highlighted the key PTMs that are partly responsible for the progression of ECM remodelling in PF. Previous literature has focused on the correlation of changes in ECM quantity with PF; however, the changes in ECM quantity have not been demonstrated as the main initiator of PF, which may result from other processes.

Our speculation based on a review of the data is that PTMs of lung ECM proteins in coherence with quantity are part of some of the key processes responsible for the progression of PF. The PTMs most commonly affecting the quality of the ECM included proteolytic cleavage, oxidation and cross-linking. This has been proven by the example that removal of the source of cross-linking can ameliorate remodelled lung tissue. We reported evidence that the ECM has more than structural functions and is indeed a regulator of various tissue diseases. This has been proven as specific proteolytic cleavage of collagen or the entire matrix resulted in reduced fibrosis and even ameliorated lung ECM remodelling. This indicates that PF can be reversed once the ECM quality is restored.

**Future Perspectives**

As no current approved methods are able to diagnose severe pulmonary disorders before a certain level of severity is reached, it can be concluded that new markers for the early diagnosis of pulmonary diseases are needed. Recent data suggests that ECM quality is important in the progression of PF. Biochemical marker targets that represent lung ECM quality may therefore aid in PF diagnosis and prognosis. The correlation between PF and quantitative changes is, however, evident. Therefore, markers or a single marker able to detect both qualitative and quantitative changes in the lung ECM are needed.

A key topic in modern medicine is customized treatment. State-of-the-art diagnostic and prognostic biochemical markers could help identify the treatment needed for individual patients. As mentioned, some total protein biomarkers may be upregulated during several diseases, which complicates the prescription of a single therapy. This may be significantly improved by measuring the protein fingerprints that are generated during a specific pathology. These are more specific markers than the total protein measurement and may offer a more disease-specific marker for diagnosis, prognosis and response to intervention. Some neo-epitopes may contain several PTMs, and biochemical markers targeting these would increase the specificity for diseases such as IPF.

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PTMs Contribute to IPF Initiation

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