

Revisiting mTOR and Epithelial–Mesenchymal Transition

In the lungs, alveolar epithelial cells (AECs) are essential for the maintenance of alveolar structure and lung homeostasis. The alveolar epithelium is composed of flat type 1 cells (AT1), which are in close proximity to capillaries and mediate gas exchange, and cuboidal type 2 cells (AT2), which regulate surfactant production and secretion (1). In recent years, several lines of evidence suggest that lung diseases can result from failure of lung repair. For example, in the adult lung, AT2 cells can proliferate to self-renew and differentiate into AT1 (2, 3). Investigators have suggested that the self-renewal capacity in AT2 cells is limited, such that repeated injury or aging preclude normal epithelial regeneration, perhaps contributing to the pathobiology of fibrotic lung diseases, including idiopathic pulmonary fibrosis (IPF) (4). The disassembly of cell–cell junctions, loss of epithelial identity, and upregulation of the expression of mesenchymal markers has been termed epithelial–mesenchymal transition (EMT) and has been suggested to contribute to lung fibrosis (5, 6). However, direct evidence of EMT using genetic lineage tracing tools in murine models or humans with IPF is lacking (7, 8).

The serine/threonine kinase mTOR plays an essential role in cell proliferation, differentiation, growth, and survival. mTOR forms two different protein complexes: the mTOR complex 1 (mTORC1; rapamycin sensitive) and the mTOR complex 2 (mTORC2; rapamycin insensitive), both of which sense and integrate intracellular and environmental signals to mediate vital cell functions (9). Investigators have previously implicated mTOR signaling in fibroblasts in the pathogenesis of IPF. For example, the activation of mTOR is involved in the metabolic reprogramming of fibroblasts and exacerbates TGF- β -induced collagen biosynthesis (10). Moreover, IPF-derived lung fibroblasts show a persistent activation of this kinase, which is associated with apoptosis resistance (11). However, the role of mTOR activation in AT2 cells is incompletely understood.

In this issue of the *Journal*, Saito and colleagues (pp. 699–708) report findings from a transgenic mouse that has constitutive activation of mTORC1 in AT2 cells (Sftpc-mTOR^{SL1 + IT} Tg) (12). In the uninjured lung, Sftpc-mTOR^{SL1 + IT} Tg mice did not exhibit a detectable phenotype, but expression of the tight junctional proteins ZO-1 and Cav-1 was reduced. When these mice were given bleomycin, the recruitment of inflammatory cells into the lungs and the resulting fibrosis were worse. The authors provide supportive data in cultured epithelial cells suggesting that activation of *Angptl4* (angiopoietin-like 4) acts downstream of mTOR signaling to alter the expression of tight junction proteins. They propose this as a mechanism for their observations but do not provide causal data *in vivo*. Their hypothesis is supported by findings in breast cancer cells in which TGF- β upregulates *Angptl4* to promote lung metastases (13). Moreover, deficiency of *Angptl4*

reduces inflammatory cell recruitment in influenza and LPS-induced models of lung injury (14, 15).

The findings of Saito and colleagues support a link between mTOR signaling in the epithelium and the regulation of tight junctional integrity and inflammatory cell recruitment (12). This finding is consistent with recent reports by Wu and colleagues, who found that loss of a small GTPase *Cdc42* that regulates cell division and cell polarization promoted the development of lung fibrosis after pneumectomy (16). However, their suggestion that *Angptl4* promotes EMT during pulmonary fibrosis is likely to be met with skepticism. To make such a claim, the investigators would need to show that labeled AT2 cells become fibroblasts during fibrosis when mTOR signaling is activated. Careful studies of this kind have been conducted by other laboratories and have failed to find evidence of EMT in the bleomycin model of pulmonary fibrosis (17). Several other limitations of these studies should be noted. Most importantly, the transgenic mouse used in this study has constitutive mTOR activation during development, raising the possibility that compensatory or alternative pathways may have compensated for the chronic activation of mTOR, contributing to the observed phenotypes. Although these studies suggest a potential new line of investigation, studies combining inducible systems with genetic lineage tracing and careful phenotyping of epithelial, immune, and mesenchymal populations during fibrosis will be required to understand the role of mTOR signaling in the lung epithelium during fibrosis. ■

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