

Forum Review

Transforming Growth Factor- β Activation in the Lung: Focus on Fibrosis and Reactive Oxygen Species

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ABSTRACT

Transforming growth factor- β s (TGF- β) regulate a wide variety of cellular functions in normal development and are involved in both tissue homeostasis and disease pathogenesis. The regulation of the TGF- β family of growth factors is unique because they are targeted to the extracellular matrix in a biologically inactive form. The release from pericellular matrices and the activation of TGF- β are important mechanisms in several pathophysiologic conditions. Reactive oxygen species (ROS) can activate TGF- β either directly or indirectly *via* the activation of proteases. In addition, TGF- β itself induces ROS production as part of its signal-transduction pathway. The lung is a unique organ, because its structures act as boundaries between gaseous and aqueous phases, allowing the utilization of inhaled oxygen. However, this renders pulmonary tissues vulnerable to the toxic effects of inhaled air. The oxidant pathways are especially relevant in the lung, where TGF- β is known to have a role in tissue repair and connective tissue turnover. In pulmonary fibrosis, TGF- β activation is considered as a hallmark of disease progression. More recently, the oxidative effects of cigarette smoking have been found to activate TGF- β in chronic obstructive pulmonary disease (COPD), a disease consisting of emphysema, airway fibrosis, and focal lung fibrosis. *Antioxid. Redox Signal.* 10, 333–342.

TRANSFORMING growth factor (TGF)- β plays a crucial role in the regulation of lung development and homeostasis. Aberrant TGF- β expression and activation are associated with abnormal lung development and parenchymal lung disorders, including pulmonary fibrosis and other airway diseases. In a large number of studies, alterations in the cellular redox state and increased oxidative stress have been observed to contribute to TGF- β activation. The various mechanisms of TGF- β activation offer numerous alternatives for human lung disease evolution and progression. Elucidation of these mechanisms presents new possibilities for intervention, such as potential antifibrotic drugs being targeted against the TGF- β activation-related processes.

LATENT FORMS OF TGF- β AND THEIR ACTIVATION

Because TGF- β can alter the functions of almost any given cell type, complex machinery has evolved to regulate both the local activation and the cell type specific signaling responses (36, 71). TGF- β s are secreted as latent complexes in which the dimeric mature 25-kDa growth factor is masked by a non-covalent association with the latency-associated protein (LAP). TGF- β and LAP are produced as a single proprotein, which is cleaved by furin-like proteases during secretion. Some cells have been observed to secrete TGF- β in the form of a TGF- β /LAP complex, which is also referred to as the small la-

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tent complex (71). However, most cells produce TGF- β as a large latent complex, in which latent TGF- β binding protein (LTBP) is associated through its third 8-Cys repeat with the small latent TGF- β . LTBP-1 and -3 can bind all three small latent TGF- β isoforms; in contrast, LTBP-4 seems to bind only TGF- β 1 (20, 87). LTBPs target the transport of the large latent TGF- β complex into the extracellular matrix (ECM), and thus LTBPs can regulate the activation process and in that way control the availability of TGF- β s (50). Several mechanisms have been described for the activation of different TGF- β isoforms, and the currently known physiologically important mechanisms are reviewed (see Fig. 1).

Thrombospondin-1-mediated TGF- β activation

Thrombospondin-1 and -2 are trimeric matricellular proteins involved in a variety of biologic processes including tissue remodeling and angiogenesis (16). Thrombospondins function through binding to other macromolecules such as proteoglycans, sulfated glycolipids, and integrins. Thrombospondin-1 can bind to both small and large latent TGF- β complexes and bring about the release of active TGF- β (76). A specific peptide sequence within thrombospondin-1, KRFLK, mediates TGF- β activation through its association with a sequence (LSKL) near the amino terminus of LAP. The KRFLK peptide, also referred to as the activating peptide, releases mature TGF- β by inducing conformational changes in the protein. The physiologic role of thrombospondin-1 in the activation of TGF- β is well illustrated by the overlapping phenotypes of TGF- β 1 and thrombospondin-1 null mice. Treatment of mice with the TGF- β activating peptide of thrombospondin-1 can prevent the lung and pancreatic abnormalities observed in thrombospondin-1 null mice (26). However, the TGF- β 1 null phenotype is severe and not fully overlapping with the thrombospondin-1 phenotype, emphasizing the

importance for other TGF- β activating mechanisms. Thrombospondin-1 appears to mediate TGF- β activation in a rat model of renal disease, glomerulonephritis (29). Recently, thrombospondin-1 also was linked to angiotensin II-induced TGF- β activation in mesangial, cardiac, and renal cells (77, 114). In addition, angiotensin II receptor antagonism can prevent aortic aneurysms in a mouse model of Marfan syndrome, which is characterized by excessive TGF- β activation (46).

Integrins in TGF- β binding and activation

Many integrins can bind to the RGD sequence present in the LAP of TGF- β 1 and - β 3, but thus far only two, α v β 6 and α v β 8, have been shown to activate the TGF- β complex (74, 75). TGF- β 2 lacks the critical RGD sequence, and therefore, it cannot be activated by integrins. Interestingly, activation by the two α v-containing integrins is carried out differently. The integrin α v β 6 activates large latent TGF- β complexes containing LTBP-1 by a fibronectin-dependent mechanism. Matrix targeting of the complex mediated by fibronectin in addition to LAP-mediated interaction with the cell surface integrin is believed to create the traction necessary for the release of mature TGF- β (2, 38, 56). Under normal conditions, epithelium-specific expression of α v β 6 is present, but after tissue injury, the expression levels increase rapidly (17). Mice lacking β 6 integrins develop excessive inflammation but are protected from pulmonary fibrosis because of their decreased TGF- β activation, emphasizing the importance *in vivo* of integrin-mediated TGF- β activation (75). The role of the blood coagulation cascade in the development of acute lung injury in mice may be partially due to the proteinase-activated receptor 1 (PAR1)-mediated enhancement of α v β 6-dependent TGF- β activation (54).

In contrast to α v β 6-mediated TGF- β activation, proteolytic activity is necessary for TGF- β activation by α v β 8 (74). A com-

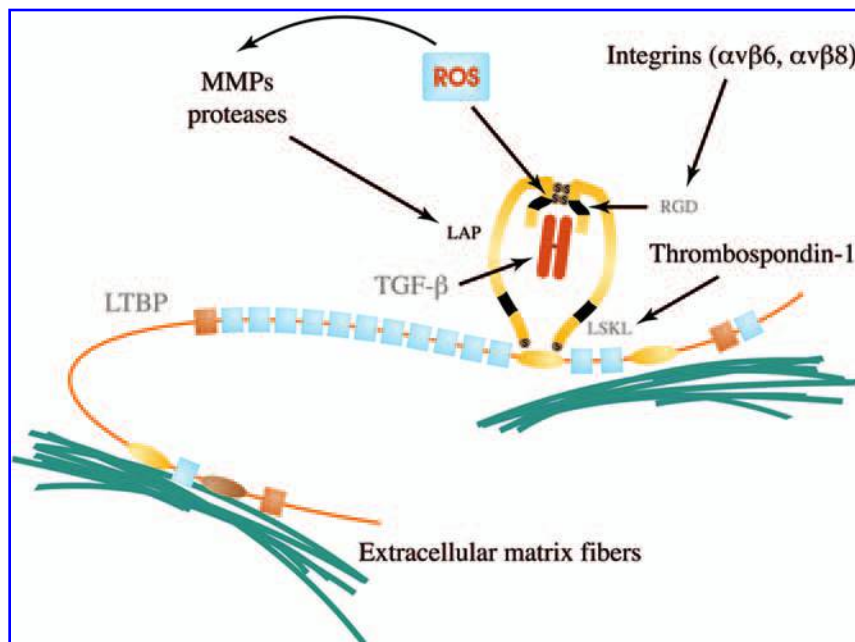


FIG. 1. Activation of latent TGF- β complexes. Large latent TGF- β consists of the mature 25-kDa polypeptide dimer (TGF- β), latency associated protein (LAP), and latent TGF- β binding protein (LTBP). The complex is targeted to the extracellular matrix structures via LTBP. Disruption of the non-covalent association between TGF- β and LAP is needed for the release of the active TGF- β , which is then able to bind to the cell-surface receptors. Thrombospondin-1 binds to the LSKL sequence in LAP, which leads to conformational changes and TGF- β activation. Integrins, in turn, bind to the RGD recognition sequence in LAP, leading to release of TGF- β either by tractional force directed against the TGF- β complex (α v β 6) or by MT1-MMP-dependent proteolytic activity (α v β 8). Reactive oxygen species (ROS) can activate TGF- β directly through oxidation induced conformational change in LAP or indirectly through the activation of proteolytic enzymes.

plex made up of the integrin, latent TGF- β , and membrane-type 1 matrix metalloproteinase (MT1-MMP) is formed at the cell surface, and a proteolytic event leads to the release of active TGF- β . This type of activation seems to be important for epithelial homeostasis in the lung, because normal human airways express all of these three proteins. During development, both α v β 6- and α v β 8-mediated TGF- β activation mechanisms appear to play important roles in epithelial mesenchymal interactions of the lung (5). The expression of α v β 8 is often lost during malignant transformation, and re-establishment of α v β 8 expression in lung carcinoma cells reduced tumor growth in nude mice (74). The contribution of RGD-binding integrins to TGF- β activation in the mouse was recently analyzed by using a TGF- β 1 gene mutation, which encodes a nonfunctional integrin-binding site (RGE instead of RGD). Mice expressing this mutation displayed severe abnormalities related to the TGF- β 1 null phenotype, including abnormal control of inflammation and vasculogenesis (108). These observations further emphasize the importance *in vivo* of integrins in TGF- β activation, although they also clearly point to the existence of multiple activation mechanisms. Other integrins, including α v β 5 and α v β 3, can also contribute to TGF- β activation in fibrotic fibroblasts (7, 8). Whether these integrins act directly to activate TGF- β or have indirect roles in the process is still an open question.

TGF- β activation by proteolysis

The serine protease plasmin was one of the first molecules found to cause activation of TGF- β (69). The proteolytic cleavage of LAP releases mature TGF- β , which is then free to associate with its cell surface receptors. Plasmin also can release the large latent TGF- β complex from the ECM by cleaving LTBP at the amino terminal hinge region (95). Release of the truncated complex is not necessarily associated with increased TGF- β activation, suggesting that ECM release and activation can be regulated independently. Proteolytic release of ECM-bound TGF- β complexes may also enhance activation by other mechanisms, or alternatively, they may block activation because of incorrect targeting of the complexes. The role of plasmin in TGF- β activation has been demonstrated in relation to the dissolution of blood clots during wound healing (44), as well as in smooth muscle cell function (3, 41). Interestingly, mice deficient in plasminogen, which is the inactive precursor of plasmin, display no TGF- β deficiency-related phenotypes, evidence that redundant mechanisms for TGF- β activation must exist (86). In addition to plasmin, many other proteases have been linked to the release or activation or both of TGF- β complexes. These proteases include thrombin, mast cell chymase, leukocyte elastase, and prostate specific antigen (PSA), as well as bone morphogenetic protein (BMP)-1 (28, 40, 96).

Matrix metalloproteinase activity has been implicated in both physiologic and pathologic tissue processes involved in matrix remodeling. The role of MT1-MMP in α v β 8-mediated TGF- β activation was described earlier. However, MMP-2 and -9 have also been implicated in the cleavage of LAP and the release of mature TGF- β (110). Cell surface localization of the complexes and the activation machinery plays a major role in the activation process. CD44, the hyaluronan receptor, was identified as a targeting protein for MMPs, and this is plausibly important

in malignant cell growth and tumor angiogenesis (110). MMP activity induced by ROS and RNS in the lung could therefore play a role in the excessive TGF- β activation associated with pathologic conditions such as idiopathic pulmonary fibrosis (IPF) or other fibrotic diseases. TGF- β can also regulate the expression and activation of MMPs, as well as their inhibitors, TIMPs, and in this way, it can contribute to the proteolytic microenvironment in the lung.

ROS-mediated activation of TGF- β

Ionizing radiation was found to induce rapid TGF- β activation *in vivo* (12). ROS produced by ionizing radiation proved to be the direct mediators of the activation process, which in this case does not involve any other proteins. Interestingly, ROS-mediated TGF- β activation is specific for the TGF- β 1 isoform, and the unique methionine residue (253) in the TGF- β 1/LAP functions as a redox switch center (55). Specifically, elevated levels of HO $_2$ were critical for the oxidation of LAP, and these radicals triggered the conformational change leading to release of mature TGF- β . Radiation-induced lung injury, as well as tissue responses to inflammation, can elevate ROS production, which may contribute to TGF- β activation. In addition, ROS produced by solar UV radiation can evoke TGF- β activation and biosynthesis in skin keratinocytes (104). Asbestos fibers carrying iron are known to induce ROS production through Fenton reactions in cellular and cell-free systems. TGF- β activation induced by asbestos is probably mediated through ROS (81). Lung diseases induced by asbestos exposure, such as mesothelioma and asbestosis, are characterized by excessive TGF- β activation (52, 67). Another example of the role of ROS in TGF- β activation is the TGF- β -related lens phenotype of peroxiredoxin 6 (Prx6) null mice (34). Prx6 is one of the cellular enzymes that participate in the defense against oxidative damage. In the absence of this enzyme, mouse lens epithelial cells produce excessive amounts of ROS and active TGF- β , leading to elevated levels of cataractogenic markers.

TGF- β SIGNAL-TRANSDUCTION MECHANISMS

Smad-dependent and -independent signaling

Many different cellular responses are elicited by TGF- β , and these are often cell-type specific (71). We are only beginning to understand the complicated signaling patterns triggered by cellular exposure to TGF- β . The classic response pathway involves Smad-mediated changes in target gene transcription. Other signaling pathways, including MAP kinases, PI3 kinase, and Rho-like GTPases, can modulate Smad-dependent responses as well as elicit Smad-independent responses (32). In addition, c-Abl tyrosine kinase has been identified as one mediator of Smad-independent TGF- β signaling (30). Figure 2 summarizes central TGF- β -induced intracellular signaling pathways.

The cell surface TGF- β receptor complex is composed of type I and II serine/threonine kinases (36) (see Fig. 2). TGF- β binds first to the type II receptor (TGF- β RII), after which the type I receptor (TGF- β RI, ALK-5) is recruited to the complex and activated by a phosphorylation event. The regulatory Smads

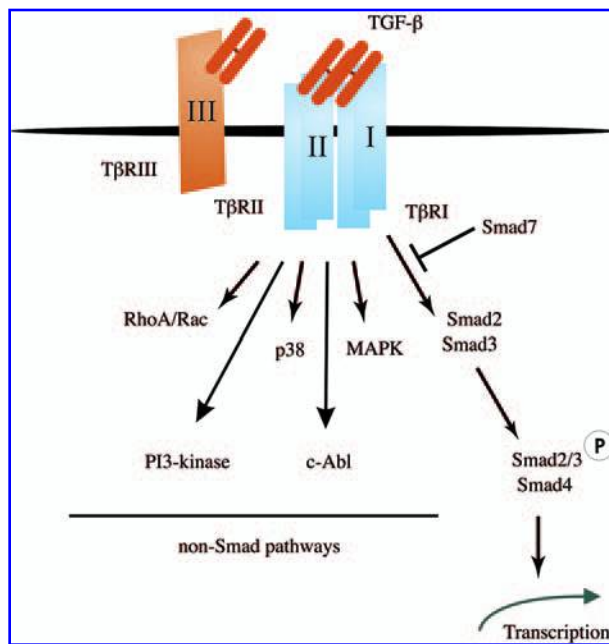


FIG. 2. TGF- β receptor signaling. The TGF- β receptor complex is composed of type I and II serine/threonine kinases. Accessory receptors, such as betaglycan or endoglin (T β RIII) can present TGF- β to the signaling receptors. The constitutively active TGF- β type II receptor (T β RII) phosphorylates the type I receptor (T β RI) on specific serine and threonine residues. Activated T β RI, in turn, directs the signal downstream by directly phosphorylating Smad2 and Smad3. Smad2 and Smad3 form complexes with Smad4, which, in combination with transcription factors, regulate gene transcription. Smad7 is an inhibitor of this pathway. Alternatively, Smad-independent pathways can be activated.

2 and 3 are phosphorylated by TGF- β RI and transported in a complex with Smad4 into the nucleus, where they can cooperate with the transcription machinery and alter gene transcription. The shuttling of Smad proteins between the nucleus and the cytoplasm, as well as their rapid turnover through ubiquitin-mediated degradation, are important as regulators of the TGF- β signaling. Specific Smad-binding elements have been identified in the promoter regions of target genes and, for example, cooperation with the AP-1 transcription factor has been described in the regulation of gene transcription (103). In endothelial cells, the ALK-1 receptor, when present in a complex with TGF- β RII, can mediate TGF- β signaling through the regulatory Smad1 (43).

TGF- β -induced ROS production

Active research on the role of ROS in cellular signaling has produced exciting new signaling paradigms. Many growth factors can induce intracellular production of ROS, which can then regulate redox-sensitive proteins *via* cysteine oxidation (100). Well-known examples of ROS-induced alterations in signaling proteins are the inactivation of protein tyrosine phosphatases (85) and the modulation of AP-1 transcription factor activity (68). TGF- β can induce intracellular ROS production through

the NADPH oxidase catalytic subunit Nox4. A biphasic ROS induction has been described, in which the rapid response is believed to be mediated through Nox4 activation and targeting to the cell membranes, whereas the slower and sustained response is associated with increased expression of Nox4 (49, 99). Cellular processes regulated by TGF- β -induced ROS include the proliferation of pulmonary artery smooth muscle cells, cytoskeletal alterations in endothelial cells, and differentiation of cardiac fibroblasts as well as angiogenesis and EMT (epithelial-to-mesenchymal transition)-related processes (27, 49, 93). TGF- β target genes CTGF, PAI-1, and p21 are dependent on ROS induction, because Nox4 knockdown can prevent the induction of these genes by TGF- β . It is also possible that Smad2/3 phosphorylation is affected by Nox4-dependent ROS production (51). Interestingly, TGF- β can induce extracellular ROS production, which points to a role for ROS in intercellular communication and matrix protein modulation (98).

Cellular alterations in gene transcription induced by TGF- β are affected by signaling cross-talk between other pathways [(53), Fig. 3]. As described earlier, in addition to the classic Smad-signaling pathway, TGF- β itself can elicit changes in ROS production and MAPK activation. This creates flexibility for cell type-specific responses to TGF- β . In addition, growth-factor or stress-activated responses leading to alterations in ROS production and MAPK activation can alter cellular TGF- β responsiveness. For example, TGF- β stimulated expression of p21 is dependent on the Smad pathway as well as ROS-mediated

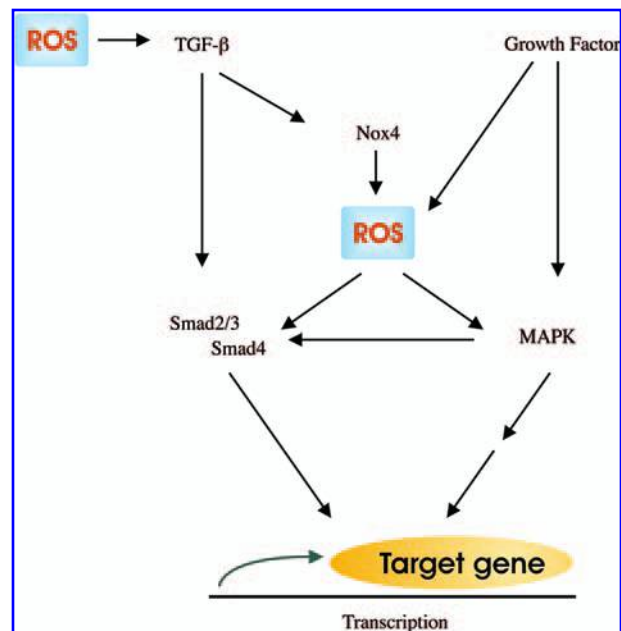


FIG. 3. TGF- β signaling cross-talk. In addition to being involved in TGF- β activation, reactive oxygen species (ROS) are part of the signal-transduction pathway leading to target gene transcription. TGF- β induces cellular ROS production through the NADPH oxidase catalytic subunit Nox4. ROS can alter the activation of Smads as well as mitogen-activated protein kinases (MAPKs). Cross-talk with other growth-factor pathways can also modify TGF- β target gene transcription.

ated ERK activation, indicative of a cooperative model for p21 induction in human keratinocytes (58).

REGULATION OF ANTIOXIDANT ENZYMES BY TGF- β

The lung possesses a cell-specific antioxidant battery, which is regulated by many different mechanisms, including cytokines and the cellular redox state (21, 22, 59, 60, 62). Only a few studies have examined the role of TGF- β in the regulation of antioxidant/detoxification enzymes; most of them point to no changes or a decrease in expression levels of antioxidant enzymes by TGF- β . This contrasts with the effects of inflammatory cytokines, such as tumor necrosis factor (TNF)- α , which generally induce the expression of these enzymes both *in vitro* and *in vivo* (21, 59, 83, 84). Manganese superoxide dismutase (MnSOD) is induced by TNF- α , whereas some other cytokines do not seem to alter the expression of this enzyme (37). Moreover, severe hyperoxia results in decreased expression or inactivation of MnSOD in association with cell injury or lung fibrosis or both (18, 24, 63, 70). A possible downregulation of extracellular SOD (ECSOD) by TGF- β may occur in human alveolar epithelial cells (61). In addition, similar changes have been observed with epidermal growth factor (EGF), platelet-derived growth factor (PDGF), and granulocyte macrophage colony stimulating factor (GM-CSF) in vascular smooth muscle cells (91).

Glutamate cysteine ligase (GCL), the rate-limiting enzyme in glutathione (GSH) synthesis, is induced by Nrf2-dependent transcriptional regulation through ARE (antioxidant response element) (21). The level of GCL, or at least the heavy subunit of this enzyme, is induced by oxidants and cytokines, but again, TGF- β 1 downregulates the levels of GCL mRNA and immunoreactive protein (6, 102). The TGF- β induced decrease in the levels of the catalytic subunit of GCL correlates with a decrease in cellular GSH and an increase in cellular ROS (11). Interestingly, the TGF- β -dependent downregulation in ARE-dependent GCL expression is mediated by Smad3-ATF3. The

expression of glutaredoxins (Grxs), another family of enzymes associated with the GSH homeostasis, is also decreased by TGF- β (80), further suggesting that TGF- β , in general, downregulates the expression of antioxidant enzymes. These *in vitro* results are in agreement with the low/absent immunoreactivities of MnSOD, ECSOD, GCL, thioredoxin, and Grx1 in the fibrotic lung lesions of patients with IPF (histopathology of usual interstitial pneumonia, UIP) (61, 65, 80, 101, 102) and the decline/proteolysis of ECSOD in experimental lung fibrosis (35). In addition to endogenous antioxidant enzymes, exogenously administered antioxidants such as SOD-mimetics evoke a significant reduction of TGF- β (51). Overall, the effects of TGF- β in combination with oxidative stress *in vivo* may have multiple consequences in the defense system of human lung.

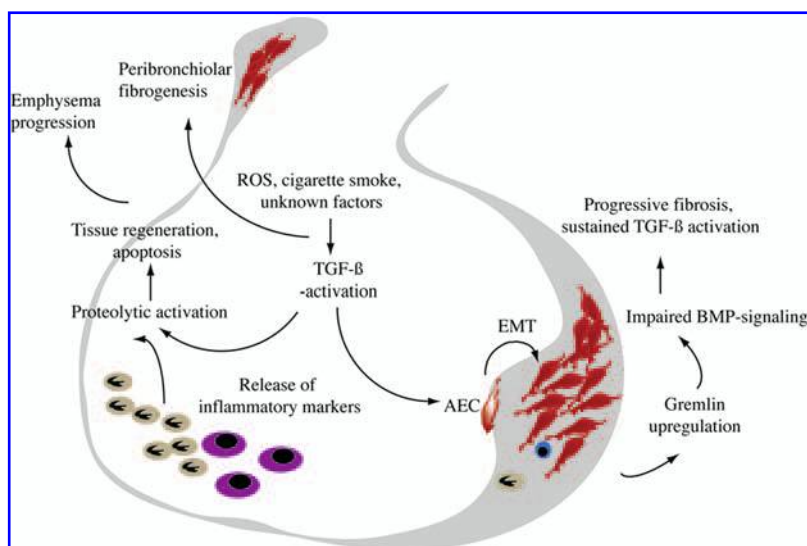
TGF- β IN HUMAN FIBROTIC LUNG DISEASES

The lung tissue can respond to external factors (such as tobacco smoke) in various ways, leading either to parenchymal fibrosis (formation of excess connective tissue) or emphysema (loss of parenchymal tissue). The current conception of fibrosis and emphysema pathogenesis is summarized in Fig. 4.

Pulmonary fibrosis

Although the initial pathogenic factors and mechanisms behind IPF and other idiopathic parenchymal disorders are poorly understood, enhanced expression and activation of latent TGF- β is considered a hallmark of fibrosis progression. Genotypic variances that enhance the cellular TGF- β secretion might act as susceptibility factors for IPF and subsequent posttransplant pulmonary fibrosis (chronic rejection) in the same patient (9, 33). Active TGF- β has been detected from patients with fibrotic pulmonary disease, whereas in healthy individuals, TGF- β exists mostly in a latent form (14, 107). Figure 5 shows phosphorylated Smad2-positive cells in the alveolar epithelium

FIG. 4. Activation of TGF- β in the lung. Extracellular matrix-associated LTBP/TGF complexes are susceptible to activation by environmental factors. TGF- β activation can result in the chemotactic accumulation of inflammatory cells and fibroblasts, disturb the pericellular proteolytic balance, and induce epithelial-to-mesenchymal transition (EMT). Genetic, environmental, and unknown factors determine the outcome of TGF- β activation and subsequent events: either the accumulation of connective tissue to the alveolar wall (fibrosis) or the disappearance of alveolar structure (emphysema).



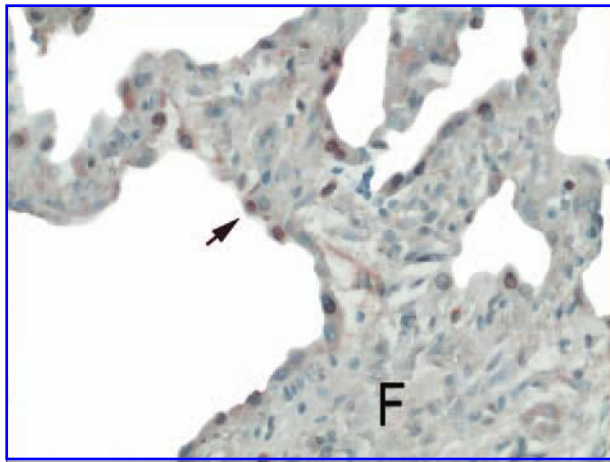


FIG. 5. Photomicrograph of an advanced lesion of a patient with IPF/UIP, stained with phosphorylated Smad2 antibody. An epithelial cell showing nuclear Smad2 positivity (red-brown) is pointed with an *arrow*. Activated, hyperplastic epithelial cells around the thickened lung parenchyma and a fibroblast focus (F) are seen, and most of these cells are Smad2 positive. Magnification $\times 400$.

around a fibroblast focus (our unpublished results). In experimental animal models of pulmonary interstitial disease, such as the mouse bleomycin model, enhanced levels of TGF- β expression, activation, and downstream signaling have been observed (57, 88, 112). Several approaches have been used to interfere with ROS production and TGF- β activation. Animal studies on direct or indirect inhibition of TGF- β or its receptor have yielded numerous promising compounds, but these have not been tested in the treatment of human IPF. Knockout studies have shown that Smad3 is a central mediator of experimental fibrosis (113) and that overexpression of the inhibitory Smad7 can protect from fibrosis (78). TGF- β can also alter other growth-factor pathways, including BMP signaling during fibrosis development (64). Receptor tyrosine kinase inhibitors, developed mainly for cancer treatment, have been used to block TGF- β action directly [ALK 5 inhibitor (48)] or indirectly [imatinib, Abl tyrosine kinase inhibition (1, 30)]. Bearing in mind the connection between thrombospondin-1 induced and angiotensin II-induced TGF- β activation (77, 114), recent results obtained in mice provide interesting evidence that the angiotensin II type 1 receptor inhibitor losartan may have an antifibrotic effect (109). Although a large body of knowledge from vascular biology suggests that angiotensin II mediates smooth muscle cell and cardiac muscle structure alterations toward fibrotic remodeling, less attention has been paid to the potential role of angiotensin II in pulmonary fibrosis. In human IPF tissue, angiotensin peptides (angiotensin II precursors) are generated locally within the fibroblasts and alveolar type II epithelial cells, and they colocalize with apoptotic alveolar epithelium (66), indicating that they may have extravascular functions in the lung. The future/ongoing clinical studies on all of the previously mentioned drugs (tyrosine kinase inhibitors, AT/ACE-inhibitors) will be among the first human studies in which an antifibrotic approach instead of an antiinflammatory treatment strategy is used.

So far, positive preliminary results have been obtained in human studies with the antioxidant glutathione precursor *N*-acetylcysteine (NAC). Glutathione is a small-molecular-weight antioxidant abundantly available in the epithelial lining fluid of alveoli. It was initially thought that NAC might be able to restore the antioxidant capacity of the fibrotic lung, but more recently, other antifibrotic mechanisms of action have been proposed. *In vitro*, NAC induces TGF- β type II receptor and PDGF receptor proteolysis and TGF- β and PDGF ligand inactivation *via* monomerization (72, 79). Furthermore, NAC abrogates TGF- β induced Smad2/3 phosphorylation and induces Smad7 mRNA expression. Both mechanisms are mediated by the displacement of TGF- β from endoglin and ligand inactivation by monomerization in hepatic profibrogenic cells (72). Another intensively studied repressor of profibrotic signaling, γ -interferon, although an indisputable TGF- β repressor in experimental studies (45), has been found to be disappointing in the clinic (4, 10).

Chronic obstructive pulmonary disease (COPD)

IPF is considered the prototype of human interstitial pneumonias that lead to a progressive increase in lung parenchymal ECM components. In addition to IPF, several other interstitial lung diseases exhibit areas of lung fibrosis that may have developed *via* TGF- β -mediated mechanisms. The lungs of patients with COPD, in contrast, display another type of lung parenchymal injury, in which cigarette smoke has induced the loss of tissue architecture and volume. Although major differences are found in the histopathology of human COPD and UIP/IPF, COPD offers some illuminating perspectives for research into lung fibrosis [reviewed in (39)]. In addition to the destruction of lung parenchyma (pulmonary emphysema), airway narrowing (obstruction) with peripheral airway fibrosis is observed. Airway fibrosis and peripheral/basal fibrotic lesions can also be detected in the parenchyma of the COPD patient's lungs. The emphysematous areas of COPD that consist of enlarged/destructed airspaces express several fibrosis associated matrix genes and proteases. This suggests that both their absolute levels and balance dictate in which direction the lung damage will proceed (either emphysema or fibrosis). In simplistic terms, when considering the outcome of TGF- β signaling and its regulation, it can be hypothesized that the regulatory pathways that are induced in fibrosis appear to be downregulated in the emphysematous lung.

Genetic association analyses have revealed a significant association in the single-nucleotide polymorphisms of the promoter and genomic regions of TGF- β and COPD (19). The latent TGF- β binding protein-4 (LTBP-4) and TGF- β 1 are associated with variable COPD phenotypes (47). The emphysematous lung undergoes a significant decline in the TGF- β mRNA levels (42). Recent studies on the lung tissues of COPD patients have suggested lower TGF- β and TGF- β receptor expression in COPD lung, as assessed by semiquantitative immunohistochemical scoring (111), and decreased release of TGF- β from the macrophages of COPD patients (82). However, the situation is not necessarily the same in the distinctly fibrotic areas of the same COPD lung. Local areas of the lungs reveal increased expression of TGF- β (RT-PCR) in the bronchial airways of patients compared with healthy smokers

and upregulation of TGF- β type II receptor in the pulmonary arteries of severe COPD (13) pointing to a role for TGF- β , at least in the development of airway fibrosis and pulmonary arterial hypertension in COPD (31, 97). These findings from human lungs are in line with the observations of increased TGF- β in the airways of smoke-exposed mice (23), and the release of active TGF- β and nuclear immunostaining of phosphorylated Smad2 after the exposure of rat tracheal explants to cigarette smoke (106). Importantly, those changes could be prevented by the oxidant scavenger tetramethylthiourea. Relatively minor, if any, changes in the expression of Smads 2-4 have been found in COPD, whereas a significant downregulation of Smad 6/7 is found, suggesting that also intracellular feedback mechanisms in TGF- β signaling are disturbed in COPD (90).

The effects of cigarette smoke have been widely investigated *in vitro*. These studies have revealed variable effects on the release/activation of TGF- β , depending on the duration and dose of the exposure, as well as the density of the cultured cells (105). Observations of experimental pulmonary emphysema may also be difficult to extrapolate directly to human COPD, because many studies describe developmental changes/septal formation and the development of emphysema-like lesions without cigarette-smoke exposure. However, these studies have revealed important associations between TGF- β homeostasis and alveolar formation/emphysema. TGF- β null mice die of inflammation within 1 month after birth, which has limited their use for the investigation of emphysema (89). Mice homozygous for the disrupted allele for LTBP-4 develop severe emphysema, profound defects in the structure of their elastic fibers, and reduced deposition of TGF- β and phosphorylated Smad2 proteins in their epithelial cells (92). Interestingly, LTBP-3 deficiency, with a temporary decrease in TGF- β signaling, correlates with the inhibition of septation and the development of emphysema (25). These findings are in line with the loss of integrin-mediated activation of TGF- β and age-dependent pulmonary emphysema through alterations in the expression of matrix metalloproteinase-12 [metalloelastase, a proteinase associated with smoking-related emphysema (73)]. Overall, these and related studies (15) suggest that a balance in the activities of the TGF- β and Smad3 is required to maintain the alveolar integrity so that excessive signaling results in fibrosis (excessive repair) or defective signaling in destruction (lack of repair). The glutathione precursor *N*-acetylcysteine (NAC) has been investigated in relation to COPD. This compound induces GSH synthesis, decreases TGF- β induced Smad2/3 phosphorylation, and induces Smad7 mRNA expression. The results with NAC have been equivocal, but in systematic analysis, it did prove to be beneficial in a subset of patients with COPD (94).

CONCLUSIONS

Although TGF- β activation is considered to be a central mechanism in the pathogenesis of many diseases, the exact mechanisms of TGF- β expression and activation, its tissue responses, as well as the regulation of ROS in the human lung are still incompletely understood. Experimental and clinical studies have revealed complex oxidative pathways involved in TGF- β activation and signal transduction, which may be related

to the initiation or progression of pulmonary disorders such as IPF and COPD. Clearly, an understanding of such pathways and their reciprocal regulation is crucial before one can attain specific drug development for these intractable diseases. Simplified mouse models of pulmonary fibrosis and COPD provide novel mechanistic insights into lung enzyme and growth factor networks, whereas novel methods for the analysis of human tissues generate an increasing amount of information on the molecular background of the pathogenesis of fibrosis. When results from animal models and clinical studies are summarized, it seems that TGF- β -mediated and ROS-mediated profibrotic signals can be considered putative targets for the treatment of pulmonary fibrosis.

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ABBREVIATIONS

ARE, antioxidant response element; BMP, bone morphogenetic protein; COPD, chronic obstructive pulmonary disease; ECSOD, extracellular superoxide dismutase; EGF, epidermal growth factor; GCL, glutamate cysteine ligase; GM-CSF, granulocyte-macrophage colony-stimulating factor; GSH, glutathione; Grx, glutaredoxins; IPF, idiopathic pulmonary fibrosis; LAP, latency-associated protein; LTBP, latent TGF- β -binding protein; MT1-MMP, membrane-type 1 matrix metalloproteinase; MMP, matrix metalloproteinase; NAC, *N*-acetylcysteine; PAR1, proteinase-activated receptor 1; PSA, prostate-specific antigen; PDGF, platelet-derived growth factor; Prx, peroxiredoxin; RNS, reactive nitrogen species; ROS, reactive oxygen species; MnSOD, manganese superoxide dismutase; TGF- β , transforming growth factor β ; TIMP, tissue inhibitor of matrix metalloproteinase; UIP, usual interstitial pneumonia.

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