Epithelial–mesenchymal transition in lung development and disease: does it exist and is it important?

Domokos Bartis, Nikica Mise, Rahul Y Mahida, Oliver Eickelberg, David R Thickett

ABSTRACT

Epithelial–mesenchymal transition (EMT) is a process when epithelial cells gradually transform into mesenchymal-like cells losing their epithelial functionality and characteristics. EMT is thought to be involved in the pathogenesis of numerous lung diseases ranging from developmental disorders, fibrotic tissue remodelling to lung cancer. The most important question—namely what is the importance and contribution of EMT in the pathogenesis of several chronic lung conditions (asthma, COPD, bronchiolitis obliterans syndrome and lung fibrosis)—is currently intensely debated. This review gives a brief insight into the mechanism and assessment methods of EMT in various pulmonary diseases and summarises the recent literature highlighting the controversial experimental data and conclusions.

WHAT IS EPITHELIAL–MESENCHYMAL TRANSITION?

Epithelial–mesenchymal transition (EMT) is a process in which epithelial cells gradually acquire a mesenchymal (fibroblast-like) cell phenotype. EMT has been shown to be essential for embryonic development, gastrulation, and the development of the neural crest, heart and other organs. EMT is also implicated in tissue repair, organ fibrosis and cancer progression. EMT is associated with the progression of many type of tumours and is involved in their metastasis and treatment resistance.

CELLULAR CHANGES IN EMT

During EMT, epithelial cells undergo profound changes which can be categorised into four broad cellular functions: changes in transcriptional regulation; changes in cytoskeleton and motility; changes in cell adhesion; and changes in the synthesis of extracellular matrix (ECM) components.

Several transcription factors such as Snail, Slug, ZEB-1, ZEB-2, Twist, β-catenin and Tcf/LEF have been identified as key regulators of EMT, and are the ‘master switches’ important for cell reprogramming (figure 1).

Cytokeratins are the characteristic intermediate filaments in epithelial cells. During EMT cells are reprogrammed to express vimentin instead.

Other cytoskeletal changes involve de novo expression of fibroblast specific protein (FSP)-1 (also called S100A4) in the epithelium, which has been associated with increased migratory capacity, a more invasive phenotype in tumours and also worse prognosis in lung cancer. α-Smooth muscle actin (α-SMA) is also a frequently assessed marker in EMT. Expression of α-SMA is characteristic for myofibroblasts which are laying down an excessive amount of ECM and thus are responsible for tissue remodelling and fibrosis (figure 1).

Early molecular signs of EMT involve the dissociation of cell–cell junctions induced by downregulation and/or disassembly of junctional components, such as occludins, ZO-1, claudins and E-cadherin.

The gradual loss of E-cadherin—considered a hallmark of EMT—is accompanied by the simultaneous gain of N-cadherin, a mesenchymal marker. This change is commonly termed the ‘cadherin switch’ (figure 1).

Cells undergoing EMT also begin to synthesise ECM components like fibronectin and collagen type I.

ASSESSMENT OF EMT IN LUNG TISSUE

EMT is thought to be a gradual process, meaning that there are intermediate cellular phenotypes during the transition. An epithelial cell undergoing EMT will express a set of different marker genes during this process. Since changes in gene expression have also been detected during injury, activation or dedifferentiation of epithelial cells, it is obviously rather challenging to identify with certainty epithelial cells undergoing EMT in complex pathological conditions.

It is well established that during the physiological repair process following epithelial injury, loosening of epithelial–epithelial cell contacts (eg, tight junctions and adherent junctions), alteration of cell–ECM contacts, and cytoskeletal activation (migration) and morphological changes (spreading) occur during wound repair. These phenotypic changes are thought to be mediated by EMT transcription factors. However, we have to emphasise that during physiological wound repair mesenchymal markers expressed by epithelial cells do not necessarily mean transdifferentiation to fibroblasts or myofibroblasts. Although acquiring mesenchymal features and molecular markers, migrating epithelial cells in wound repair do not downregulate E-cadherin and tight junction proteins; there is rather an intercellular redistribution of these proteins.

There are numerous articles demonstrating that epithelial cells coexpress mesenchymal and epithelial markers in various lung diseases in humans.

Other methods commonly used to identify EMT are to show the activation of signalling pathways and transcription factors thought to regulate EMT. These mechanisms—for example, the activation of transcription factors of the Snail family and the...
consequent downregulation of E-cadherin—show striking similarities between fibrosis, developmental programmes involving EMT and carcinogenesis, suggesting a common molecular regulatory background is present. However, these experimental methods only provide a ‘snapshot’ of a process stretched over a period of time and thus are criticised for not being suitable to follow a dynamic process like EMT. To solve this ongoing controversy there is a need for methods which are able to track the transdifferentiation process more reliably, like intravital microscopy or cell fate mapping. Currently there are no publications available describing the use of intravital microscopy to evaluate EMT of lung epithelial cells in real time. Faulkner et al. found that kidney interstitial fibroblasts do not derive from tubular epithelial cells in renal fibrosis and it was described that activation of intrinsic transforming growth factor β (TGF-β) signalling is essential in blood-borne metastasis formation in breast cancer cells using in vivo imaging techniques.

However, the most important question remaining is whether EMT causally contributes to lung disease and, if yes, to what extent? Lung conditions with chronic inflammation and persistent injury result in scarring, fibrosis and tissue remodelling, leading to a decrease of lung function, respiratory failure and death. Recently, experiments using genetic cell fate tracking of lung epithelial cells were performed to address this issue in mouse models of lung fibrosis and allergic asthma. These studies found that approximately 30–50% of murine lung fibroblasts in lung fibrosis and allergic asthma were derived from epithelial cells which had undergone EMT as identified by genetic tagging. In these models, β galactosidase was used as a genetic label. Criticism of this method highlighted that the enzymatic reaction using X-gal and β galactosidase does not allow high-resolution confocal imaging contrary to fluorescent tags. Because of this, the borders between neighbouring cells are obscure and the possibility of false-positive identification of cells cannot be excluded. Additionally, these lineage-tracking studies used transgenic mice in which the recombination was driven by a 3.7 kb fragment of the human surfactant protein C (Sftpc) promoter, which is somewhat different from the endogenous murine Sftpc promoter which drives the recombination in other animal models. Also in vitro culture of alveolar epithelial cells (AECs) after isolation may result in experimental artefacts, which raises doubt as to whether EMT actually contributes to in vivo fibroblast formation.

Recently published data have challenged the idea that a significant fraction of myofibroblasts in the diseased lung derive from epithelial cells in animal models and humans. These contradictory results from different laboratories have resulted in an intensive debate on lung fibrosis, and kidney injury and liver fibrosis. Rock et al used a transgenic mouse strain with a
EMT IN LUNG DEVELOPMENT AND PAEDIATRIC DISEASES

The first EMT event described occurs in gastrulation—the earliest stage of embryonic development. During this process, the primary mesenchyme is formed, giving the first distinction between epithelial and mesenchymal phenotypes. The epithelial and mesenchymal cell phenotypes are not irreversible, and during embryonic development, cells can convert between the epithelial and mesenchymal states through the process of EMT or mesenchymal-to-epithelial transition (MET).36 37 Sometimes, several rounds of EMT and MET are required to give a rise to specialised cell types needed for organ formation. During development, EMT provides flexibility in cell fate; however, the development of specialised tissues during embryogenesis requires additional epithelial cell plasticity that slightly differs from classical EMT. Epithelial cell plasticity is essential throughout the process of branching morphogenesis in numerous organs, including the lung.38 39 Lung-branching morphogenesis requires reciprocal signalling between the epithelium and surrounding mesenchyme that is mediated by coordinated activity of TGF-β/bone morphogenetic protein, Wnt, Sonic hedgehog, fibroblast growth factor (FGF) or retinoic acid signalling.40 Dysregulation of these signalling pathways is implicated in aberrant lung branching, alveologenesis and pulmonary vascular development, events critical for normal lung development. In addition to genetic factors, pre-natal and post-natal environmental exposures, including epigenetics, play a significant role in programming lung morphogenesis and development of paediatric lung disease.

Bronchopulmonary dysplasia (BPD) is a chronic lung disease that occurs in very premature infants and is characterised by impaired alveologenesis and vascular development. BPD develops as a result of injury or infection on a very immature lung. Interstitial fibrosis is recognised as a prominent feature of BPD as a consequence of repetitive lung injury. Deng and coworkers,41 using transgenic reporter mice, showed that lung fibroblasts in BPD could arise from bone-marrow-derived ATII cells that have undergone EMT. Noseda and colleagues,42 43 revealed that expression of Notch1 or Notch4 in endothelial cells can cause transition to a mesenchymal phenotype via endothelial-to-mesenchymal transition, a process very similar to EMT. Constitutive Notch1 activation, together with inhibitor studies in lung organ cultures, identified a role for Notch signalling together with TGF-β in mesothelial EMT.44 Que et al45 have also shown that mesothelial cells covering the lung surface can migrate into the organ itself and give rise to various cell types, including mesenchymal cells, within the developing lung.

Taken together, these findings have important implications for our understanding of lung developmental defects; however, the casual impact of EMT to BPD has yet to be determined.

EMT IN ASTHMA

Airway remodelling comprises thickening of the basement membrane accompanied by sub-epithelial fibrosis, epithelial shedding and smooth muscle hypertrophy/hyperplasia.17 Under normal conditions, the damaged epithelium is able to repair itself quickly. However, constant damage inflicted by chronic inflammation in asthma results in a greatly reduced number of ciliated cells, leaving the basal membrane surface only partially covered with basal cells which are more resistant to apoptosis.17 Loss of E-cadherin as a hallmark of EMT in airway epithelial cells of patients with asthma is also described.14 44 47 Fibroblasts and myofibroblasts are responsible for the increased production of ECM proteins, for example, collagen and proteoglycans, and also serve as storage for cytokines and growth factors like TGF-β, which play important roles in fibrosis and the regulation of fibroblast–myofibroblast differentiation in inflamed airways.48 49

Recent experimental data indicate that T helper 2 dominant chronic inflammation leads to elevated TGF-β1 levels in airways via increased production of TGF-β by eosinophils and macrophages, in addition to fibroblasts, endothelial and smooth muscle cells. TGF-β is stored in the ECM and in turn induces EMT and sub-epithelial fibrosis.29

Concerning the pathogenesis of asthma, does EMT contribute to tissue remodelling and sub-epithelial fibrosis? Johnson and colleagues28 found evidence for this phenomenon in a house dust mite (HDM) allergen sensitised transgenic murine model. They demonstrated that β-galactosidase-tagged large airway epithelial cells gradually lose epithelial characteristics, gain expression of mesenchymal markers, for example, vimentin, and migrate into the sub-epithelial compartment.29 In vivo cell fate tracking of genetically labelled epithelial cells provides evidence for epithelial cell transdifferentiation in this mouse model of chronic asthma. Other studies use primary human bronchial epithelial cell (hBEC) cultures to study the role of allergen sensitisation in EMT. HDM sensitisation of the airways synergises with TGF-β1 and results in the loss of E-cadherin expression,47 caveolin-1 internalisation and consequent loss of epithelial barrier function.46 Hackett et al44 investigated EMT using air–liquid interface cultures of hBECs isolated from patients with asthma and non-asthmatic controls. The authors found that basal cells of the stratified airway epithelium are the most susceptible to TGF-β1-induced EMT. Interestingly, they found no histological evidence for expression of mesenchymal markers in the bronchial epithelium of matched patients with asthma, rather an increased number of cytokeratin-5+ (KRT5+) positive cells, indicating a differentiation shift towards the basal epithelial cell phenotype.14 The results discussed above highlight the controversy and discrepancy between research data concerning EMT.

EMT IN BRONCHIOLITIS OBLITERANS SYNDROME

Bronchiolitis obliterans syndrome (BOS) is a major cause of allograft dysfunction in lung transplant recipients. Hodge et al43 found increased expression of mesenchymal proteins by large airway bronchial epithelial cells (BECs) in patients with BOS after lung transplantation to be a clear indicator of the presence of
EMT is a primary mechanism of action. Currently there are multiple therapeutic approaches targeting Wnt signalling in lung fibrosis and tissue remodelling, and malignant lung diseases. However, despite the growing body of evidence, there is still no direct proof in humans that EMT actually happens as a dynamic process in tumour metastasis formation.

WHAT IS THE CLINICAL IMPORTANCE OF EMT?
Two disease groups need to be considered concerning the clinical importance of EMT in the lung: conditions with fibrosis and tissue remodelling, and malignant lung diseases.

It has been recently highlighted that various forms of lung fibrosis and tissue remodelling are present in all chronic respiratory diseases. Current research data highlight that we have to be careful on judging how much EMT contributes to the actual fibrosis, scarring and tissue remodelling. Among the identified targets is the TGF-β pathway and other growth factors, like PDGF, CTGF, FGF and vascular endothelial growth factor, which are considered to trigger EMT and have a proven pathogenic role in fibrotic lung diseases. Most of these molecular targets have been tested in animal models but there has been no success so far in translating these findings to the clinic. Pirfenidone is the only licensed therapy for IPF but the mechanism of action is obscure and there are no in vivo data available of its effects on EMT.

As Wnt signalling pathways have been shown to be important in the pathogenesis in several lung diseases, such as fibrosis, asthma, COPD and lung cancer, they could serve as another promising therapeutic target. Currently there are multiple therapeutic approaches targeting Wnt signalling in lung...
A large majority of studies on EMT in lung diseases use methods which take only a ‘snapshot’ of this dynamic process—for example, immunohistochemistry, western blotting or flow cytometry. Although there have been moves to standardise the molecular markers of EMT,\textsuperscript{5} 33 there are doubts as to whether EMT can only be defined by the coexpression of certain epithelial and mesenchymal markers,\textsuperscript{46} since similar molecular changes occur in epithelial cells during wound repair.\textsuperscript{11} 12

In conclusion, much recent research has highlighted the potential of EMT to be involved in lung development and disease responses. The precise clinical importance of EMT outside of tumour biology remains to be determined, but the development of drugs that target growth factors known to promote EMT suggest that modulation of EMT processes in the clinical setting may soon be possible. Whether these are clinically effective remains to be seen.

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**Provenance and peer review** Not commissioned; externally peer reviewed.

**REFERENCES**


33 Quaggini SE, Kapus A. Scar wars: mapping the fate of epithelial–mesenchymal–


<table>
<thead>
<tr>
<th>Disease</th>
<th>Reference</th>
<th>Model</th>
<th>Methods/Treatment</th>
<th>Markers</th>
<th>Other markers</th>
<th>Main results</th>
</tr>
</thead>
<tbody>
<tr>
<td>BPD</td>
<td>Dong C et al.(1)</td>
<td>Murine model of hyperoxia-induced BPD, GFP-tagged bone marrow (BM) chimera mice</td>
<td>60% oxygen for 14 days, CXCL12 chemotaxis assay</td>
<td>N Y N</td>
<td>S100A4, TTF-1, Pro-Surfactant Protein-B, Collagen I, CXCR4</td>
<td>GFP-tagged BM-derived fibroblasts were engrafting the lung in active fibrotic areas; there were significantly more BM-derived CXCR4+ fibroblasts in the lungs of O2 treated animals than in controls; BM-derived TTF-1+ epithelial cells were detected in injured lungs</td>
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<tr>
<td>Asthma</td>
<td>Heijinkl et al.(2)</td>
<td>Bronchial epithelial cell line, Primary bronchial epithelium (hBEC), in vitro</td>
<td>TGF-β1, House dust mite (HDM) allergen</td>
<td>Y N Y</td>
<td>EGFR,α-catenin activation, cytokeratin (KRT), Myosin light chain phosphorylation</td>
<td>HDM allergen acted synergically with TGF-β1 in inducing EMT in primary hBECs.</td>
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<tr>
<td></td>
<td>Hackett T-L et al.(3)</td>
<td>hBEC from patients with asthma (8) and healthy controls (10)</td>
<td>TGF-β1 SMAD3 siRNA, BMP-7</td>
<td>Y N Y</td>
<td>Fibronectin (FN), collagen-1, occludin-1</td>
<td>In vitro evidence for EMT in hBEC; basal epithelial cells are especially sensitive to EMT as in vitro data suggest; no histological evidence for EMT in sections from matched asthmatic patients</td>
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<tr>
<td></td>
<td>Hackett T-L et al.(4)</td>
<td>hBEC cell lines 16HBE and BEAS-2B; primary hBEC from healthy controls and from patients with asthma</td>
<td>HDM allergen; epidermal growth factor (EGF)</td>
<td>Y N N</td>
<td>Caveolin-1 (Cav-1), β-catenin, Thymic Stromal Lymphopoietin (TSLP),</td>
<td>Cav-1 levels, junctional E-cadherin and β-catenin were significantly lower, TSLP levels were higher in asthma patients compared to controls; EGF and HDM treatment induced E-cad redistribution and Cav-1 internalization in 16HBE cells. Cav-1-specific siRNA inhibited E-cad internalisation and barrier dysfunction in 16HBE cells; Cav-1 overexpression restored barrier dysfunction and reduced TSLP levels in BEAS-2B cells.</td>
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<tr>
<td></td>
<td>Johnson Jl et al.(5)</td>
<td>HDM-induced asthma in ROSA-26/SPC-Cre-LacZ reporter mice</td>
<td>HDM for 15 weeks</td>
<td>Y Y Y</td>
<td>TGF-β1, occludin, pro-collagen I, SNAIL</td>
<td>LacZ+/α-SMA+ cells were incorporated into airway smooth muscle; LacZ+/Vim+ cells were present in the sub-epithelium; 30% of Vim+ cell were also LacZ+</td>
</tr>
<tr>
<td>BOS</td>
<td>Hodge et al.(6)</td>
<td>Bronchial brushings from lung transplant (LTX) patients with (6) or without BOS (16)</td>
<td>N/A</td>
<td>N Y N</td>
<td>Flow cytometry, S100A4 FN, HLA-DR; TGF-β1 and HGF levels in BALF-ELISA</td>
<td>EMT markers α-SMA, S100A4 FN and HLA-DR were increased in epithelial cells from BOS patients compared to stable LTx patients; Increased levels of HGF but not TGF-β1 in the BALF of BOS patients.</td>
</tr>
<tr>
<td>BOS</td>
<td>Ward et al.</td>
<td>Endobronchial biopsy and brushings from 16 stable LTx patients</td>
<td>TGF-β1</td>
<td>N N N</td>
<td>S100A4 IHC, MMP-2, 7 and 9 zymography, invasion assay</td>
<td>A median 15% of the biopsy epithelium stained for S100A4 and MMP-7 in stable lung transplant recipients; Epithelial cultures from lung allografts were positive for S100A4 and MMP-2 and 9 showed zymographic activity. MMP total protein and activity was increased after TGF-β1 treatment; Both TGF-β1 stimulated and non-stimulated epithelial cells were invasive, invasion capacity was higher in TGF-β1 stimulated cells.</td>
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<tr>
<td>BOS</td>
<td>Bortwick et al.(7)</td>
<td>In vitro culturing of hBEC form obtained via bronchial brushing from stable LTx patients, co-culture with THP-1 cells</td>
<td>TGF-β1 with or without P. aeruginosa cell lysate (lab. strain and clinical isolates (9))</td>
<td>Y Y Y</td>
<td>IL-8, IL-1β, TNF-α, FN, KRT-19</td>
<td>Supernatants, but not co-cultures of THP-1 cells treated with P. aeruginosa accentuated EMT on cultured hBECs. Clinical isolates of P.aeruginosa induced significantly higher production of inflammatory cytokines in THP-1s than the reference strain.</td>
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<td>BOS</td>
<td>Authors</td>
<td>Description</td>
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<tr>
<td>BOS</td>
<td>Borthwick et al. (8)</td>
<td>In vitro culturing of hBEC form obtained via bronchial brushing from stable LTx patients</td>
<td>TGF-β, TNF-α</td>
<td>Y</td>
<td>FN, KRT-19, S100A4, MMP-9 zymography, Matrigel invasion assay, collagen synthesis</td>
<td>Bronchial epithelium upregulating EMT and downregulating epithelial markers in BOS but not in stable transplants; epithelial cells; TNF-α accentuates TGF-induced EMT and cell migration, but not ECM deposition.</td>
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<tr>
<td>BOS</td>
<td>Milana et al. (9)</td>
<td>In vitro culture of hBECs isolated from small airways (&gt;1mm) of non-smokers (5), smokers (12) and COPD patients (15); IHC of tissue samples</td>
<td>Cigarette Smoke Extract (CSE)</td>
<td>Y</td>
<td>collagen type I, NOX4, ZO-1 (IHC); TGF-β1, cAMP and MMP-9 (EUSA) ERK1/2 and Smad3 phosphorylation (WB)</td>
<td>hBECs from smokers and COPD patients but not from controls show EMT; CSE-induced EMT is mediated by the ROS and downregulation of cAMP;</td>
</tr>
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<td>BOS</td>
<td>Zou et al.</td>
<td>HBEC cell line</td>
<td>Nicotine, Wnt-3a, TGF-β1 siRNA</td>
<td>Y</td>
<td>MMP-9, Collagen-I</td>
<td>Nicotine treatment leads β-catenin to nuclear translocation, E-cad downregulation, αSMA, Vim, Col-1, MMP-9 and TGF-β1 upregulation in HBECs; Knockdown of Wnt3a and TGF-β1 using specific siRNA constructs prevented these effects..</td>
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<td>COPD</td>
<td>Sahai et al. (10, 11)</td>
<td>Endobronchial biopsies from non-smokers (15); ex-smokers with COPD (15), smokers with normal lung function (16) and current smokers (17)</td>
<td>N/A</td>
<td>e-SMA, Vimentin</td>
<td>IHC for S100A4, MMP-9, KRT and EGFR</td>
<td>Evidence for Rbm fragmentation/remodelling, increased EGFR expression of epithelial cells in COPD patients and smokers compared to non-smoker control (11), 7.2% of basal epithelial cells and cells in the Rbm frequently co-express KRT and S100A4 suggesting EMT in vivo (10).</td>
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<tr>
<td>COPD</td>
<td>Wang et al.</td>
<td>Lung tissue samples obtained during lobectomy from 25 non-smokers, 25 smokers with and 18 smokers without COPD; Human primary small airway epithelial cells (SAEC)</td>
<td>CSE extract, uPAR-1 and 2-specific siRNA constructs;</td>
<td>e-SMA, α-catenin, N-cadherin, p-Akt, p-GSK-3β</td>
<td>Increased expression of EMT markers and uPAR small airway epithelium (SAE) of patients with COPD compared to controls; Vimentin and uPAR expression are correlated in SAE; CSE-induced EMT in SAEC was associated with high uPAR expression; Targeted silencing of uPAR inhibited CSE-induced EMT; uPAR mediates EMT in SAEC through the PI3K/Akt signaling pathway.</td>
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<td>COPD</td>
<td>Chung et al.</td>
<td>C57Bl/6 mice were exposed to cigarette smoke for up to 6 months</td>
<td>Smoke of 2R1 Kentucky research cigarettes in various doses</td>
<td>e-SMA, Vimentin</td>
<td>Procollagen, TGF-β1, platelet-derived growth factor (PDGF)-A, PDGF-B, connective tissue growth factor (CTGF), p-ASMAD2</td>
<td>With a single smoke exposure, increases in procollagen, CTGF, TGF-β1, PDGF-A and -B expression were seen after 2 h of smoke exposure; With chronic smoke exposures increases in procollagen, CTGF, PDGF-B expression persisted through 1 wk, 1 mo, and 6 mo; Increased p-Smad2 was present at all time points, indicating constitutively active TGF-β signalling; Small airways in smoke-exposed mice had more collagen at 6 mo.</td>
</tr>
<tr>
<td>COPD</td>
<td>Milana et al.</td>
<td>Air-liquid interface (ALI) cultures were set up from HBECS from non-smokers (n=5), smokers (n=12) and patients with COPD (n=15)</td>
<td>CSE exposure</td>
<td>e-SMA, Vimentin</td>
<td>collagen-I, NOX4, ZO-1, MMP-9</td>
<td>EMT markers were upregulated and epithelial markers were downregulated in HBECS of smokers and patients with COPD compared to non-smokers; CSE exposure caused EMT within 72 h in vitro differentiated HBECS; CSE effects were mediated by intracellular reactive O2 species, autocrine action of TGF-β1, activation of ERK1/2 and Smad3 and by the downregulation of cAMP.</td>
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<tr>
<td>IPF</td>
<td>Kim et al. (12, 2)</td>
<td>ROSA-26/SPC-Cre-LacZ reporter mice, in vitro culture of transgenic ATIs</td>
<td>Intranasal Adeno-TGF-β1, culturing ATIs on Matrigel or FN, TGFR kinase inhibitor SB431542</td>
<td>e-SMA, Vimentin</td>
<td>Pro-SP-C, FN, N-cad, p-SMAD2, TUNEL</td>
<td>Lung injury induced by TGF-β1 expressing adenovirus causes massive EMT AECs; genetic fate tracking proves epithelial origin of myofibroblasts. Culturing genetically tagged AECs on FN but not on Matrigel induces EMT by activating intracellular TGF-β/SMAD signalling through αvβ6 integrin.</td>
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<tr>
<td>IPF</td>
<td>Tanjore et al. (13)</td>
<td>ROSA-26/SPC-Cre-LacZ reporter mouse, in vitro culture of transgenic ATIs</td>
<td>IT bleomycin (single 0.08U dose)</td>
<td>N</td>
<td>Y</td>
<td>N</td>
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<tr>
<td>IPF</td>
<td>Deagryse et al. (14)</td>
<td>ROSA-26/SPC-Cre-LacZ reporter mice</td>
<td>IT bleomycin (0.04U given biweekly 8 times)</td>
<td>N</td>
<td>Y</td>
<td>N</td>
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<tr>
<td>IPF</td>
<td>Harada et al. (15)</td>
<td>13 patients with UIP histology; 11 IPF, 2 autoimmune; 10 control patients w/ normal lung function</td>
<td>N/A</td>
<td>N</td>
<td>Y</td>
<td>Y</td>
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<tr>
<td>IPF</td>
<td>Rock et al. (16)</td>
<td>ROSA-26/ Sftpctm1-Cre-Tomato transgenic reporter mice</td>
<td>IT bleomycin (1.25 U/kg – 5 U/kg body weight dose) in a single injection</td>
<td>N</td>
<td>Y</td>
<td>Y</td>
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<tr>
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<td>Lung Cancer</td>
<td>Prudin et al. (17)</td>
<td>Tissue from human lung cancers: squamous metaplasia (13), squamous dysplasia (34) &amp; carcinoma in situ (20), Brain metastases: adenocarcinoma (37), squamous cell (11).</td>
<td>N/A</td>
<td>E-cad N Y Vimentin N Y</td>
<td>N-Cadherin, Integrin αvβ6, MMP-9, and phosphorylated EGFR. Methods: Tissue microarray construction, IHC, EGFR mutation analysis.</td>
<td>EMT phenotype was commonly expressed in dysplastic lesions, lung squamous cell carcinoma and adenocarcinoma. Brain metastases from these tumours expressed higher levels of E-cadherin than primary tumours implicating the occurrence of MET after dissemination.</td>
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<tr>
<td>Lung Cancer</td>
<td>Pirzda et al. (18)</td>
<td>A549s (control) and LC31 (lung cancer primary cell line). LC31 cells grown as pneumospheres were subcutaneously injected in NOD/SCID mice.</td>
<td>TGF-β1 2ng/ml: A549s for 30 days, LC31s for 80 days</td>
<td>E-cad N Y Vimentin N Y</td>
<td>KRT, N-cad, CD90, SLUG, TWIST, β-catenin. Stem markers: Oct4, Nanog, Sox2, c-kit, CD133.</td>
<td>TGF-β1 lung cancer cells underwent EMT showing mesenchymal phenotype and LC31s also showed over-expression of stemness markers. TGF-β1 treatment increased the pneumosphere-forming capacity and invasiveness of LC31s in NOD/SCID mice.</td>
</tr>
<tr>
<td></td>
<td>Ren et al. (19)</td>
<td>Cell lines: Doxetacel (DTX) sensitive and resistant human NSCLC line SPC-A1. Animal model: SPC-A1/DTX cells injected into nude mice.</td>
<td>ZEB1 siRNA knockdown. DTX treatment.</td>
<td>E-cad N Y Vimentin N Y</td>
<td>N-cad, KRT-19, TWIST. Methods: apoptosis assay, colony formation assay, wound healing assay, migration/invasion assays.</td>
<td>Acquisition of DTX resistance coincides with EMT/mesenchymal phenotype, an increased migratory and invasive capacity, increased ZEB1 expression. ZEB1 knockdown was found to reverse the EMT phenotype and inhibit the migratory ability of SPC-A1/DTXs, enhanced the chemo-sensitivity.</td>
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<td>Tominga et al. (20)</td>
<td>Human NSCLC lines: A549, PC-9, RERF-LC-KJ, and LC-2/lad</td>
<td>Cell lines were transfected to over-express miR-1</td>
<td>E-cad N Y Vimentin N Y</td>
<td>Vinculin, occludin, SNAI1, SLUG, ZEB1</td>
<td>miR-1 expression was down-regulated in lung cancer cell lines. Overexpression of miR-1 endowed A549 cells with epithelial features upregulated E-cad by inhibiting SLUG. miR-1 suppressed the migratory &amp; invasive capacity of A549s.</td>
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<td>Wika et al. (21)</td>
<td>21 NSCLC cell lines were used: squamous (4), large cell (5), adeno-carcinoma (10), &amp; bronchiolo-alveolar (2).</td>
<td>Gefitinib, HDAC inhibitor (MS-275). E-cad transfection.</td>
<td>E-cad N Y Vimentin N</td>
<td>EGFR, ZEB1</td>
<td>Gefitinib sensitivity correlated with E-cad and ZEB1 expression. E-cad overexpression restored gefitinib sensitivity. HDAC inhibitor (MS-275) treatment induced E-cadherin &amp; EGFR, and led to a growth-inhibitory &amp; apoptotic effect with gefitinib treatment, even in resistant cell lines harbouring EGFR mutations.</td>
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