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Epithelial-Mesenchymal Transition Contributes to Pulmonary Fibrosis via Aberrant Epithelial/Fibroblastic Cross-Talk

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Abstract

Idiopathic pulmonary fibrosis (IPF) is the prototypic progressive fibrotic interstitial lung disease. Median survival is only 3 years, and treatment options are limited. IPF is thought to be a result of a combination of genetic and environmental factors with repetitive micro-injuries to alveolar epithelial cells playing a central role. IPF is characterised by aberrant extra cellular matrix (ECM) deposition by activated myofibroblasts. Epithelial-mesenchymal transition (EMT) is a process where polarised epithelial cells undergo molecular changes allowing them to gain a mesenchymal phenotype, with a subsequent enhanced ability to produce ECM components and increased migration and/or invasion. The source of myofibroblasts in IPF has been debated for many years, and EMT has been proposed as a source of these cells. However, lineage tracing in transgenic mice suggests the contribution of epithelial cells, which have undergone EMT, to the fibroblast population may be negligible. Instead, recent findings suggest that alveolar epithelial type II (ATII) cells undergoing EMT promote a pro-fibrotic microenvironment through paracrine signalling activating local fibroblasts. This review paper explores the contribution of ATII cells, which have undergone EMT, in the context of pulmonary fibrosis.

Introduction and Discussion

Idiopathic pulmonary fibrosis (IPF)

IPF is a chronic, progressive and fibrotic lung disease of unknown cause, which typically occurs in older adults. Alveolar architecture is destroyed and healthy tissue is replaced by altered extra cellular matrix (ECM), with progressive dyspnoea and impairment of lung function ultimately leading to death[1,2]. IPF is the most common type of idiopathic interstitial pneumonia and occurs with similar frequency to stomach, brain and testicular cancer[3]. Although the cause of IPF is unknown, interacting genetic and environmental factors are thought to play a role in its development[2]. Repetitive injury to aged alveolar epithelium is proposed to trigger aberrant wound healing processes, initiating an accumulation of ECM deposited by myofibroblasts[2]. Current approved therapies only slow IPF disease progression highlighting the need for better understanding of the disease process and the identification of new molecular targets.

Epithelial-mesenchymal transition (EMT)

EMT is a dynamic, reversible process which has been implicated in embryonic development, wound healing, cancer metastasis and fibrosis and is associated with an increased migratory and/or invasive ability[4]. The role of EMT in cancer is detrimental

whereas, in wound healing, EMT as a response to injury can be beneficial, however, if the wound healing process is exaggerated it may lead to fibrosis. During EMT, epithelial cells lose apical-basal polarity, tight and adherens junctions in favour of front-back polarity, N-cadherin junctions and vimentin stress fibres[4,5]. The change in morphology is accompanied by molecular change initiated by several pathways and signalling factors which regulate expression of transcription factors (EMT-TFs), including Snail, ZEB, Twist and others[6]. Pleotropic signalling factors such as transforming growth factor β (TGFβ), fibroblast growth factor (FGF), Wnt/β-catenin and epidermal growth factor (EGF) can initiate EMT, in turn, these factors regulate expression of EMT-TFs. These promote the repression of epithelial features by suppressing E-cadherin expression, and induction of mesenchymal features, in part, through the activation of mesenchymal genes N-cadherin, vimentin and fibronectin, which are responsible for cell-cell adhesion, cell motility, and migration[6–11].

Induction of EMT in fibrosis has been linked to a variety of processes including endoplasmic reticulum (ER) stress, smoking, Epstein Barr virus protein LMP1 (latent membrane protein 1)[12–14] and EGF receptor (EGFR) signalling[15]. A number of studies have implicated EGFR activation[16–18], mutations[19] and increased expression[20] in IPF patients. An increase in transforming growth factor α (TGFα) and EGFR in rats with bleomycin-induced lung injury[16] has been observed. TGFα was also increased in response to asbestos and hyperoxia[17,18]. Transgenic mice that constitutively express TGFα develop progressive and severe lung fibrosis[21], chronic expression of TGFα in new born transgenic mice resulted in remodelling of lung during postnatal alveolarisation resulting in pulmonary fibrosis[22]. Further, mice treated with inhibitors of the EGFR pathway display resistance to bleomycin-induced fibrosis[23]. Gene network analysis of publicly available microarray data (GSE24206) of IPF and control lung tissue has identified the EGFR-ERK pathway to be a top-ranked pathway[15]. Further, RAS signalling is a key pathway downstream of EGFR activation and RAS activation has been demonstrated to induce EMT in other contexts[24,25]. Together, these results highlight the potential importance of EGFR activation in IPF. Elucidating the downstream mechanisms and processes which could be activated as a result of this, may provide new targets for treatment. Of relevance to IPF is the demonstration that EGFR activation induces EMT in ATII cells, where they undergo a change in morphology, with reorganisation of actin cytoskeleton, accompanied by an increase in vimentin, ZEB1 and a reduction in E-cadherin[15]. It has been demonstrated through inhibition of AKT or ERK that RAS activation induces EMT in ATII cells via ERK pathway. Further, RNA interference (RNAi)-mediated knockdown of EMT-TFs confirmed that RAS-induced EMT in ATII cells is specifically via ZEB1[15]. Consistent with this, analysis of human IPF lung tissue demonstrates that in comparison with control lung tissue, strong nuclear staining of ZEB1 is present in fibroblast foci[15,26,27] and also in epithelial cells of thickened alveoli septae, where collagen deposition in the interstitium is evident[15].

Contribution of EMT to pulmonary fibrosis

In the distal region of the lung there are two types of alveolar epithelial cells; type I and type II, with the first providing thin-walled gas-exchange surface and the latter functions as stem cells, contributing to alveolar renewal and repair[28]. The origin of myofibroblasts in IPF is controversial but it has been proposed that ATII cells that have undergone EMT may be a source of myofibroblasts in fibrosis. Myofibroblasts are understood to be critical in the pathogenesis of IPF, with increased fibroblast foci associated with worse prognosis[29].

Human IPF tissue demonstrated co-localisation of epithelial and mesenchymal markers[26,27,30–32]. Laser capture microdissection has also been performed to isolate RNA from epithelial cells in IPF lungs which confirmed expression of mesenchymal markers by epithelial populations[33], suggesting that EMT may contribute to the mesenchymal population. However, in mouse models of lung fibrosis, the conclusions of lineage tracing studies investigating the contribution of EMT to the mesenchymal population have been varied. Several studies have suggested that EMT may contribute to the pathogenesis of IPF *in vivo*[34-39]. Conversely, other lineage tracing studies found relatively small numbers of fibroblasts arise from epithelial cells[40,41]. In addition, it was shown that α-smooth muscle actin (α-SMA) did not co-localise with EMT-derived cells, suggesting that although they may have undergone EMT, they did not transition to myofibroblasts[36,37]. Similarly, we reported that ATII cells which have undergone RAS-induced EMT produce extremely low levels of ECM genes[15]. Thus, the significance of EMT and these cells' ability to contribute towards the mesenchymal population are still somewhat controversial.

Studies in renal fibrosis have proposed that tubular epithelial cells are able to promote myofibroblast differentiation and fibrogenesis without directly contributing to the population by relaying signals to the interstitium. It was demonstrated that reactivation of Snail1 in renal epithelial cells was required for the development of fibrosis in the kidney. In a murine model, damage-mediated Snail1 reactivation induced EMT but these cells did not contribute to myofibroblast or interstitial cell population. Epithelial cells which have undergone EMT did subsequently relay signals to the interstitium to promote myofibroblast differentiation and fibrogenesis[42]. In mouse models of experimentally induced renal fibrosis, *Snai1* or *Twist1* deletion led to inhibition of EMT, while restoring

proliferation, repair and regeneration ultimately attenuated interstitial fibrosis[43]. In renal fibrosis TGFβ induces EMT via Snail1 (*SNAI1*), in turn, this induces TGFβ expression generating an autocrine loop sustaining myofibroblast differentiation[42]. Snail1 has also been demonstrated to be up-regulated in mouse models of acute liver fibrosis during tissue remodelling[44].

In the context of pulmonary fibrosis, it has also been reported that ATII cells appear to promote fibrogenesis without direct contribution to the population. We demonstrated that conditioned media (CM) from RAS-activated ATII cells was able to potentiate fibroblast activation in the presence of TGFβ, which could be produced as a result of damage to alveolar epithelial cells. RNAi-mediated knockdown of ZEB1 abolished the effects of the RAS-activated CM on fibroblast, therefore ZEB1 was demonstrated to be a key regulator of the paracrine signalling between alveolar cells and fibroblasts[15]. Further, it was determined that ZEB1 controls tissue plasminogen activator (tPA) expression, which subsequently affects fibroblast activation induced by TGFβ[15]. tPA has previously been identified in the context of kidney fibrosis and was shown to promote TGFβ-mediated α-SMA and type I collagen expression[45]. Quantitative analysis of CM from RAS-activated ATII cells identified secreted proteins, expression of these was then compared with a publicly available dataset[46] and 25 genes/proteins were identified in both. *PLAT* which encodes tPA was the most up-regulated in ATII cells, and was identified in this list. A ZEB1 binding site was identified in the promoter region of *PLAT*, mRNA expression of *PLAT* was increased upon RAS-activation and this was repressed by ZEB1 RNAi[15].

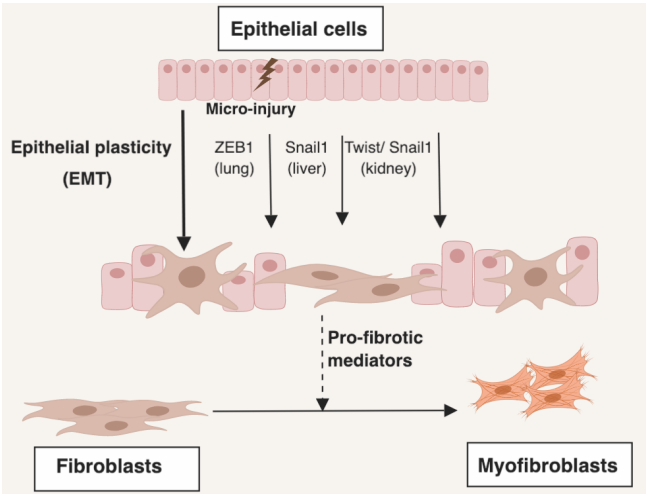

Figure 1: EMT of epithelial cells dysregulates signalling between epithelial and mesenchymal cells leading to a pro-fibrotic microenvironment. Repetitive micro-injury to epithelial cells creates a pro-fibrotic environment. A number of EMT transcription factors (EMT-TFs) have been demonstrated to induce EMT programs in a variety of tissues in the context of fibrosis. In pulmonary fibrosis, ZEB1 is responsible for RAS-induced EMT[15]. In the liver Snail1 has been demonstrated to induce EMT[44]. In the context of renal fibrosis, Snail1 and Twist1 have been demonstrated to induce EMT[42,43]. However, lineage tracing studies suggest these fibroblasts do not contribute significantly to the myofibroblast population[40,41]. These EMT-TFs do appear to mediate creating a pro-fibrotic microenvironment[15,42,43].

In both pulmonary and kidney fibrosis, it appears that although epithelial cells do not directly contribute to myofibroblast populations via EMT, they are able to promote myofibroblast differentiation through secreted factors (Figure 1), and that these could potentially be the source of novel targets of treatment.

Conclusion

Epithelial cells undergoing EMT produce relatively low levels of ECM and lineage-tracing studies have demonstrated that they do not significantly contribute directly towards the mesenchymal population. Recent studies have identified that across organs, EMT may instead promote a pro-fibrotic microenvironment by dysregulating paracrine signalling between epithelial and mesenchymal cells. Targeting EMT inducers might have therapeutic potential in fibrotic conditions, with such therapies currently undergoing development in the context of malignancy[47,48].

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