



SERIES “SIGNALLING AND TRANSCRIPTIONAL REGULATION IN INFLAMMATORY AND IMMUNE CELLS: IMPORTANCE IN LUNG BIOLOGY AND DISEASE”

Edited by K.F. Chung and I.M. Adcock

Number 3 in this Series

The contribution of transforming growth factor- β and epidermal growth factor signalling to airway remodelling in chronic asthma

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ABSTRACT: Asthma is increasing in prevalence in the developing world, affecting ~10% of the world's population. It is characterised by chronic lung inflammation and airway remodelling associated with wheezing, shortness of breath, acute bronchial hyperresponsiveness to a variety of innocuous stimuli and a more rapid decline in lung function over time.

Airway remodelling, involving proliferation and differentiation of mesenchymal cells, particularly myofibroblasts and smooth muscle cells, is generally refractory to corticosteroids and makes a major contribution to disease chronicity. Transforming growth factor- β is a potent profibrogenic factor whose expression is increased in the asthmatic airways and is a prime candidate for the initiation and persistence of airway remodelling in asthma.

This review highlights the role of transforming growth factor- β in the asthmatic lung, incorporating biosynthesis, signalling pathways and functional outcome. *In vivo*, however, it is the balance between transforming growth factor- β and other growth factors, such as epidermal growth factor, which will determine the extent of fibrosis in the airways.

A fuller comprehension of the actions of transforming growth factor- β , and its interaction with other signalling pathways, such as the epidermal growth factor receptor signalling cascade, may enable development of therapies that control airway remodelling where there is an unmet clinical need.

KEYWORDS: Asthma, fibroblast, fibrosis, myofibroblast, transforming growth factor- β

Asthma is a chronic inflammatory disease of the airways characterised by recurrent respiratory symptoms, such as wheezing, breathlessness, chest tightness and coughing. Airway remodelling is the general description for the thickening and restructuring of the airways seen in asthma patients (fig. 1 and 2). The characteristics of airway remodelling include subepithelial fibrosis, myofibroblast hyperplasia, myocyte hyperplasia and hypertrophy, together

with epithelial damage, goblet cell metaplasia, oedema [1] and increased vascularity. Mathematical models suggest that the remodelling and thickening observed in the airway of asthmatic subjects will enhance airway narrowing in response to bronchospasm during an asthma attack [2, 3]. Remodelling is also considered to be responsible for the more rapid decline in lung function over time experienced in the asthmatic compared with the nonasthmatic population [4].

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Received:

November 13 2004

Accepted after revision:

July 07 2005

Previous articles in this series: No. 1: Fan J, Heller NM, Gorospe M, Atasoy U and Stellato C. The role of post-transcriptional regulation in chemokine gene expression in inflammation and allergy. *Eur Respir J* 2005; 26: 933–947. No. 2: Georas SN, Guo J, De Fanis U and Casolaro V. T-helper cell type-2 regulation in allergic disease. *Eur Respir J* 2005; 26: 1119–1137.

European Respiratory Journal
Print ISSN 0903-1936
Online ISSN 1399-3003

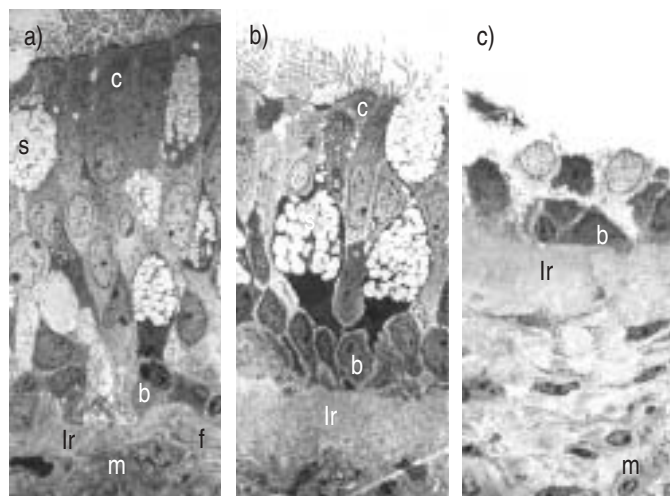


FIGURE 1. Transmission electron micrographs showing a) normal, b) mild and c) severe asthma airway epithelia. The epithelium is frequently damaged in asthmatic airways, revealing denuded areas where the basal cells are exposed (c). b) shows an increase in goblet cells in the epithelial layer. Transmission electron micrographs b) and c) of the asthmatic airway show thickening of the lamina reticularis. b: Basal cell, c: columnar epithelial cells, f: (myo)fibroblast, lr: lamina reticularis, m: mast cell, s: secretory goblet cells. Reprinted with permission from [6].

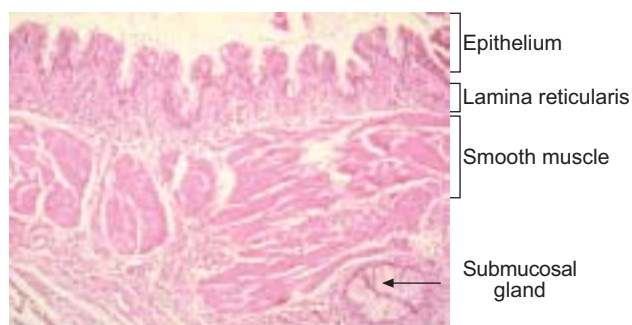


FIGURE 2. An increase in smooth muscle mass and thickening of the lamina reticularis are phenomena frequently observed in asthmatic airways as a result of remodelling. Reprinted with permission from [7].

Furthermore, it has been reported that airway hyperresponsiveness is associated with features of both remodelling and airway inflammation [5].

This review initially discusses the current findings in the field of remodelling in asthma. Recognising the role of transforming growth factor (TGF)- β as a central mediator of tissue fibrosis and structural remodelling, the mode of action and cell type-specific effects of TGF- β will then be discussed, with a view to understanding the advantages and disadvantages behind the application of anti-TGF- β therapies in the clinic. The review will continue by describing how the ultimate balance of growth factors in the lung can alter the delicate equilibrium that determines whether the epithelium has the capacity to repair after insult without triggering uncontrolled fibrosis. This will focus on the relationship between TGF- β and members of the epidermal growth factor (EGF) receptor ligand family, both of which show dysregulation in asthma. These growth factors

are not only connected historically, as TGF- α and TGF- β were originally co-purified as “transforming growth factor” on the basis of anchorage-independent growth assays [8], but also demonstrate many archetypal properties as regulators of epithelial and mesenchymal cell behaviour.

AIRWAY REMODELLING IN ASTHMA

Epithelial changes

The lung epithelium is continually subjected to environmental insults, such as air pollution, viruses and bacteria, as well as allergens, such as grass pollen and house dust mite allergens. Some irritants, such as house dust mite allergens, exert protease activity and can degrade the tight junctions of the epithelium [9]. Although shedding of the epithelium is part of airway homeostasis, it has been suggested that the epithelium of asthmatics is more susceptible to environmental insults compared with that of nonasthmatics. Indeed, clumps of attached ciliated epithelial cells (creola bodies) have been observed in bronchoalveolar lavage (BAL) fluid from asthmatics [10]. The extent of epithelial injury observed in asthmatics is controversial, with some reports showing no differences between normal and mild-to-moderate asthmatic biopsies [11]. However, this study was based on morphometry and did not use markers of epithelial repair to discriminate between damage that had occurred *in vivo* and artefactual damage that inevitably arises due to the bronchoscopy procedure [12]. More recent ultrastructural studies have provided further insight into the structure of the asthmatic epithelium, where it has been suggested that reduced desmosomal contact may be an important factor in the epithelial shedding observed in patients with asthma [13]. *In vitro* studies have also identified functional differences in the responses of asthmatic epithelial cells to environmental injury. For example, WARK *et al.* [14] showed that asthmatic cells have a defective innate immune response following infection with rhinovirus (RV-16), while BUCCHIERI *et al.* [15] showed that asthmatic bronchial epithelial cells are more susceptible to apoptosis in response to oxidant stress than normal epithelial cells. Additionally, PUDDICOMBE *et al.* [16] reported that p21waf, a cyclin-dependent kinase inhibitor, is expressed at a higher level in asthmatic epithelium compared with healthy controls. Expression of p21waf was also induced by TGF- β and oxidants, suggesting that these agents may contribute to a slower repair response within the context of airway inflammation and remodelling.

Other characteristic features of the asthmatic epithelium are an increase in the number of mucus-containing goblet cells [17] (fig. 1) and an increase in the size of submucosal glands [18] in asthmatic airways, resulting in an excessive release of mucus. The increased production of mucus can lead to the formation of plugs that can extend to the membranous bronchioles and contribute to airway obstruction, although, interestingly, mucus release into the BAL fluid was not found to be affected either 1 or 24 h after allergen challenge [19]. Mucin glycoproteins (MUC) are the major macromolecular component of mucus and are expressed as two major forms: membrane-tethered mucins and secreted mucins. Immunohistochemical staining for MUC5AC, one of the major gel-forming secreted mucins, has revealed abundant staining in goblet cells situated in the epithelial surface lining and glandular ducts of tissues

from patients with fatal asthma [20]. MUC2 and MUC4 mRNA expression has also been reported to be increased in asthmatic bronchial biopsies [21].

Thickening of the lamina reticularis

The "true" basement membrane, comprising the lamina rara and lamina densa, separates the airway epithelium from the mesenchyme. While the lamina rara and lamina densa in airways of asthmatic subjects are not reported to differ from nonasthmatics, the lamina reticularis is altered in asthmatics (fig. 1). This region, which is composed of collagen I, collagen III, collagen V, fibronectin and tenascin, and is situated just below the basement membrane, has an overall thickness of $\sim 3\text{--}4\ \mu\text{m}$ in nonasthmatics, while in asthma this is increased two- to three-fold [22, 23]. Although increased collagen deposition in the lamina reticularis is a characteristic of asthma, it may not explain the differences in severity of asthma [24]. Functionally, thickening of the lamina reticularis has been linked to reduced airway distensibility and increased airflow limitation in asthma [25], suggesting that this altered structure has a negative impact on lung function. However, it has been suggested that thickening of the lamina reticularis may actually serve as a protective mechanism by increasing the stiffness of the airways to attenuate the sporadic bronchoconstriction [2, 26].

Increased numbers of structural mesenchymal cells

Fibroblasts and myofibroblasts are the main structural cells of the mesenchyme that mediate the majority of the events contributing to the subepithelial fibrosis in remodelled airways. A number of studies have shown that there is an increase in myofibroblasts [22] in the submucosal layer of asthmatics. BENAYOUN *et al.* [27] demonstrated that there were significantly greater numbers of fibroblasts in bronchial biopsy samples from severe asthmatic compared with normal subjects. The number of fibroblasts in the submucosa of asthmatic subjects has also been significantly correlated with thickening of the subepithelial lamina reticularis [28].

In addition to an increase in the number of myofibroblasts, a number of reports describe smooth muscle hyperplasia in asthmatic airways. For example, WOODRUFF *et al.* [29] demonstrated a 50–83% ($p < 0.005$) increase in the amount of smooth muscle in the submucosa of asthmatics. It was reported that tritiated thymidine incorporation was increased in asthmatic airway smooth muscle cells *in vitro* compared with normal cells, indicating that airway smooth muscle proliferation may be increased in asthma, thus contributing to the hyperplasia [30]. In 2004, JOHNSON *et al.* [31] suggested that the increased proliferation may be attributable to the altered matrix deposition by asthmatic smooth muscle cells. Specifically, extracellular matrix (ECM) rich in perlecan and collagen I, but with lower amounts of laminin $\alpha 1$ and collagen IV deposited by asthmatic cells, enhanced the proliferation of nonasthmatic smooth muscle *in vitro*. There are conflicting reports as to whether there is also a difference in the size (hypertrophy) of asthmatic smooth muscle cells. BENAYOUN *et al.* [27] described hypertrophic smooth muscle cells with an accompanied increase in myosin light-chain kinase expression from severe persistent asthmatic subjects compared with those with milder disease. Conversely, in mildly to moderately severe subjects, WOODRUFF *et al.* [29] measured no differences in cell size.

DULIN *et al.* [32] report that smooth muscle isolated from asthmatic tissues exhibits normal sensitivity to constrictor agonists when studied during isometric contraction. The sheer increase in smooth muscle mass was suggested to be responsible for generating more contractile force than that experienced in the nonasthmatic airways. The increased muscle bulk can also reduce the luminal circumference and alter the pattern of mucosal folding, resulting in a reduced number of folds and enhanced airway narrowing.

THE EPITHELIAL-MESENCHYMAL TROPHIC UNIT

In order to help explain some of the structural changes that occur in asthmatic airways, it has been proposed that the epithelium and the underlying fibroblasts communicate through autocrine and paracrine mechanisms, effectively forming the epithelial-mesenchymal trophic unit. The epithelial-mesenchymal trophic unit functions during development and is crucial to the process of branching morphogenesis. It is postulated that reactivation of developmental pathways contributes to the structural alterations of airways in asthma [33]. Thus, it is proposed that, in asthma, epithelial susceptibility to injury and repair of the wounded bronchial epithelium leads to perpetuation of a chronic inflammatory cycle [33]. During exacerbations, activated inflammatory cells interact with the epithelium to produce an array of T-helper cell type-2 cytokines and chemokines. As well as having a protective role, the inflammatory cells can have a detrimental effect by causing further damage to the epithelium through the release of free radicals and proteases.

The epithelium can also communicate with the underlying mesenchyme (fig. 3). TGF- β is released from damaged epithelial cells [34] and can mediate its effects by interacting with TGF- β receptors on fibroblasts. This interaction can promote the transformation of fibroblasts into myofibroblasts. Myofibroblasts are more biosynthetic in nature and can synthesise and release an array of growth factors and cytokines, resulting in remodelling of the airways and continuation of the chronic inflammatory events. This is amplified by release of various factors, such as endothelin-1, a mitogen for smooth muscle, eotaxin, a chemoattractant for eosinophils and vascular endothelial growth factor, an angiogenic factor that promotes the growth of new blood vessels [35, 36].

EGF receptor (EGFR) ligands can also be released from epithelial cells, fibroblasts and smooth muscle cells. EGFR ligands can promote either proliferation or differentiation. It is proposed that ligands of the EGF family are released from the damaged epithelium and cause the proliferation of the underlying mesenchymal cells, as demonstrated in TGF- α transgene mice [38].

REMODELLING IN CHILDHOOD ASTHMA

The chronology of events leading to the onset of disease is currently a subject of much discussion. It is widely accepted that susceptible subjects go on to develop atopic asthma after sensitisation to a particular allergen. The precise initiation of remodelling events in the airways is less certain, although recent studies suggest that remodelling (or pre-modelling) may be an early event in the aetiology of disease linked to the function of the epithelial-mesenchymal trophic unit [39].

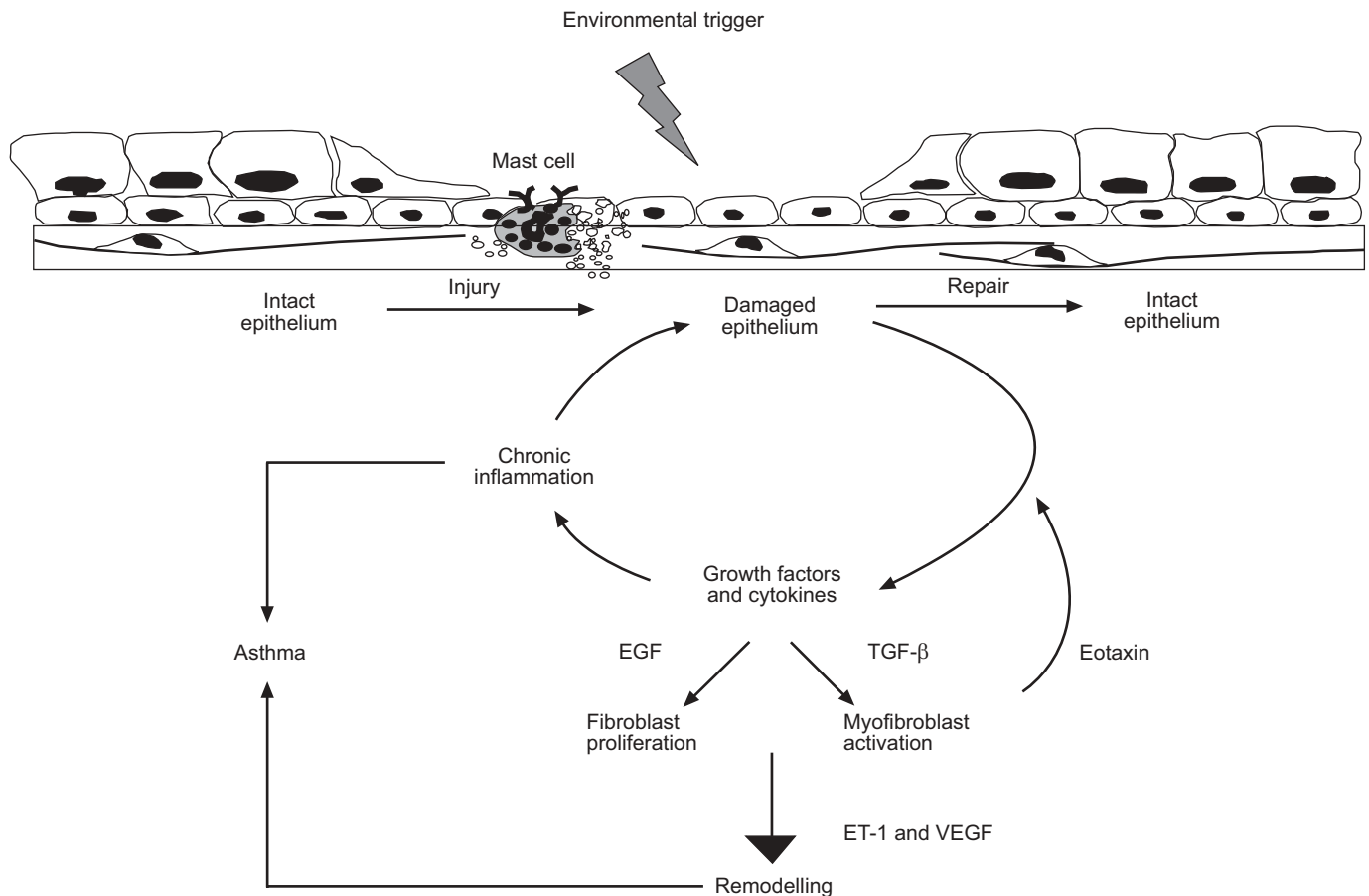


FIGURE 3. The epithelium and the mesenchyme can communicate in asthmatic airways due to the release of soluble growth factors. The epithelium can release pro-inflammatory and profibrogenic growth factors that can mediate remodelling and perpetuate the chronic inflammatory cycle. Activated fibroblasts can in turn release factors that promote inflammation as well as remodelling processes, such as smooth muscle hyperplasia and angiogenesis. It is postulated that the remodelling and inflammation attenuate the normal repair of the damaged epithelium and ultimately lead to the development of asthma. Modified from [37]. EGF: epidermal growth factor; TGF- β : transforming growth factor- β ; ET-1: endothelin-1; VEGF: vascular endothelial growth factor.

Indeed, the impact of remodelling may be greater during the childhood years, as children's lungs grow rapidly in the first few years of life.

In addition to the more complex ethical issues surrounding bronchoscopies performed on children, it is often very difficult to differentiate between wheeze induced by viral infections and bronchial asthma in the preschool child. In the studies that have been carried out in paediatric asthma, it appears that a number of phenomena associated with remodelling are present at an early age. For example, COKUGRAS *et al.* [40] studied biopsy samples from 10 children with moderate asthma and demonstrated thickening and hyalinisation of the sub-basement membrane region in nine patients. Although eosinophils were present in only one sample, 60% had degranulating mast cells in the submucosa. NAJAFI *et al.* [41] performed BAL on 39 newly diagnosed wheezy children. The study found that children >2 yrs of age had larger amounts of ciliated columnar and goblet cells in the BAL fluid compared with older children, suggesting acute inflammation of the airways early in life. A study comparing the degree of remodelling in asthmatic children prescribed with 1,600 $\mu\text{g}\cdot\text{day}^{-1}$ of an inhaled steroid to adult asthmatics

revealed that lamina reticularis thickening is present in children with difficult asthma at a similar level to that observed in biopsies obtained from adult asthmatic subjects [42]. However, there was no association with age, symptom duration, lung function, or concurrent eosinophilic airway inflammation. In a separate study, FEDEROV *et al.* [39] showed thickening of the lamina reticularis in asthmatic biopsies with increased deposition of collagen III. As in adults, there was an asthma-related increase in epithelial EGFR and this correlated with the thickness of the lamina reticularis, suggesting a link between subepithelial fibrosis and epithelial damage and/or activation [39].

IS REMODELLING POSITIVELY CORRELATED TO DISEASE SEVERITY?

The majority of studies carried out to compare the effect of disease severity suggest that tissue remodelling is more advanced in subjects with severe asthma. HARMANCI *et al.* [43] demonstrated that bronchial wall thickening was more prominent with increased severity, decreased forced expiratory volume in one second (FEV₁) values and the duration of asthma. The submucosa of asthmatic subjects contained more

blood vessels; this also correlated with the severity of the disease [44].

BENAYOUN *et al.* [27] revealed that mucosal eosinophilia, neutrophilia, epithelial damage and subepithelial basement membrane thickness were not related to disease severity. However, a number of observations distinguished patients with severe persistent asthma from patients with milder disease. These included increased numbers of fibroblasts, larger areas of mucous gland and smooth muscle, smooth muscle hypertrophy, increased collagen type III deposition, and higher myosin light-chain kinase expression. CHAKIR *et al.* [45] described an association between disease severity and collagen deposition. In contrast, CHU *et al.* [24] found no identifiable differences in collagen deposition or TGF- β expressing cells in the large airways of mild when compared with severe asthmatics.

REVERSIBILITY OF REMODELLING?

Airway remodelling has been considered to be an irreversible process, although there is evidence to suggest that early use of corticosteroids can delay or even reverse the structural changes [46]. A 5-yr follow-up study comparing subjects treated with corticosteroid early in the course of their disease to a delayed treatment group showed that early use of corticosteroids (budesonide) significantly improved lung function and increased exercise tolerance. Furthermore, the early treatment group used reliever medication less, had fewer exacerbations and, after 5 yrs, 17% were able to stop using budesonide when compared with 3% in the delayed treatment group [47]. Furthermore, in a randomised, double-blind clinical trial of 7,241 patients in 32 countries performed by the START (Steroid Treatment As Regular Therapy) investigators group [48], treatment with budesonide (in addition to their usual asthma medication) in patients who had mild persistent asthma for ≤ 2 yrs had fewer courses of systematic steroids and more symptom-free days than those on placebo. FEV₁ readings, pre- and post-bronchodilator, from patients taking budesonide (400 μ g for adults, 200 μ g for children aged 5–11 yrs) were significantly increased after 3 yrs. Although the outcomes of the study were beneficial to the patients, it was noted that growth over 3 yrs was suppressed by 1.34 cm in children aged >11 yrs in the treatment group.

A number of studies have directly examined the effect of corticosteroids on remodelling by performing bronchoscopies. A study carried out by SONT *et al.* [49] showed that subjects treated with corticosteroids over a period of 2 yrs experienced a lower rate of mild exacerbations, an improved FEV₁ and a reduction in the thickness of the subepithelial layer compared with the control group. In a double-blind study of 28 asthmatic subjects, HOSHINO *et al.* [50] demonstrated that treatment with the inhaled steroid beclomethasone dipropionate significantly reduced the vessel number and vascularity in the airways of steroid treated patients. Further study showed that biopsy samples taken before and after treatment with an inhaled steroid revealed a decrease in inflammatory cells and a reduced amount of epithelial damage after 10 yrs, although bronchial hyperresponsiveness remained the same [51]. The majority of investigations carried out do suggest that early and prolonged use of corticosteroids can provide some improvement in lung function and may minimise some of the

remodelling events, although it should be remembered that long-term use of corticosteroids can in itself bring about other adverse effects, such as adrenal suppression and arterial hypertension. Furthermore, the absence of an effect of corticosteroids on bronchial hyperresponsiveness suggests that some of the underlying structural changes and/or disease mechanisms are poorly responsive to the effects of corticosteroids.

INCREASED DEPOSITION OF EXTRACELLULAR MATRIX

The ECM is a complex network of secreted polysaccharides and proteins that creates a microenvironment which has the capacity to influence the behaviour of cells in very distinct, as well as cooperative, ways. Thus, in addition to forming a scaffold on which tissues are organised, ECM molecules, such as proteoglycans, can modify the binding of cytokines to their cell surface receptors, or they can lead to the storage of the soluble factors in the matrix. This is particularly important in the case of TGF- β , which can be sequestered by a number of different binding proteins, including decorin, biglycan, type IV collagen, fibronectin and elastin [52].

In asthma, there is an altered profile of ECM proteins present in the submucosal layer below the lamina reticularis. It is proposed that this is due not only to the increased number of synthetic cells present, but also due to differences in the degradation of the existing proteins. The “true” basement membrane in asthma contains less collagen IV than normal, although the submucosa of asthmatic airways contains more collagen I, III and V [28, 31, 45, 53]. Additionally, the orientation and fibre thickness of collagen I appears to be altered in asthmatics [23, 54]. DUBE *et al.* [55] suggested that differences in collagen expression were due to post-translational modifications, as baseline procollagen production was not found to differ between nonasthmatic and asthmatic fibroblasts.

There are a number of reports demonstrating increased levels of ECM proteins in the submucosa of asthmatics. For example, tenascin [56], lumican, biglycan and versican [57] are all present at elevated levels in the submucosa of asthmatic subjects. WESTERGREN-THORSSON [58] reported that subjects with the most hyperresponsive airways produced up to four-fold more total proteoglycan than subjects with less responsive airways. Laminin β_2 and α_1 staining [59] was also higher in biopsies from asthmatic subjects. Elastin fibres are needed to maintain bronchial patency and contribute to the elastic recoil of the lungs. BOUSQUET *et al.* [60] reported that biopsy samples from asthmatics showed altered elastin staining. In addition, VIGNOLA *et al.* [61] showed that the enzyme responsible for elastin degradation, elastase, was increased in sputum samples from asthmatics compared with healthy controls. Apart from elastin degradation, it is proposed that neutrophil elastase can also act as a smooth muscle mitogen [62] and promotes mucin gene expression by cleavage of EGF receptor ligands [63].

Matrix metalloproteinases (MMPs) were first recognised for their ability to degrade many ECM proteins, including collagens, fibronectin, laminin, proteoglycans and elastin. However, it is now clear that MMP activity also causes the release of cryptic information from the ECM by cleaving large insoluble ECM components to liberate bioactive fragments and

growth factors that can have marked effects on cell behaviour. Thus, in combination with proteases, the ECM is a dynamic environment, where small changes in levels of MMPs and other enzymes may alter the equilibrium of a range of bioactive proteins in the submucosal layer.

An altered expression profile of ECM-degrading enzymes has been reported in asthma. For example, asthmatic bronchial fibroblasts produce less MMP-3 (stromolysin) than normal fibroblasts [64]. LALIBERTÉ *et al.* [65] demonstrated that baseline MMP-2 (gelatinase A) secretion was lower in asthmatic fibroblasts when compared with those from normal airways. The group also showed that asthmatic fibroblasts displayed a decreased capacity to degrade collagen by phagocytosis.

MMP-9 (gelatinase B), a metalloproteinase responsible for cleaving collagen IV and degrading denatured collagen, is reportedly expressed at higher levels in eosinophils isolated from asthmatics compared with nonasthmatics [66]. A significant increase in both the level of circulating MMP-9 [67] and its activity in BAL fluid [68] was also seen in patients after exacerbation compared with patients with asthma. Additionally, MMP-9 staining in the subepithelial basement membrane region was reportedly higher in severe asthmatic biopsies than in control subjects [69]. These findings may account for the decreased expression of collagen IV in the basement membrane of asthmatic subjects.

Tissue-specific inhibitors of metalloproteinases (TIMPs) can inhibit activation of the MMPs by binding an MMP in a 1:1 stoichiometric fashion. LALIBERTÉ *et al.* [65] hypothesised that a compromised balance between TIMP-1 and MMP-1 levels may be responsible for the increase in collagen deposition observed in asthmatic airways. Indeed, TIMP-1 mRNA and protein levels were elevated in asthmatic alveolar macrophages isolated from BAL fluid, a finding demonstrated by OHNO *et al.* [66]. Additionally, CATALDO *et al.* [70] reported that MMP-1 and TIMP-1 levels were increased at the mRNA level in induced sputum from asthmatic subjects compared with nonasthmatics. Recent studies using computed tomography have linked induced sputum MMP-9/TIMP-1 ratios to thickening of the airway wall in asthmatics [71, 72].

The A Disintegrin And Metalloprotease (ADAM) family of proteins belongs to the metzincin subgroup of zinc-dependent proteases; it encompasses a large number of proteins, 40 to date [73], although only 23 are expressed in humans. ADAM9, -10, -15 and -17 are ubiquitously expressed in human tissue, whilst the majority of the ADAMs display restricted expression in the testis and are involved in spermatogenesis and egg fertilisation.

Approximately half of the ADAM family contains a zinc-binding consensus motif in their metalloprotease domain; this is essential for enzymatic activity. In regard to the processing of EGFR ligands, ADAM9, -10, -12, -17 and -19 have all been reported to play a role in pro-growth factor cleavage. Proteolytic ADAM activity can be inhibited *in vivo* by TIMPs. For example, TIMP-3 can inhibit ADAM17 [74] and ADAM12 [75], whilst ADAM10 activity can be inhibited by both TIMP-1 and TIMP-3 [74].

Using positional cloning, the 33rd member of the ADAM family has been linked to asthma and bronchial hyperresponsiveness [76]. ADAM33 contains a zinc-binding consensus sequence in its metalloprotease domain [77], which has been shown to be catalytically active in an α_2 -macroglobulin complex formation assay [78]. Expression of the purified metalloprotease domain in *Drosophila* S2 cells also showed that the domain has some functional activity, although ZOU *et al.* [79] reported cleavage of only four synthetic peptides. While the metalloprotease activity of ADAM33 represents a potential target for therapeutic intervention, the only single nucleotide polymorphism that has been identified that could cause a coding change within the metalloprotease domain has a weak association with bronchial hyperresponsiveness [76]. Furthermore, POWELL *et al.* [80] have reported that the metalloprotease domain is spliced out over 95% of transcripts in bronchial fibroblasts, suggesting that other domains of ADAM33 play important functional roles. Similarly, in bronchial biopsies, transcripts encoding the metalloprotease domain are of low abundance and there is no clear disease-related difference in ADAM33 expression [81]. These data suggest that simple up- or downregulation of ADAM33 is unlikely to explain its contribution to the development of asthma. A more likely explanation is that polymorphic variation in ADAM33 may have functional effects, possibly by affecting its regulation within the cell. Ongoing work in the field should hopefully reveal its role in asthma pathogenesis. In this context, it is noteworthy that ADAM33 is selectively expressed in mesenchymal cells [76], strongly implicating it in airway remodelling. Consistent with this proposal, a rare allele of the S₂ polymorphism of ADAM33 is significantly associated with excessive decline in FEV₁ in asthmatic subjects [82] and chronic obstructive pulmonary disease patients [83]. Furthermore, in a prospective birth cohort study, polymorphisms in ADAM33 predict impaired early-life lung function [84].

TGF- β SIGNALLING AND ITS ROLE IN ASTHMA

In asthma, it has been hypothesised that an enhanced expression of TGF- β in the airways may have far reaching effects in the pathophysiology of the disease. TGF- β released from inflammatory cells, the epithelium and (myo)fibroblasts can promote remodelling by inducing expression of a wide range of ECM components. Although TGF- β is anti-inflammatory (for a recent review see [85]) and can promote cellular migration [86], an excess of TGF- β can inhibit subsequent epithelial cell proliferation that is required during early wound healing. The net result of excessive TGF- β in the airways in asthma may explain many of the morphological changes that occur in airway remodelling (fig. 4).

More than 30 members of the TGF- β superfamily have been identified [87]. The superfamily is divided into four main families: 1) TGF- β family; 2) bone morphogenetic (BMP) family; 3) inhibin/activin family; and 4) the Müllerian-inhibiting substance family. There are three TGF- β isoforms identified in mammals, namely TGF- β ₁, - β ₂ and - β ₃. It should be noted that, for much of the early work on TGF- β , it would not have been possible to distinguish which isoform of TGF- β was responsible for the observed effect, hence these studies refer simply to TGF- β . Although TGF- β was first isolated and characterised from human platelets [88], it is produced by most

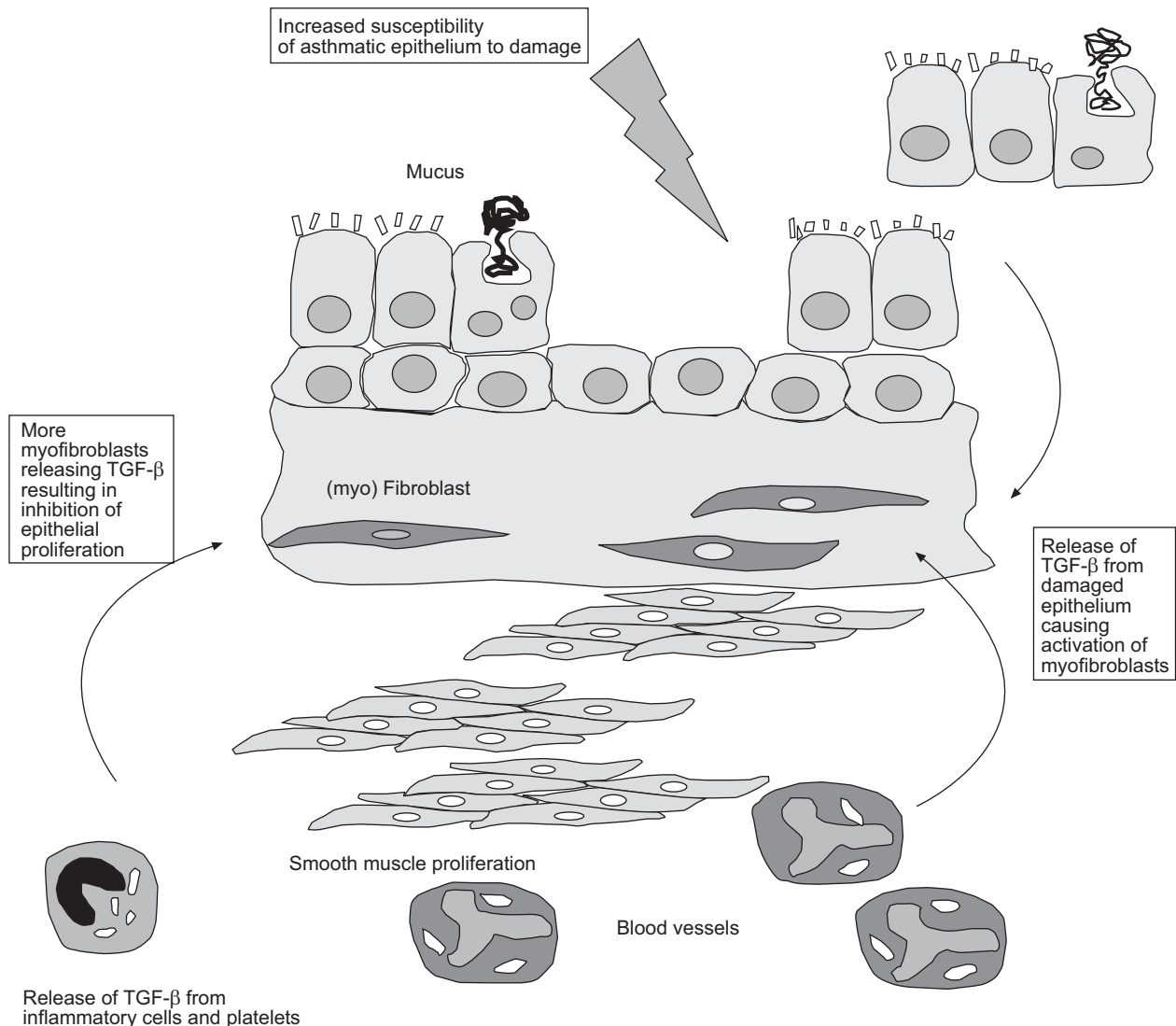


FIGURE 4. Studies have revealed that there is an increased expression and release of transforming growth factor (TGF)- β in asthmatic airways. TGF- β is released from the epithelium, fibroblasts, smooth muscle cells and inflammatory cells, and is proposed to have a major role in the fibrosis associated with airway remodelling.

cell types, including fibroblasts, smooth muscle, epithelial and inflammatory cells.

TGF- β is encoded as a biologically inactive large precursor peptide termed pre-pro-TGF- β . Endopeptidases catalyse the cleavage of the precursor molecule, yielding the mature 25 kDa protein. The mature TGF- β dimerises and associates noncovalently with latency associated peptide, the precursor cleavage product, to form small latent TGF- β . TGF- β is secreted from the cell as either small latent TGF- β or, more often, as large latent TGF- β (small latent TGF- β bound to latent TGF- β binding protein). TGF- β can then be rapidly sequestered by a number of different binding proteins, including decorin, biglycan, type IV collagen, fibronectin and elastin [52]. The binding protein also has the ability to bind to sites in the ECM [89].

The mechanism by which latent TGF- β is activated *in vivo* remains elusive, although a number of molecules have been implicated *in vitro*. TGF- β can be activated by thrombospondin, which binds to latency-associated peptide and induces a

conformational change [90, 91]. Plasmin, low-dose radiation, low pH, reactive oxygen species [92] and nitric oxide nitrosylation [93] have all been suggested to play a role in TGF- β activation.

TRANSFORMING GROWTH FACTOR- β RECEPTORS

There are six types of TGF- β receptor (RI–VI). Most of the information in the literature concerns RI, RII and RIII. TGF- β RIV [94] and RVI [95] bind TGF- β , but are not known to propagate downstream signalling. TGF- β RV is a serine/threonine kinase like RI and RII, and further investigation may reveal its importance in controlling downstream signalling events [96]. Betaglycan and endoglin comprise the two types of TGF- β RIII. Endoglin is expressed only on endothelial and myeloid cells. Betaglycan is expressed on most cell types and has a variable molecular weight due to the heparan sulphate and glycosaminoglycan chains attached to it. The receptor is responsible for binding TGF- β and presenting the ligand to the type II receptor. This enables the local concentration of ligand

to be increased and may also have a role in stabilising TGF-β in the optimal conformation for binding to the type II receptors. TGF-β₂ has a weak affinity for the type II receptor alone and can only signal *via* interaction with betaglycan [97] where the short cytoplasmic tail of the receptor acts to enhance TGF-β₂ signalling. In contrast, TGF-β₁ can signal directly through TGF-β RII.

The type II receptor is a 70 kDa constitutively active serine/threonine kinase. Upon ligand binding, the receptor recruits and phosphorylates the type I receptor in the GS domain and juxtamembrane regions. Whilst the type II receptor can bind TGF-β₁ independently of betaglycan, recruitment of the type I receptor is still required for downstream signalling. The type I receptor is a 55 kDa protein, responsible for downstream signalling *via* a cascade of Smad proteins. There are seven type I receptors. ALK-1 (mainly associated with endothelial cells) and ALK-5 are type I receptors for TGF-β [98], ALK-4 is the receptor for activin and ALK-2, -3 and -6 are receptors for the BMPs [99, 100]. TGF-β receptor-associated protein 1 binds to the inactive type I receptor but is released when the receptor is activated by ligand binding [101]. The activated receptor complex is a heteromeric complex consisting of two type II and two type I receptors (fig. 5).

DOWNSTREAM SIGNALLING

TGF-β mediates intracellular signalling *via* the “Smad” proteins. Mad was the first member of the Smad family to be identified in *Drosophila*. Its discovery led to the identification of Mad homologues in *Caenorhabditis elegans*; these were named Sma-2, -3 and -4 because of their small size. Smad (Smad/Mad-related) proteins were later identified as TGF-β signalling molecules in vertebrates (fig. 6). Receptor Smads, *i.e.* Smad-2 and -3, reside in the cytoplasm in their inactivated state. Smad-2 exists as a monomer due to a structural element in the MH1 domain that inhibits protein–protein interactions in the basal state. Smad-3 has multiple oligomeric states and Smad-4 most likely exists as a trimer [102]. The Smads are serine phosphorylated by the type I receptor after ligand-dependent activation. The interaction of the Smad anchor for activation protein [103] with the receptor allows interaction with Smad-2 and Smad-3. Smad-2 signalling is dependent

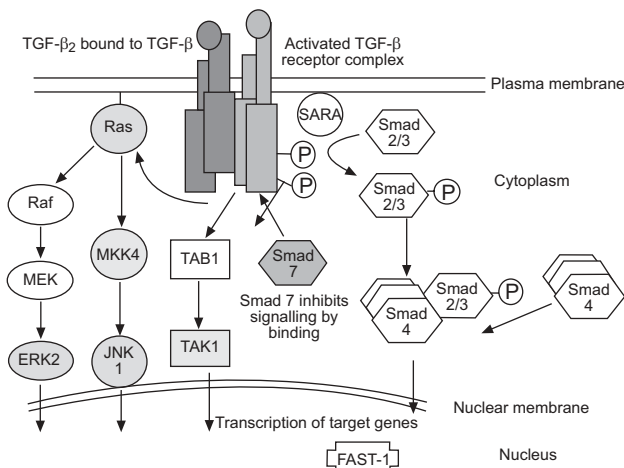


FIGURE 6. Transforming growth factor (TGF)-β can signal *via* Smads or a mitogen-activated protein MAP kinase-like pathway, resulting in transcription of target genes. Nuclear transcription of target genes occurs either by Smads binding directly to Smad-binding elements of target genes or by functional co-operation with transcription factors, such as fork-head activin signal transducer 1 (FAST-1). Phosphorylation changes are only indicated on the Smad pathway for ease of interpretation. MEK: MAP kinase kinase; ERK2: extracellular-regulated protein kinase 2; MKK4: MAP kinase kinase 4; JNK1: Jun N-terminal kinase 1; TAK1: TGF-β-activated kinase 1; TAB1: TAK1-binding protein; SARA: Smad anchor for activation; Smad: TGF-β signalling molecules.

upon the Smad anchor for activation but the Smad 3/Smad anchor for activation interaction is not required for downstream signalling [104]. The phosphorylated receptor Smads bind Smad-4 (a co-Smad), and the complex translocates to the nucleus. There is evidence to suggest that TGF-β receptor-associated protein 1 interacts with Smad-4 (fig. 6) and may act as a chaperone protein [105].

The Smads can bind directly to the Smad-binding element of various genes, such as junB, c-jun and immunoglobulin (Ig) A [106, 107]; they can also mediate gene transcription via functional co-operation with other transcription factors, such as FAST-1 [108]. TGF-β-activated Smad-2 and -3 can also bind to co-repressors, *e.g.* cAMP response element-binding (CREB)-binding protein and p300, which can in turn interact with transcription factors to modify gene transcription [109]. HOCEVAR *et al.* [110] described Smad-4 independent activation of TGF-β with resultant induction of fibronectin synthesis. The mechanism involves TGF-β activation of mitogen-activating protein kinase (MAPK) kinase 4, which activates Jun N-terminal kinase 1; this in turn phosphorylates c-jun, promoting the formation of the c-jun-ATF 2 heterodimer. These heterodimers can bind to cAMP-response elements in the fibronectin promoter and thus promote fibronectin synthesis.

There are other possible pathways by which TGF-β receptors can transmit signals. Protein farnesyltransferase-α [111] and FK506 binding protein-12 (FKBP-12) [112] have both been shown to bind to the TGF-β receptors, although FKBP-12 might act as a negative regulator of TGF-β receptor endocytosis [113]. It is also possible that a MAPK-like pathway is involved in the propagation of signals from the membrane to the nucleus, *via* TAB1 and TAK1 (MAPK kinases) [114, 115].

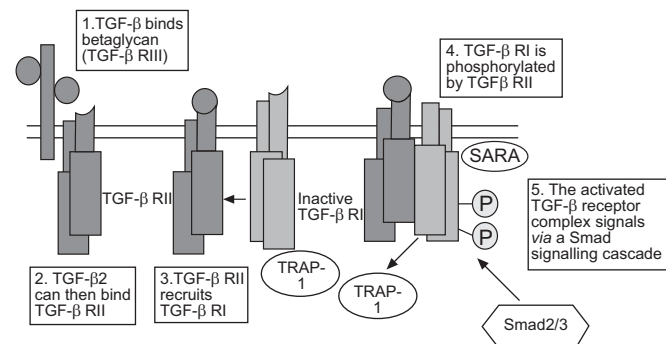


FIGURE 5. Scheme showing steps involved in forming the activated transforming growth factor (TGF)-β receptor complex. Betaglycan (TGF-β RIII) binds TGF-β₂, enhancing the affinity of the growth factor for TGF-β RII. Once bound, TGF-β RII recruits and phosphorylates TGF-β RI, thus promoting downstream signalling. TRAP-1: tumour necrosis factor-associated protein 1.

REGULATION OF TGF- β SIGNALLING

After ligand binding, a process of endocytosis typically downregulates growth factor receptors. In fibroblasts, heteromeric TGF- β receptors are internalised whereas homomeric receptors are recycled back to the membrane [116, 117]. The diversity of TGF- β signalling is controlled in part by the residues phosphorylated on the receptor in response to ligand stimulation. SAITOH *et al.* [118] observed that serine 172 and threonine 176 of TGF- β RI are dispensable for ECM protein production but essential to epithelial growth inhibition mediated by TGF- β . LUO and LODISH [119] demonstrated that autophosphorylation of serine 213 on TGF- β RII is essential for activation of the TGF- β RII kinase, activation of TGF- β RI and TGF- β -induced growth inhibition.

There are two mammalian antagonistic Smads, Smad-6 and Smad-7, which can inhibit BMP signalling; TGF- β signalling can be inhibited by Smad-7. Smad-6 inhibits BMP/Smad-1 signalling by competing with Smad-4, forming a Smad-1/Smad-6 inactive complex [120]. Smad-7 acts as an antagonist of TGF- β RI [121] and is induced by TGF- β . Conversely, EGF can induce the mRNA levels of Smad-7, providing evidence of cross-talk between the pathways [122]. Serine-threonine kinase receptor-associated protein (STRAP) stabilises the association between the type I receptor and Smad-7, preventing the receptors association with Smad-2 or -3 and thus preventing signalling [123].

Another form of negative regulation of Smads is by the interaction with MAPK. The linker region between the MH1 and MH2 domain of the receptor Smads can be phosphorylated, which prevents the Smad-2/Smad-4 complex from entering the nucleus and eliciting gene transcription. There are also a number of inhibitory transcription factors, such as Evi-1 [124], c-ski [125] and SnoN [126], which can prevent activated Smads from binding to Smad-binding elements on DNA. Transforming growth- interacting factor is an example of a co-repressor that can compete with p300 for Smad-2 association, preventing TGF- β -mediated signalling [127].

TGF- β AND THE EPITHELIUM

TGF- β 1 regulates the migratory phase of epithelial repair. BOLAND *et al.* [128] reported that 1–10 ng·mL⁻¹ TGF- β 1 inhibited the proliferation of primary epithelial tracheal cells but enhanced cell migration. TGF- β also induced cell spreading, reduced the number of cell–cell contacts and increased cell-substratum anchorage, thus favouring a migratory phenotype. Furthermore, HOWAT *et al.* [129] showed that TGF- β 1, but not TGF- β 2, could progressively increase the migration of damaged bronchial epithelial monolayers at concentrations down to 250 pg·mL⁻¹.

TGF- β 1 can inhibit cell proliferation of epithelial cells by a number of different mechanisms involving the downregulation of c-myc [130], and the upregulation of the cyclin-dependent kinase inhibitors, p15INK4B, p21waf1 and p27kip1 [131]. p21waf1 is over-expressed in asthmatic epithelium, which is strongly suggestive of cell stress and growth arrest [16].

TGF- β , FIBROBLAST AND MYOFIBROBLASTS

Fibroblasts comprise the major structural cell in the mesenchyme in its resting state. Quiescent fibroblasts are involved in

the baseline secretion of proteins, such as collagen, contributing to the normal turnover of ECM in the airways. Upon insult to the tissue, fibroblasts become activated and capable of migrating to the site of injury. In order to carry out this function, the fibroblasts secrete collagen and fibronectin fibrils to enable orientation of the cell, thus creating both a migratory meshwork as well as lines of stress and mechanical tension.

Myofibroblasts are generally viewed as morphological intermediates of fibroblasts and smooth muscle cells. They are the predominant cell type found in wound granulation tissue, but they play a major role in fibroproliferative diseases when unregulated. Myofibroblasts are more biosynthetic in nature than the fibroblasts and are capable, due to activation of myosin light chain kinase and Rho kinase, of both rapid contraction and a more sustained contraction, respectively. *In vivo*, the myofibroblast is a transient cell type and is normally activated upon connective tissue injury. A combination of TGF- β 1 and extra domain A fibronectin [132–134] induces the transformation of proto-myofibroblasts into myofibroblasts (fig. 7). TGF- β induces α -smooth muscle actin (α SMA) and smooth muscle protein 22- α (SM22 α) *via* interactions with the TGF- β controlling element and two serum response element regions in the α SMA promoter of fibroblasts [135]. THANNICKAL *et al.* [136] reported that expression of a stable myofibroblast phenotype is dependent upon both TGF- β - and adhesion-dependent signals. Inhibition of TGF- β 1-induced phosphorylation of focal adhesion kinase on tyrosine 397, a cell adhesion-dependent event, resulted in inhibition of α SMA expression. TGF- β 1 was found to increase integrins α 4, α 5 and β 1 as well as fibronectin in human lung fibroblasts. The authors proposed that TGF- β -induced fibroblast differentiation occurs *via* a Smad-mediated, adhesion-independent signalling pathway followed by a delayed adhesion-dependent pathway involving focal adhesions that are essential for maintenance of the phenotype. Studies of wound healing suggest that myofibroblast disappearance occurs *via* apoptosis [137]. TGF- β promotes the transformation from fibroblast to myofibroblast

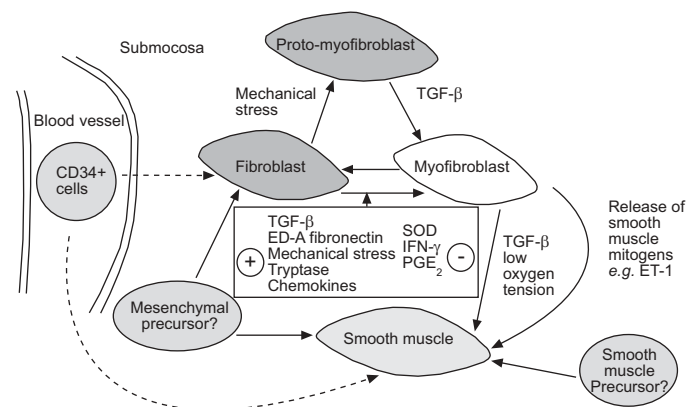


FIGURE 7. Although the established dogma describes fibroblasts transforming into myofibroblasts under the influence of transforming growth factor (TGF)- β , there are reports of other precursor cells and a number of other inducers of the myofibroblast phenotype. There is also some evidence to suggest that myofibroblasts may act as smooth muscle precursors. ED-A: extra domain A; SOD: superoxide dismutase; IFN- γ : interferon- γ ; PGE₂: prostaglandin E₂; ET-1: endothelin-1.

as well as enhancing the survival of myofibroblasts by inhibiting interleukin (IL)-1 β -induced apoptosis [138].

The cytokines IL-4 and -13 have been reported to induce the myofibroblastic phenotype in a time- and dose-dependent manner [139, 140]. However, RICHTER *et al.* [35] demonstrated that IL-4 and -13 were relatively ineffective in promoting myofibroblast transformation directly, although transformation was effective through IL-4 or -13-mediated TGF- β_2 release from epithelial cells [35]. *In vivo*, the myofibroblast is only present transiently. VOZENIN-BROTONS *et al.* [141] reported that addition of superoxide dismutase to porcine dermal myofibroblasts reduced the levels of α SMA and collagen production, an event not associated with an increase in cell death. Interferon- γ (IFN- γ) has been implicated in preventing the generation of myofibroblasts and can also moderately inhibit the production of α SMA in TGF- β -induced myofibroblasts [142, 143]. Prostaglandin E₂, signalling *via* E prostanoid receptor 2, has also been reported to prevent the TGF- β -induced fibroblast undergoing myofibroblast transition in primary foetal and adult lung fibroblasts [144].

The accepted view is that myofibroblasts are derived from fibroblasts. A recent study, however, has identified another potential source of myofibroblasts. SCHMIDT *et al.* [145] suggest that bronchial myofibroblasts can originate from fibrocytes, blood-borne cells that can home to sites of tissue damage (fig. 7). These cells are CD34+, express both collagen I and α SMA, and localise to areas of collagen deposition below the epithelium. By tracking labelled circulating fibrocytes in a mouse model of allergic asthma, the authors showed that fibrocytes are recruited into the bronchial tissue following allergen exposure and differentiate into myofibroblasts.

The potential involvement of fibrocytes in airway remodelling in asthma has been further highlighted in a study by LARSEN *et al.* [146] who found activated and mobile fibroblasts in BAL fluid of subjects with mild asthma.

In addition to induction of myofibroblast differentiation and deposition of ECM proteins, TGF- β also has a role in fibroblast proliferation. TGF- β has been reported to have different effects on the proliferation of fibroblasts DUBE *et al.* [55] reported that TGF- β_1 had no significant effect on bronchial fibroblast proliferation. KAY *et al.* [147] reported that corneal stromal fibroblasts produce fibroblast growth factor-2 in response to TGF- β , and this is suggested to be a direct stimulator for TGF- β -mediated cell proliferation. It was further reported by THANNICKAL *et al.* [148] that TGF- β_1 (2 ng·mL⁻¹) upregulated fibroblast growth factor R-1 and -2 in a time-dependent manner, thus contributing to the proliferative response. MCANULTY *et al.* [149] also demonstrated that TGF- β (5 pg·mL⁻¹) could stimulate fibroblast proliferation.

TGF- β -treated fibroblasts also have indirect effects on inflammation by releasing a number of chemoattractants. For example, release of eotaxin in response to TGF- β and IL-13 can act as a chemoattractant for eosinophils [150]. TGF- β -induced CCL-2 (monocyte chemoattractant protein-1) acts as a chemoattractant for monocytes [151]. TGF- β is also reported to induce fibroblast-like synoviocytes from rheumatoid arthritis and osteoarthritis patients to induce CXCL-8 (IL-8), a neutrophil attractant, and CCL-3 (macrophage inflammatory

protein 1- α) mRNA which can recruit monocytes, macrophages and T-cells [152].

RELATIONSHIP BETWEEN TGF- β AND AIRWAY SMOOTH MUSCLE

Smooth muscle is primarily under the control of the autonomic nervous system and can develop an isometric force per cross-sectional area equal to skeletal muscle, although the speed of contraction is much slower than skeletal muscle. Airway smooth muscle plays a major role in the pathophysiology of a number of airway diseases, including asthma. As described previously, the smooth muscle layer in asthma is significantly increased in size due to hyperplasia and possibly hypertrophy. In addition to its role as regulator of bronchomotor tone, smooth muscle can also secrete cytokines and growth factors, thus contributing to the inflammation and remodelling of the airways.

It has been proposed that TGF- β_1 and TGF- β_2 are responsible for the conversion of myofibroblasts into smooth muscle cells (fig. 7). Microarray analysis of foetal lung fibroblasts have shown that TGF- β can induce expression of a number of smooth muscle-specific genes, including smooth muscle myosin heavy chain, basic calponin and smoothelin [153]. However, expression of some of these genes appears to be further regulated at the translational level [154]. Furthermore, there is evidence that rabbit bladder myofibroblasts are able to transform into smooth muscle cells after treatment with TGF- β for 21 days [155]. The smooth muscle transition has also been reported to occur independently of TGF- β . For example, a study by JONES and JACOBSON [156] identified interstitial rat lung fibroblasts as the source of perivascular smooth muscle cells in response to low oxygen levels.

It is possible that the role of TGF- β is to induce the expression of smooth muscle mitogens, such as endothelin-1 [35], and thus play a more indirect role in smooth muscle differentiation. Alternatively, YEH *et al.* [157] demonstrated that adult peripheral blood CD34+ cells can transdifferentiate into smooth muscle cells *in vivo*, and that this is augmented significantly by local tissue injury.

ROLE OF TGF- β AND EXTRACELLULAR MATRIX FORMATION

Activated smooth muscle cells and fibroblasts can release ECM proteins in response to TGF- β . For example, TGF- β induces α_1 collagen I mRNA and α_2 collagen protein in human lung fibroblasts [158]. EICKELBERG *et al.* [159] showed that the percentage of collagen deposited in the ECM was higher in TGF- β_1 -treated human lung fibroblasts compared with controls. TGF- β_1 has also been shown to stabilise tropoelastin mRNA in human foetal lung fibroblasts [160].

TGF- β also has indirect effects through the upregulation of inhibitors of ECM proteases, such as plasminogen activator inhibitor-1 (PAI-1) [161], TIMP-1 [162] and TIMP-3, [163], and the downregulation of degrading ECM proteases, such as interstitial collagenase [164].

INVOLVEMENT OF TGF- β IN ASTHMA

Increased TGF- β immunoreactivity is found in mucosal bronchial biopsies from asthmatic subjects compared with

controls [165, 166]. Indeed, a significant correlation has been found between the number of epithelial or submucosal cells expressing TGF- β in asthma and the thickness of the basement membrane and fibroblast number. Elevated phosphorylated Smad-2 levels have been demonstrated in bronchial biopsies obtained from asthmatic subjects [167], indicating that TGF- β signalling downstream from the receptor is also enhanced in asthma.

CHU *et al.* [168] reported that unstimulated bronchial epithelial cells express five times more TGF- β_2 than TGF- β_1 . Although no differences in TGF- β_1 expression were observed between normal and asthmatic bronchial epithelial cells, there were significantly higher amounts of TGF- β_2 protein in asthmatic compared with normal epithelial cells. TGF- β_2 was shown to induce MUC5AC mRNA and protein *in vitro*, although interestingly TGF- β_1 did not induce mucin expression.

TGF- β_1 is released in higher amounts in basal and allergen-challenged sites in the BAL fluid of asthmatic patients [169] than in controls [170]. Although TGF- β_1 levels are raised in the plasma of nonatopic asthmatics, this is not seen in atopic asthma [171]. TGF- β_1 levels are also increased in eosinophils from severe asthmatics at the mRNA level [172, 173]. Recently, BALZAR *et al.* [174] reported that there were more TGF- β_2 positive cells in endobronchial tissue biopsies from eosinophilic severe asthmatics. Furthermore, the tissue eosinophils from eosinophilic severe asthmatics constantly co-localised with the TGF- β_2 -positive cells. Alveolar macrophages from asthmatic subjects also release greater amounts of TGF- β compared with control subjects [165].

TGF- β has been implicated as a key mediator in asthma, responsible for a number of remodelling events. Four polymorphisms of TGF- β have been identified. A single polymorphism (C/T at position -509) in the TGF- β_1 promoter has been linked to elevated TGF- β_1 plasma levels [175] and IgE levels [176]. A later study by SILVERMAN *et al.* [177] has revealed that the T allele of C-509T is associated with the diagnosis of asthma and may increase transcription by altering TGF- β promoter-reporter activity by interacting with the transcription factor Yin Yang 1. PULLEYN *et al.* [178] demonstrated that there is a greater relative frequency of homozygosity for this allele in severe asthmatics compared with a control group. Conversely, BUCKOVA [179] showed that the polymorphism was not linked to elevated IgE levels in the Czech population.

A mouse model has been described where BALB/C mice were intratracheally instilled with either TGF- β_1 or buffered saline [180]. An increase in collagen I and III mRNA was seen in the airways after 1 week and an increase in total collagen was detected after a month following TGF- β treatment. There was also a detectable increase in airway hyperreactivity in the growth factor-treated mice, thus highlighting the importance of TGF- β in the pathogenesis of remodelling.

TGF- β AS A THERAPEUTIC TARGET

Due to the physical nature of TGF- β , mature growth factor is bound in close proximity to the cell, attached to binding proteins within the ECM. As a result, increased production of TGF- β will affect only those cells in the nearby vicinity.

Experiments on adult skin revealed that TGF- β mRNA is induced in response to wounding, whereas no upregulation was detected in human foetal skin under similar conditions. This explains why foetal wounds heal without the deposition of scar tissue. SHAH *et al.* [181] demonstrated that treating dermal wounds in adult rats with a neutralising TGF- β antibody prevented the formation of scar tissue. In a later study, SHAH *et al.* [182] showed that administration of anti-TGF- β_1 or anti-TGF- β_2 antibodies to wounds could increase wound-healing time and reduce scarring, as can addition of TGF- β_3 directly to wounds. Anti-TGF- β_2 antibodies have also been utilised in the field of conjunctival scarring and significantly improved glaucoma filtration surgery outcome in animal models [183].

A number of small molecule inhibitors of the type I TGF- β receptor have been identified. For example, SB-431542 inhibits TGF- β_1 -induced Smad-3 translocation to the nucleus, as well as inhibiting TGF- β_1 -induced fibronectin mRNA and collagen $\text{I}\alpha_1$ induction in renal epithelial carcinoma A498 cells [184]. More recently another type I TGF- β receptor, SB-505124, has been shown to display three to five times the potency of SB-431542 [185] against ALK5, as well as concentration-dependently inhibiting the activity of ALK4 and ALK7.

A novel small compound, SMP-534, has been shown to reduce ECM production induced by TGF- β in normal rat kidney fibroblasts [186]. SMP-534 selectively inhibited TGF- β -induced p38 MAPK activation, but did not inhibit EGF-induced extracellular regulated protein kinase-2 (ERK) activation. Encouragingly, in a rat anti-Thy-1 nephritis model, oral administration of SMP-534 dose-dependently lowered hydroxyproline levels in the cortex. SMP-534 or a similar drug may have a therapeutic benefit in the asthmatic lung, acting to reduce TGF- β -mediated fibrosis associated with airway remodelling without suppressing EGF-mediated restitution of the injured epithelium.

Inhibition of TGF- β signalling may be a beneficial target in asthma. In theory it would have far reaching effects in reducing remodelling by lifting the inhibition on epithelial proliferation, preventing myofibroblast transformation, repressing the proliferative effect on myofibroblasts and inhibiting the excessive production of ECM components. A potentially negative effect would be the alleviation of immunosuppression and thus the possible accentuation of inflammation. Epithelial cells release TGF- β in order to initiate cellular migration in the process of epithelial repair. Therefore, an inhibition of this process may be detrimental to airway remodelling.

MODULATION OF TGF- β AND DOWNSTREAM EFFECTS

NOGAMI *et al.* [187] reported that TGF- β_1 decreased the number of β -adrenoceptors on human tracheal smooth muscle cells. TGF- β treatment partially suppressed the β_2 -agonist stimulated increase in cAMP, an observation that may explain the defective relaxation to β_2 -agonists shown by some asthmatics. ISHIKAWA *et al.* [188] showed that IFN- γ could suppress this TGF- β response. Interestingly, mucosal adenoviral IFN- γ gene transfer can effectively attenuate established allergen-induced airway inflammation and airway hyperresponsiveness in ovalbumin-sensitised mice [189], although human trials have not been so successful [190].

Glucocorticosteroids are the mainstay therapy for the majority of mild to severe, persistent asthmatic subjects. Glucocorticoids exert an anti-inflammatory effect, but can also have an anti-fibrotic action (for a review see SHUKLA *et al.* [191]) by decreasing collagen synthesis. Dexamethasone, for example, has been shown to block TGF- β -induced collagen synthesis in rats [192]. In a murine model of prolonged allergen challenge [193], budesonide was shown to regulate TGF- β signalling by reducing phospho-Smad-2 expression and increasing Smad-7 in lung tissue.

In human samples, WEN *et al.* [194] reported a significant inhibition of TGF- β_1 and TGF- β_2 production and a reduced expression of autoinduced TGF- β_1 and TGF- β_2 mRNA in response to glucocorticoid treatment in human foetal lung fibroblasts. Furthermore, flunisolide can decrease TGF- β and fibronectin release from mild-to-moderate asthmatic sputum cells cultured for 24 h [195].

Connective tissue growth factor (CTGF) is a potential target to combat the remodelling seen in asthma. CTGF is considered to be an immediate early gene for TGF- β [196]. CTGF antisense constructs and neutralising antibodies have been reported to block the effect of TGF- β on fibroblast collagen production and proliferation [197–199]. CTGF is also profibrogenic *per se*, for example, it can stimulate collagen I, fibronectin and α_5 integrin expression in NRK cells [200], as well as inducing lysyl oxidase and collagen in human gingival cells [201]. Recently, it has been reported that the N-terminal domain of CTGF mediates myofibroblast differentiation and collagen synthesis, while the C-terminal domain of CTGF regulates fibroblast proliferation [202].

In 2003, BURGESS *et al.* [203] reported that the fold induction of CTGF in response to TGF- β was greatest in the airway smooth muscle cells isolated from asthmatic subjects, and that the induction occurred earlier, in comparison to nonasthmatic airway cells. A study by KUCICH *et al.* [204] suggested the possible use of protein kinase C inhibitors in suppressing CTGF levels. Protein kinase C was found to phosphorylate Smad-3 directly, inhibiting its ability to bind DNA and enhance transcription.

FU *et al.* [205] demonstrated that both the natural ligand (15-deoxyprostaglandin J [2]) and a synthetic ligand (GW7845) for the peroxisome proliferator-activated receptor gamma (PPAR- γ) could significantly inhibit TGF- β -induced CTGF production in a dose-dependent manner in human airway smooth muscle cells. It was further reported that PPAR- γ could physically interact with Smad3, highlighting a potential mechanism of action for the ligand. More recent studies have shown that PPAR- γ ligands can prevent TGF- β_1 -induced fibronectin in mesangial cells [206] and skin fibroblasts [207].

Ligands for PPAR- γ represent important anti-fibrotic targets, which potentially could be manipulated in asthma. For example, in a murine asthma model, ciglitazone, a synthetic PPAR- γ agonist used in the treatment of diabetes, inhibited a number of remodelling events [208]. Specifically, ciglitazone nebulisation reduced mucus gland hyperplasia and airway occlusion caused by the mucus hypersecretion. Increases in collagen levels and basement membrane thickness were suppressed and TGF- β levels were decreased by 54%.

Additionally, ciglitazone has been shown to decrease both eosinophil numbers and T-helper cell type-2 cytokine (IL-4, IL-5 and IL-13) levels in murine airways [209]. Natural and synthetic ligands of PPAR- γ can also inhibit serum-induced smooth muscle proliferation more effectively than dexamethasone, as well as inhibiting the release of GM-CSF, a survival factor for leukocytes [210].

Interestingly, PPAR- γ expression is increased in the submucosa, smooth muscle layer and epithelium of bronchial tissue in asthmatics [211]. Indeed, TGF- β can indirectly activate cytosolic phospholipase A2alpha (cPLA2- α), *via* p38 and ERK activation, resulting in activation of PPAR- γ activation [212] in human liver epithelial cells. HAN *et al.* [212] demonstrated that overexpression of cPLA2- α or PPAR- γ could block TGF- β_1 -induced Smad transcriptional activity. Both Smad-7 and PPAR- γ therefore act as negative feedback pathways and further elucidation of the pathways in asthma may yield exciting new targets to combat remodelling.

A novel approach to combating the TGF- β -induced fibrotic response is the use of the human pregnancy hormone, relaxin. Relaxin has been shown to inhibit the TGF- β -induced expression of both collagen and fibronectin in human lung fibroblasts, as well as inducing levels of MMP-1 [213]. The hormone also stimulated wound healing of bronchial epithelial cells *in vitro* [214] and, in a murine model, relaxin restored bleomycin-induced collagen accumulation back to normal levels [213].

A QUESTION OF BALANCE

This review has appraised the actions of TGF- β in the airways and other tissues. However, it would be a naive to suppose that TGF- β is the only fibrotic mediator in the airways or even that in the milieu of growth factors present in the lung that it was solely responsible for fibrosis associated with remodelled asthmatic airways. The actions of TGF- β are controlled not only by the expression levels of this growth factor in the lung and the ability of cells to respond to this signal, but also on the balance of fibrotic *versus* anti-fibrotic factors produced as a result of wound healing.

TGF- β can interact with a large number of different growth factors and cytokines in the lungs, each affiliation mediating a different outcome. Attempting to unscramble the interconnecting pathways of only two growth factors among the thousands of potential couplings that exist in the plethora of growth factors in the lung is a daunting task. The current authors have focussed on the interactions between TGF- β and EGF chosen because of their much published and often opposing actions in proliferation and differentiation.

EPIDERMAL GROWTH FACTOR RECEPTOR

EGFR (ErbB1), a member of the ErbB family, is expressed on the majority of cell types, including fibroblasts and epithelial cells of the respiratory tract. The receptors have a restricted expression pattern in polarised lung epithelial cells, with ErbB receptors expressed basolaterally and, thus, are exposed only after epithelial damage. Immediately following a mechanical injury, ErbB ligands can activate EGFR [215] or ErbB2 [216] at the edge of the wound, thus hastening the restoration of epithelial integrity. Mammalian ligands for the EGFR include

EGF, TGF- α , amphiregulin, betacellulin, heparin-binding epidermal growth factor-like growth factor (HB-EGF), epiregulin and epigen [217]. A number of EGFR ligands are present in all cell types, although the expression profile of the individual ligands varies. For example, HB-EGF, amphiregulin and EGF have a widespread tissue distribution pattern, although TGF- α is expressed mainly in epithelial cells, macrophages and eosinophils. Immunolocalisation studies have revealed that EGF is primarily expressed in bronchial glands [218, 219], although there is weak expression in the bronchial epithelium and smooth muscle [220]. Interestingly, stronger EGF immunoreactivity has been demonstrated in the bronchial epithelium, glands, smooth muscle [220] and submucosa [165] of asthmatic subjects compared with nonasthmatics. TGF- α , amphiregulin, betacellulin and HB-EGF expression has also been observed in airway epithelium, but does not differ in asthma [221].

FUNCTIONS OF EGFR LIGANDS

Proliferation is the most well studied function of EGFR signalling. All of the EGFR ligands are capable of promoting mitogenesis, although their potency is dependent on cell type. For example, amphiregulin induces proliferation of epithelial cells, whereas HB-EGF is a potent smooth muscle mitogen. EGFR ligands can also promote a migratory phenotype in cells, a response clearly illustrated by EGF. For example, EGF can enhance the repair of the mechanically damaged monolayers of bronchial epithelial cells [215]. EGF-dependent cell motility is regulated by phospholipase c - α activation [222, 223] and MAPK activation [224]. EGF can stimulate the disassembly of focal adhesions and alter components of the adherens [225] and desmosomal junctions, thus decreasing cell-cell contact and contributing to cell motility [226]. Therefore, TGF- β and EGF can have opposing roles in terms of proliferation, but similar roles in terms of migration.

The TGF- β and EGF signalling pathways are not discrete pathways as they share many downstream signalling molecules. TGF- β and EGF can both mediate distinct cellular events *via* activation of ERK1 and ERK2 and, as a result, TGF- β can act synergistically, antagonistically or independently to EGF signalling. There are a number of reported examples of cross-talk between the two pathways at the level of receptor-ligand interactions. A study by THOMPSON *et al.* [227] using normal rat kidney fibroblasts indicated that TGF- β was capable of increasing expression of EGFR. Conversely, DANIELPOUR *et al.* [228] showed that stimulation by EGF in the same cell type could induce the secretion of TGF- β ₁. TGF- β can also regulate expression of other members of the EGF family. For example, a study by BENNETT *et al.* [229] showed that TGF- β treatment reduces the level of expression of amphiregulin in the human lung adenocarcinoma cell line A549.

TGF- β and EGF are known to mediate a number of different cellular events, including growth, migration and branching morphogenesis of the lung. MISHIMA *et al.* [230] demonstrated that TGF- β could antagonise EGF-induced attachment of cells onto a fibronectin matrix, migration over corneal stroma, and proliferation of corneal epithelial cells. TGF- β was also found to inhibit the EGF-induced filopodia extension associated with migrating human bronchial epithelial cells [231]. Both TGF- β and EGF can control lung branching in the developing foetus. TGF- β causes growth arrest of the developing airways

[232–235], whereas EGF has been reported to cause significant elongation of the bronchial tubes [236]. In combination, TGF- β promotes cell arrest, allowing EGF to induce branching in the outgrowing terminal buds.

These examples show how the action of TGF- β can influence EGF-signalling pathways and *vice versa* in a number of ways. Regulation of the pathways occurs at a number of different levels and the signalling outcome is dictated by the relative balance between the TGF- β and EGF signalling pathways. No signalling-mediated event can occur in isolation in the cell, but the TGF- β -EGF axis is distinct in its degree of overlap, especially when the antagonistic nature of the two growth factors is taken into consideration. The balance between EGF-driven proliferation and TGF- β -mediated differentiation of fibroblasts is therefore of potential importance in the pathogenesis of airway remodelling in asthmatics.

EPIDERMAL GROWTH FACTORS AND ASTHMA

EGFR, ErbB2 and ErbB3 receptors are expressed in the epithelium of the upper and lower airways, as well as in primary cultures of human bronchial epithelial cells and human bronchial epithelial derived cell lines, such as H292 and 16HBE 14o- [217, 219]. In asthma, it has been observed that the expression of EGFR is increased on the remaining epithelial cells around the site of damage, and on the apical side of the exposed basal cells [219]. EGFR expression levels are increased in asthma and correlate to disease severity [215]. This increase in EGFR expression is a typical response to tissue injury; however, in asthma there is no evidence that this is coupled with an increased proliferative response [16]. Furthermore, EGFR expression is insensitive to the effects of corticosteroids [215, 237].

Increased expression of EGFR ligands has been reported in asthmatic airways. AMISHIMA *et al.* [220] reported that EGF was expressed at higher levels in the bronchial epithelium and glands of asthmatic subjects compared with normals. Additionally, TGF- α release was enhanced in asthmatic epithelial cells in response to pro-inflammatory cytokines, in particular tumour necrosis factor- α and combinations of IL-4, IL-13 and allergen [238].

VARGAFTIG and SINGER [239] demonstrated that AG1478, an EGFR antagonist, could inhibit bronchial hyperresponsiveness, inflammation and lung remodelling induced by ovalbumin in a murine model. EGF and TGF- α have been implicated in induction of MUC5AC expression, a mucin released from goblet cells, *via* activation of the EGFR/Ras/Raf/ERK-signalling pathway [240]. TAKEYAMA *et al.* [241] demonstrated a positive correlation between EGFR immunoreactivity and the area of MUC5AC-positive staining. Increased release of EGFR ligands into the luminal space, such as EGF, coupled with increased EGFR expression, may account for the increase in mucus secretion by asthmatic epithelial cells.

The inflammatory cell profile in severe asthma is characterised by high numbers of circulating neutrophils. HAMILTON *et al.* [242] demonstrated that damage to the epithelium has the potential to contribute to neutrophilic inflammation through enhanced production of CXCL-8 (IL-8) *via* EGFR-dependent mechanisms, which again are insensitive to corticosteroids.

MODULATION OF EGFR EXPRESSION IN ASTHMA

β_2 -agonists can stimulate cAMP release, causing activation of protein kinase A and subsequent serine phosphorylation of the EGFR [243]. Phosphorylation of serine residues on the EGFR deactivates the receptor, thus preventing signalling downstream from the receptor. Additionally, KIMURA and OGIHARA [244] showed that increasing concentrations of the β_2 -agonist metaproterenol markedly reduced the proliferative effects of TGF- α in adult rat hepatocytes. These observations provide an example where a pre-existing therapy could indeed be counter-productive and prevent epithelial repair in the airways of asthmatics.

Studies have revealed that corticosteroids do not alter either EGFR expression [215] or activation [237]. A study by KIBE *et al.* [245] reported that corticosteroid treatment inhibited eotaxin expression and eosinophil accumulation, but had no effect on airway hyperresponsiveness, MUC5AC overexpression, or goblet cell hyperplasia induced by IL-13 in a murine model. Corticosteroids have also been shown to have no effect on the expression of p21waf expression, a cyclin-dependent kinase inhibitor.

EGF/EGFR AS A NOVEL THERAPEUTIC TARGET IN CHRONIC ASTHMA

EGFR can regulate mucin production in the airways [246]. A treatment whereby secretion is reduced would be beneficial to the asthma sufferer, although complete inhibition of mucus secretion may indeed be counter-productive. Controlled mucus secretion plays a protective role in the innate immune system and helps to eliminate airborne allergens *via* ciliary action. Inhibitors of EGFR would potentially also suppress EGFR-mediated signals needed to initiate repair of the damaged epithelium, evident in asthmatic airways. Therefore, targeted downstream interventions may be appropriate.

A number of studies have concentrated on the effect of blocking nonreceptor tyrosine kinases in inflammatory cells (as reviewed by WONG and LEONG [247]). Binding of allergen to immunoreceptors causes stimulation of nonreceptor tyrosine kinases, such as Lyn, Lck, Syk and Fyn. Use of both nonselective and selective tyrosine kinase inhibitors can induce a number of beneficial effects. For example, the Jak-3-specific inhibitor WHI-P97 was reported to suppress leukotriene synthesis, airway hyperresponsiveness and recruitment of eosinophils after ovalbumin challenge in a mouse model [248]. However, in some cases, inhibition of tyrosine kinases can be counter-productive, *e.g.* Lck is also required for downregulating TCR expression by increasing the internalisation and degradation of receptors [249].

CONCLUDING COMMENTS

Transforming growth factor- β is a potent fibrogenic growth factor, which is overexpressed in the asthmatic lung. The growth factor appears to play an essential role in mediating the fibrosis associated with the remodelled airways of asthmatics. In addition to transforming growth factor- β , abnormal epidermal growth factor receptor function may account for the excess mucus production in asthma. However, it is likely that the ultimate response *in vivo* will not depend solely on the balance between pro-fibrogenic and anti-fibrogenic growth factors.

Although complete ablation could cause a whole host of new problems, as is shown in knockout mice, restoration of the balance between different growth factors may be of therapeutic benefit, for example, through the use of neutralising antibodies. Hopefully, the fuller comprehension of how signalling pathways interact in the asthmatic lung can be manipulated to provide novel therapeutic targets to combat the remodelling and maybe attenuate the chronic inflammation, so intimately linked to the altered structure of the lungs.

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