

ROLE OF SMADS IN RESPIRATORY DISEASE PATHOGENESIS

RUOLO DEGLI SMADS NELLA PATOGENESI DELLE MALATTIE RESPIRATORIE

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Abstract.

Transforming Growth Factor beta (TGF β) cytokine plays an important role in normal pulmonary morphogenesis and function as well as in the pathogenesis of lung diseases. The principal signaling pathway downstream to activate TGF β is the Smad pathway. Even though many studies have focused on Smads' structural features and pathway, less is known about the possible relationship between protein and mRNA expression of Smads and lung diseases. This review will focus on Smads and sum up what is known about their role in some respiratory diseases: COPD, asthma and fibrosis.

KEYWORDS: TGF β , Smads, Lung disease, COPD, pulmonary fibrosis.

Riassunto.

La citochina TGF β (Transforming Growth Factor beta) gioca un ruolo importante nella normale morfogenesi e funzione polmonare nonché nella patogenesi delle malattie respiratorie. Il principale pathway di trasduzione del segnale indotto dal TGF β attivato è quello degli Smads. Anche se molti studi si sono soffermati sull'analisi delle caratteristiche strutturali e sui meccanismi alla base del pathway, poco si sa circa la possibile correlazione tra l'espressione proteica e trascrizionale degli Smads e le patologie polmonari. Questa review analizzerà le caratteristiche degli Smads e riassumerà le informazioni riguardanti il loro ruolo nelle patologie respiratorie: asma, COPD e fibrosi.

PAROLE CHIAVE: TGF β , Smads, malattie polmonari, COPD, fibrosi polmonare.

Introduction

COPD (Chronic Obstructive Pulmonary Disease) is characterised by a slow, progressive and partially reversible airflow limitation, which is associated with an abnormal inflammatory response of the lung to noxious particles or gases. The pathological hallmarks of COPD are typical of the principal lung diseases: mucus hypersecretion and submucosal gland hyperplasia (chronic bronchitis), collapsed airways and destruction of airways parenchyma (emphysema), tightening of the muscles around the airways (chronic asthma) followed by tissue damage and inflammation of small airways and fibrosis (1). TGF β appears to be directly involved in the development and maintenance of

pulmonary diseases. TGF β superfamily consists of secreted growth factors regulating different cellular process such as cell growth, development, differentiation, proliferation, motility, adhesion and apoptosis (Table 1) (2-4). Members of this family are secreted as latent forms, due to the presence of a propeptide, or in trapped form by binding to occluding factors. The active form is a dimer able to initiate signal by binding to a specific pair of membrane serine/threonine kinases receptors, type I and type II receptor. Destruction of the TGF β signaling system has been implicated in embryonic anomalies (5-8), cancer and tumorigenesis (4,9), autoimmune diseases (10-13), atherosclerosis (14-16), hypertension (17), osteoporosis

Tab. 1: TGFβ regulatory effects on target cells.

Endothelium	Epithelium	Fibroblasts
Migration Morphogenesis ⁵⁵ Growth control ⁵⁶	Cell cycle arrest Apoptosis ^{55, 57} Adhesion ECM production ⁵⁸ Cytokine production Growth control ⁵⁶ Epithelial-mesenchymal transition (EMT) ⁵⁹	ECM production ^{58,60} Proliferation ^{61,62,63} Cytokine secretion Anchorage-independent growth ⁶⁴ Growth arrests ^{56,65}

sis (18), fibrotic disease (9-19) and hereditary hemorrhagic telangiectasia (20-21). These pathological states suggest a possible involvement of Smads/TGFβ signaling in development and maintenance of these pathological conditions.

Basic features of Smads

The name "Smad" was coined in reference to its sequence similarity to the *Sma* and *Mad* proteins. Eight Smad proteins are encoded in the human and mouse genome, four in *Drosophila* and three in *C. Elegans* (22). Only five of the mammalian Smads (Receptor-regulated Smads or R-Smads: Smad1, Smad2, Smad3, Smad5 and Smad8) act as substrates for the TGFβ family's receptors; specifically Smad1, 5, and 8 serve principally as substrates for the BMP (Bone Morphogenetic Protein) and anti-Muellerian receptors, Smads2 and 3 for the TGFβ, activin, and nodal receptors. Co-Smad Smad4 serves as a common partner for all R-Smads while Smad6 and 7 are inhibitory Smads (I-Smads) that serve as decoys interfering with Smad-receptor or Smad-Smad interactions (23). Functional studies, together with the X-ray crystal structure analysis, showed that these ~500 amino acids proteins consist of two conserved globular domains (*MH1* and *MH2* domains) coupled by a flexible *linker region* rich of binding sites for Smurf (Smad ubiquitination-related factors) ubiquitin ligase, of phosphorylation sites for several classes of protein kinases and, in Smad4, a nuclear export signal (NES) involved in nucleus-cytoplasmatic translocation (23). The MH1 domain is conserved in all R-Smads and in Co-Smad, but not in I-Smads and functions as a DNA-binding site, while the MH2 domain is conserved in Smad proteins and involved in Smad-Smad interaction and in R-Smad activation/phosphorylation. Binding of TGFβ to the type I receptor triggers phosphorylation of its cytoplasmatic GS domain by the type II receptor, thus creating a repeated pS-X-pS motif, that serves as a docking site for the R-Smads. The latter are presented to the activated type I receptor by the anchor protein SARA (Smad Anchor for Receptor Activation).

In the basal state, Smads form homooligomers and remain in an inactive conformation until both activated R-Smads and Smad4 form homotrimeric complexes (24,25). In this state R-Smads decrease their affinity for SARA, and the R-Smad/Smad4 complex is translocated into the nucleus, where can directly bind DNA with DNA promoters or interact with transcription factors or co-factors (26,27) (Figure 1). Smads activation and downstream targets activation can be regulated in both cytoplasmatic and nuclear compartments by different mechanisms including inhibitory Smads activation (28), ubiquitination (29), acetylation (30), sumoylation (31) and, as recently reported, dephosphorylation by PPM subfamily phosphatases (PPM1A, PPM1B and SCP1) (32,33).

TGFβ and lung disease: role of Smads

Injury of lung tissue leads to induction of TGFβ that limits some inflammatory reactions. It is also involved in mediating fibrotic tissue remodelling, by increasing the production and decreasing the degradation of connective tissue, and acts mediating the normal tissue repair (34). In several studies, TGFβ has been shown to be a marker of activity of tissue repair and remodelling; acute, as well as chronic, lung diseases showed an increase of TGFβ protein and mRNA expression during the phase of tissue remodelling (35-36). Disruption of the TGFβ signaling system has been shown to be involved in different pulmonary diseases such as COPD and pulmonary fibrosis.

Fibrosis

The direct involvement of TGFβ in fibrosis has been observed during several studies on fibrotic diseases. The prominent hypothesis of fibrosis development is that it is caused by chronic inflammation in response to an unknown etiologic agent, leading to tissue destruction, ongoing wound healing responses, and fibrosis (37). TGFβ is a critical element of progression from inflammation to chronic fibrosis. The pro-fibrotic effects of TGFβ are numerous, including induction of myofibroblasts, increase of matrix synthesis, and inhibition of col-

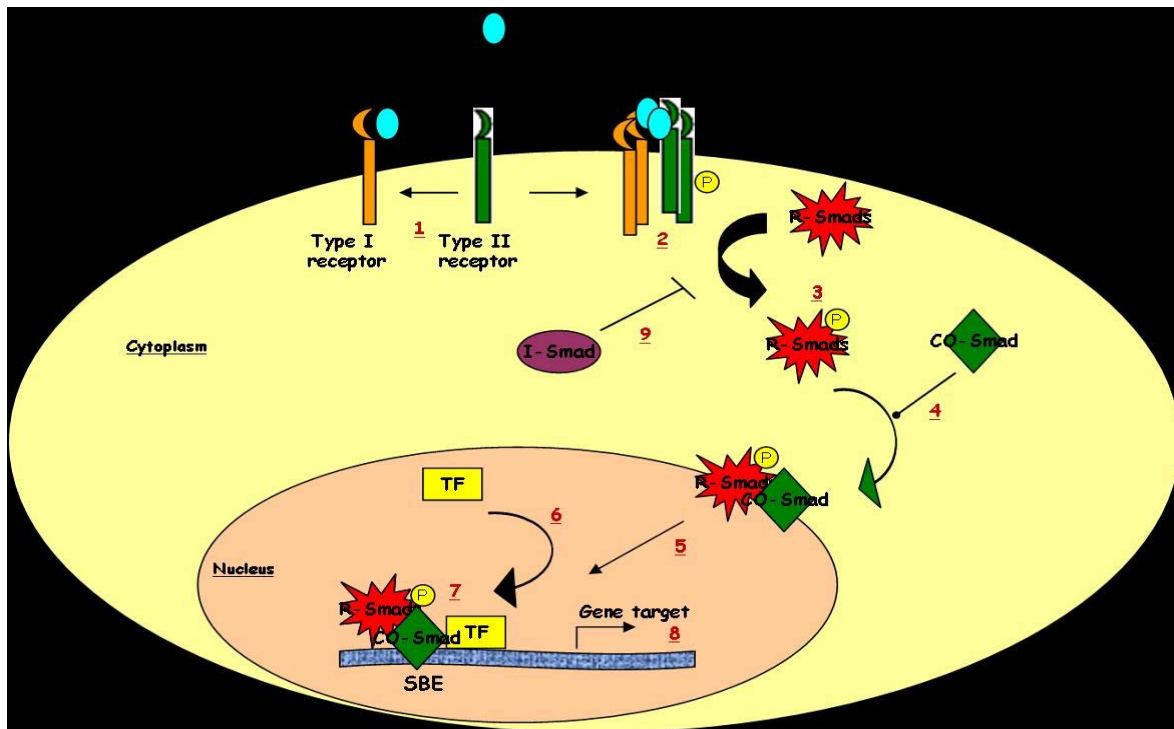


Fig. 1: Molecular mechanism of Smads pathway. **1)** Binding of TGF β to the type I and type II receptors, induces formation of multimeric receptors. **3-4)** Activated R-Smads dissociate from the receptor/SARA complex and form an oligomeric complex with Co-Smad Smad4. **5-6-7)** The complex R-Smad/Co-Smad translocates to the nucleus where it can interact with transcription factors or directly with DNA in Smad Binding Elements (SBE). **8)** Gene target transcription is activated. **9)** I-Smads (Smad7) inhibits signals competing with R-Smads for interacting with type I receptor and preventing phosphorylation.

lagen breakdown. Most of these effects are mediated through the Smad signaling pathway. Smad3 is principally related to fibrotic phenotype. Smad3 pathway is involved in pathogenic mechanisms mediating tissue destruction (lack of repair) and fibrogenesis (excessive repair); Smad3 null mice are protected from progressive fibrosis mediated by overexpression of TGF β 1 (38), do not develop lung fibrosis induced by bleomycin (39), and are protected against radiation-induced fibrosis of the skin (39). In a study by Gauldie and colleagues (41), administration of active TGF β to mice deficient in Smad3, blocked the ability of TGF β to induce matrix gene expression, enzyme inhibitors' gene expression and matrix accumulation, thus not progressing to scar formation or fibrosis. This indicates that TGF β and Smad signalling pathway, specifically Smad3, are required to initiate fibrosis and that mechanisms inducing expression of this growth factor are prominent in this disease. Loss of Smad3 was shown to confer resistance to fibrosis and resulted in reduced inflammatory cell infiltrates, reduced autoinduction of TGF- β (important to sustain the process) and reduced elaboration of collagen. Also, the key cellular mechanism of fibrosis is associated with myofibroblasts transdiffer-

entiation; myofibroblasts are generated from resident mesenchymal cells, endothelial and epithelial cells (epithelial-mesenchymal transition-EMT) (42); TGF β stimulates myofibroblast transdifferentiation through Smad3-dependent and -independent signals, contributing to the excessive matrix deposition that characterizes obliterative bronchiolitis. A significantly reduced expression of the Smad3 protein was observed in cystic fibrotic epithelial cells of nasal epithelium, and this reduction was apparently sufficient to influence the transmission of TGF β signals, including anti-inflammatory signals. (43).

COPD and Asthma

Less is known about the direct involvement of Smad proteins in COPD, even though various studies have shown that TGF β is involved in airways remodelling which characterize this disease. TGF β 1 protein and mRNA expression were increased in the bronchial and alveolar epithelium of COPD patients and correlated with the number of intraepithelial macrophages (44). Elevated levels of TGF β 1 have been observed in bronchial epithelium of smokers with COPD compared with those without COPD (45). Springer et colleagues (46) demonstrated that cigarette smoke down-regulates the inhibi-

tory Smad6 and 7 transcription in bronchial mucosal biopsies from severe COPD patients. A reduced mRNA expression of Smad7 was observed in bronchial biopsies of COPD stage II patients in comparison with controls, but no significant change was observed for Smad3 and 4. The study did not detect Smad2 transcription in the bronchial biopsies tested. In contrast, Zandvoort and colleagues (47) verified Smad2 protein expression, but found no significant differences between controls and COPD. Increased presence of TGF β 1 in the parenchyma may protect against emphysema as demonstrated in a mouse model, where constitutive expression of TGF β 1 prevented emphysema development. Absence of proper Smad3 signaling results in an ineffective repair response to damage in the lung, reduction of suppression of expression of MMPs, and susceptibility to airspace enlargement and emphysema. Disregulation of MMP expression has been shown as a key feature of smoke-exposed human lung fibroblasts in an in vitro model of COPD pathogenesis (48). Moreover Smad3-deficient animals are protected from fibrosis but are more susceptible to emphysema: Smad3 null mice are resistant to bleomycin- and TGF β -mediated fibrosis, but they develop spontaneous age-related airspace enlargement, consistent with emphysema, with a lack of ability to repair tissue damage appropriately (49). Studies on asthmatic patients showed increased levels of TGF β 1 and its transducer factors in the airways (50). Airway remodelling is one of the hallmark features of asthma. TGF β appears to be implicated in ECM proteins deposition which characterizes asthma, especially collagen. Concentrations of the active form TGF β 1 are higher in bronchoalveolar lavage fluid (BAL) of patients with severe asthma compared with controls (51). Runyan and colleagues (52) found a cross talk between Smads and PI3K (Phosphoinositide 3-kinase) pathway that enhanced TGF β -induced collagen type I expression in human mesangial cells. Recently, a different Smad2 activation was observed between asthmatic and non-asthmatic airway smooth muscle cells (ASM) with levels of phosphorylated Smad2 significantly higher in the asthmatic cells in comparison to the non-asthmatic (53). Expression levels of Smad7 in bronchial epithelial cells of asthmatic patients were inversely correlated with basement membrane thickness and airway hyperresponsiveness in asthmatic subjects, suggesting an active remodelling process resulting in a thickened basement membrane (54).

Concluding remarks

In the last ten years the attention of scientists for Smad proteins has increased, in view of

their prominent roles in the pathogenesis of lung diseases. Studies on Smads have started to explain their potential role in regulation and inhibition of TGF β effects. Modifications of Smad pathways or of their receptor systems, with a combination of genetic and environmental factors, could contribute to development of several TGF β -dependent diseases. All these information will expand the complex network about the TGF β signaling and thereby the potential role of Smad proteins in human respiratory diseases, potentially helping to design therapeutic strategies that should target TGF β signaling.

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