Chapter 3 Pericytes in the Lung



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Abstract The lung has numerous roles, including gas exchange, immune surveillance, and barrier function. Being a highly vascularized organ, the lung receives dual blood supply from both the pulmonary and bronchial circulation. Therefore, pericytes likely play a prominent role in lung physiology given their localization in the perivascular niche. New genetic approaches have increased our understanding of the origin and the diverse functions of lung pericytes. Lung pericytes are myofibroblast progenitors, contributing to development of fibrosis in mouse models. Lung pericytes are also capable of responding to danger signals and amplify the inflammatory response through elaboration of cytokines and adhesion molecules. In this chapter, we describe the molecular, anatomical, and phenotypical characterization of lung pericytes. We further highlight their potential roles in the pathogenesis of lung diseases including pulmonary fibrosis, asthma, and pulmonary hypertension. Finally, current gaps in knowledge and areas of ongoing investigation in lung pericyte biology are also discussed.

Keywords Lung pericytes \cdot PDGFR β \cdot Lung development \cdot Lung myofibroblasts \cdot Pulmonary fibrosis \cdot Lung injury \cdot Lung inflammation

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3.1 Introduction

A critical but vastly understudied cell in the lung is the pericyte. Pericytes are mesenchymal cells defined by their anatomical association with endothelial cells (Armulik et al. 2011; von Tell et al. 2006). Pericytes directly interact with microvascular endothelium, including capillaries, precapillary arterioles, postcapillary, and collecting venules, and are critical to blood vessel maturation and stability. However, it is increasingly clear that lung pericytes play important roles not only in vascular homeostasis but in lung injury and repair. In this chapter, we will review what is known about lung pericytes in normal lung homeostasis, including their developmental origins, discuss characterization of these cells in vitro and in vivo, and highlight current knowledge of lung pericytes in lung diseases, such as pulmonary fibrosis and pulmonary hypertension. Finally, we will speculate on the potential role of pericytes as a regenerative niche in the lung.

3.2 Definition of Lung Pericytes

Anatomic Characterization Pericytes are classically defined by ultrastructural localization demonstrating direct contact with microvascular endothelial cells through gaps in the shared basement membrane. Using transmission electron microscopy, Epling was the first to observe pericytes as "filament-containing cells" in bovine and porcine lungs (Epling 1966), and Weibel confirmed the presence of pericytes in capillaries of the lungs of humans and other mammals (Weibel 1974). Compared to organs such as the heart or pancreas, pericytes are more rare in the lung, and their frequency correlates with body size. For example, pericytes were readily detected in human and dog lungs but were sparser in rodent lungs and could not be found in lungs of the Etruscan shrew, the smallest mammal known (Weibel 1974). Pericytes are sensitive to oxygen levels and thus are less abundant in areas of gas exchange (Shepro and Morel 1993). The pericyte-to-endothelial ratio in the lung has been estimated to be about 1:10 (Shepro and Morel 1993), less than that in the retina and central nervous system (~1:1 to 1:3), where barrier function is paramount and pericytes play a key role in regulating permeability. By genetically tracing pericytes in mice, Kato et al. found a pericyte-to-endothelial ratio from 1:7 to 1:9 (Kato et al. 2018). Coverage of the abluminal surface of capillaries also varies by organ and ranges between 18 and 26% in bovine lungs, depending on developmental stage of the animal (Sims and Westfall 1983).

Perivascular stromal cells are found along all levels of the bronchovascular bundle. Classically, lung pericytes are defined at the level of the alveolar capillary bed (Armulik et al. 2011). Electron microscopy lungs show pericytes embedded within the capillary basement membrane of alveoli in humans, mice, and other mammals (Hung et al. 2013) (Epling 1966; Weibel 1974). In human lung samples, Weibel observed that while most of the pericyte cell body and its large cellular processes are separated from endothelial cells by the intervening basement membrane, finer processes penetrate the basement membrane and make contacts with the endothelial cells in capillaries (Weibel 1974). Some pericytes were even seen to bridge separate capillary segments (Weibel 1974). The nature of pericyte interactions with endothelial cells in larger microvessels (i.e., the arterioles and venules) of the lung has not yet been described at the ultrastructural level.

Developmental Origins Current understanding of lung pericytes indicates that they primarily originate from the mesoderm and mesothelium (Que et al. 2008). In the mouse, a multipotent cardiopulmonary progenitor positive for the transcription factors Gli1 and Isl1 and the signaling molecule Wnt2 gives rise to mesodermal lineages in the lung, including pericytes (Peng et al. 2013). We showed that the forkhead transcription factor FoxD1 is transiently expressed in pulmonary mesenchymal progenitors as they infiltrate the lung buds during mouse embryogenesis between days 11.5 and 12.5 (Hung et al. 2013). Expression of FoxD1 is then silenced by day 15.5 once the progenitors differentiate into mature mesenchymal cells, making this factor a useful marker for fate mapping these progenitors in the mouse lung (see section on Molecular Identification below). For most organs, including the lung, the PDGF-B-PDGFR β signaling axis is critical in recruiting pericytes to their proper anatomical niche within the microvascular environment during embryogenesis (Armulik et al. 2011). Disruption of this axis by knockout of PDGFR β or PDGF-B results in virtually total absence of pericytes in the mouse embryonic lung (Hellstrom et al. 1999). The developmental origin of human lung pericytes is not known, but we presume that they derive from a mesodermal precursor as well. As discussed below, PDGFR β is a key, robust marker of lung pericytes.

Molecular Identification and Pericyte Subtypes Whereas identification of pericytes in early studies of lung tissue specimens used electron microscopy to define the cells at the ultrastructural level, this method is cumbersome and difficult to carry out in most laboratories. Advances in molecular characterization of pericytes and in fate-mapping transgenic models have enabled investigators to study lung pericytes with greater ease and flexibility than in the past. Nevertheless, lack of a truly pericyte-specific marker means that researchers need to use multiple criteria including location relative to endothelial cells in situ, morphology, and genetic markers to identify pericytes.

Only in the last decade or so have a limited number of studies been undertaken to isolate and characterize pericytes from "normal" human lung (typically from failed donor organs or tissue adjacent to carcinoma). The commonalities in these studies were that pericytes were selected from dissociated lung cells using magnetic bead-linked antibodies against one or two markers and then expanded in commercial medium especially designed for growth of pericytes. In culture, isolated lung pericytes have a stellate or elongated morphology with long extensive cellular processes (Yuan et al. 2015; Wilson et al. 2018) (Fig. 3.1). In addition, lung pericytes form primitive tubelike structures on the basement membrane preparation Matrigel (Wilson et al. 2018; Bagley et al. 2006) (Fig. 3.1).



Fig. 3.1 Cell morphology and characteristics of isolated human lung pericytes. Representative phase-contrast light microscopic images of pericytes from normal lungs after plating on plastic (**a**) or MatrigelTM (**b**). Note the extensive number of elongated cellular processes emanating from the cells on plastic. On MatrigelTM, pericytes assemble into primitive networks composed of nodes of cells from which cellular processes project and connect with other nodes (**b**). Human lung pericytes are positive for PDGFRβ (**c**) and NG2 (**d**) by immunofluorescence. Scale bar = 500 μm in (**a**), (**c**), and (**d**) and 100 μm in (**b**)

Table 3.1 summarizes the markers that were used for isolation of human lung pericytes and the other markers that were detected in these cells in different studies. Expression of the proteoglycan neural glial antigen-2 (NG2 or chondroitin sulfate proteoglycan 4) (Yuan et al. 2015; Wilson et al. 2018; Bagley et al. 2005; Bichsel et al. 2015; Ricard et al. 2014) was reported in all the studies (Fig. 3.2). NG2+ cells localized to perivascular regions in human lung tissue by immunofluorescence (Sava et al. 2017; Rock et al. 2011). Most studies showed that lung pericytes are PDGFR β +, as expected (Fig. 3.2), and we used this marker in our own work for cell selection from both human and mouse lungs (Wilson et al. 2018; Hung et al. 2017a).

Other prominent mesenchymal markers found in isolated human lung pericytes include CD73 (ecto-5'-nucleotidase), CD90 (Thy1, also a fibroblast marker), and the hyaluronan receptor CD44, although not all studies examined the cells for these markers. Expression of endoglin (CD105) and PDGFR α is also characteristic of human lung pericytes. The monoclonal antibody 3G5-defined ganglioside antigen has emerged as a useful pericyte marker for the lung as well as the skin

	Yuan et al.			Bichsel et al.	Wilson et al.
	(2015)	Bagley et al.	Ricard et al.	(2015) (CD73/	(2018)
Markers	(3G5)	(2006) (NG2)	(2014) (3G5)	CD90)	(CD140b)
CD44	ND	ND	ND	+	+
CD73	ND	ND	ND	+	+
CD90	+	+	ND	+	+
CD105 (endoglin)	ND	+	ND	+	ND
CD140a (PDGFRa)	ND	ND	ND	+	+
CD140b (PDGFRβ)	+	+	ND	ND	+
CD146	+	ND	ND	-	-
NG2 (CSPG4)	+	+	+	+	+
3G5	+	+	+	ND	ND
αSMA	+	+	-	-	-
Desmin	ND	+	ND	ND	ND

 Table 3.1 Gene markers of isolated human lung pericytes

Marker(s) used for cell selection shown in parentheses. ND not done



Fig. 3.2 Fate-mapping of Foxd1 progenitor-derived pericytes identifies them as a major source of myofibroblast precursors in lung injury. (**a**, **b**) Confocal images showing fibrotic foci on d7 and d14 after bleomycin lung injury in *Foxd1-Cre; Rs26-TdT-R* mice stained for the myofibroblast marker α SMA (green). Co-expression of myofibroblast marker α SMA and the tdTomato fate marker of Foxd1-derived pericytes indicated by (**1**). Graph indicating proportion of tdTomato+ cells co-expressing α SMA+ in fibroblastic foci at indicated time points after bleomycin lung injury (mean ± SEM, *n* = 3). (**c**, **d**) Confocal images showing fibrotic foci on d7 after bleomycin lung injury in triple transgenic mouse *Foxd1-Cre; Rs26-TdT-R; Coll-GFP^{Tg}* and graph summarizing proportion of tdTomato cells co-expressing Coll-GFP in fibrotic foci (mean ± SEM, *n* = 3) (Bar = 50 µm). Modified and reprinted with permission of the American Thoracic Society. Copyright © 2018 American Thoracic Society (Hung et al. 2013). The *American Journal of Respiratory and Critical Care Medicine* is an official journal of the American Thoracic Society

(Helmbold et al. 2001a, b) and was used by two investigator teams to isolate these cells (Yuan et al. 2015; Ricard et al. 2014). There are discrepant reports on CD146 (also known as MCAM or melanoma cell adhesion molecule) expression: one study found that the cells are positive for CD146 (Yuan et al. 2015), whereas two others did not (Wilson et al. 2018; Bichsel et al. 2015). The lack of significant CD146 expression is surprising as it is a typical marker of pericytes from other organs, such as the placenta and brain (Crisan et al. 2008), and was detected in mouse lung pericytes (Hung et al. 2013). Potential explanations for these conflicting data on CD146 positivity include the presence of subpopulations of lung pericytes, differences in underlying pathology of donor lung tissue, and/or differences in culture conditions. Also, while α -SMA has been described as a pericyte marker, in general, only mural cells associated with precapillary arterioles and postcapillary venules express this contractile protein, whereas quiescent capillary pericytes do not (Nehls and Drenckhahn 1991). Further complicating interpretations, while pericytes on arterioles and capillaries are NG2+, venular pericytes are NG2-, at least in rat mesenteric and subcutaneous tissue and skeletal muscle (Murfee et al. 2005). NG2 is induced in venular pericytes during angiogenesis and vascular remodeling (Murfee et al. 2006). Although this differential expression of NG2 has not yet been established in the microvasculature of the human lung, it raises the possibility that a cell selection strategy based on NG2 may not include the entire spectrum of pericytes. Because the markers are not pericyte specific [e.g., CD146 is expressed by endothelial cells (Bardin et al. 2001) and 3G5 by mast cells (Gushi et al. 2008)], it is equally important to exclude expression of other cell-specific markers such as CD31 and CD144 (endothelial cell markers PECAM and VE-cadherin, respectively), CD45 (pan leukocyte marker), and CD326 (EpCAM, an epithelial cell marker).

Animal Models Much of our knowledge on the origin and fate of lung pericytes comes from genetic approaches in mouse models, mostly using Cre-LoxP technology (Table 3.2). In these models, Cre recombinase expression is driven by a promoter selective for pericytes or pericyte progenitors, and the recombinase activates expression of a reporter allele by targeting LoxP sequences that flank a transcriptional stop site upstream of the reporter. This technique irreversibly labels cells with active promoter expression and their progeny. We showed that expression of the transcriptional factor FoxD1 marks progenitors destined to become pericytes in the lung (Hung et al. 2013). Using triple transgenic mice expressing Cre recombinase from the FoxD1 promoter and GFP from the collagen I promoter (Yata et al. 2003), in conjunction with a tdTomato reporter allele at the ROSA locus, we found that FoxD1-derived progenitors give rise to vascular smooth muscle cells and two populations of pericytes. The major population does not express collagen I or α-SMA and is positive for PDGFR β ; a second, minor population expresses collagen I and PDGFR α rather than PDGFR β (Hung et al. 2013). In this study, all FoxD1-derived cells were negative for CD31, an important distinction given that a group has reported that FoxD1 positivity also marks endothelial progenitors in the mouse lung (Sims-Lucas et al. 2013).

Promoter	Insert	Туре	Major findings in uninjured lung	References
FoxD1	GFP-Cre	Knock-in	Cells are PDGFRβ+, CD146+, 60% NG2+, αSMA-; variable expression of collagen I and PDGFRα	Hung et al. (2013)
FoxD1	GFP- CreERT2	Knock-in, TAM inducible	Promoter active between days 11.5 and 15.5 in embryogenesis	Hung et al. (2013)
FoxJ1	CreER	Transgenic, TAM inducible	Expressed in NG2+ cells	Rock et al. (2011)
NG2	DsRedBAC	Transgenic	Cells are PDGFRβ+, CD146+, αSMA–	Ricard et al. (2014), Chow et al. (2013) and Akamatsu et al. (2013)
NG2	CreER TM BAC	Transgenic, TAM inducible	Only 15% recombination efficiency; cells are PDGFRβ+, αSMA-	Rock et al. (2011)
PDGFRβ	Cre	Transgenic	PDGFRβ expressed in other lineages in addition to pericytes during embryogenesis	Guimaraes-Camboa et al. (2017)
PDGFRβ (BAC)	CreER	Transgenic, TAM inducible	Cells are NG2+	Kato et al. (2018)

Table 3.2 Transgenic mice for identifying and tracking lung pericytes

TAM tamoxifen

One important limitation in lung pericyte research using lineage tracing animal models is the lack of a definitive marker for pericytes. Commonly recognized markers such as PDGFR β , NG2, and CD146 are not uniformly expressed in all pericytes. Moreover, their expression may be spatially and temporally dynamic throughout development and after injury. For example, PDGFR β promoter is active in multiple cell lineages during embryogenesis and is not specific to pericytes (Guimaraes-Camboa et al. 2017). Furthermore, activated myofibroblasts derived from non-pericyte populations following lung injury may upregulate expression of PDGFR β (Henderson et al. 2013; Hung et al. 2018).

Pulse labeling of pericyte populations circumvents the dynamic expression of pericyte markers that are observed in other cell lineages during development and with physiologic stress. Modification of Cre recombinase to make its activity inducible allows temporal control in labeling pericytes. For example, a tamoxifeninducible PDGFR β -CreER transgenic animal enables postnatal marking of PDGFR β + cells; tamoxifen administration at days 1 through 3 after birth labeled cells tightly juxtaposed to endothelial cells in the lung (Kato et al. 2018). Isolated labeled cells were positive for expression of PDGFR β and NG2 and were negative for markers of endothelial and epithelial cells (Kato et al. 2018).

There are important limitations to Cre-loxP models. As discussed previously, promoter activity driving Cre recombinase expression may not be restricted to pericytes, depending on the developmental stage and the presence of physiologic stress. Secondly, Cre recombinase activity is rarely 100% efficient. Promoter activity, accessibility of the target loxP sequences in the genome, and experimental conditions used to induce Cre activity in inducible models can all influence labeling efficiency. In one report, postnatal tamoxifen administration labeled only ~15% of the NG2+ lung cells in NG2-CreER mice (Rock et al. 2011), highlighting a potential drawback of these types of models. Furthermore, bioavailability of tamoxifen can influence labeling efficiency in tamoxifen-inducible Cre models. Some investigators have leveraged this property to study lineage-labeled single cells distributed throughout the lung by administering low-dose tamoxifen (Kato et al. 2018; Barkauskas et al. 2013). Finally, there is currently no single marker that identifies the entire lung pericyte population. The commonly used markers do not completely overlap, suggesting heterogeneity within the lung pericyte population. We showed that only a subset of PDGFRβ+ cells (~60%) express NG2 (Hung et al. 2013), suggesting that NG2 may not be an all-inclusive marker of mouse lung pericytes. Indeed, NG2 has been described as a marker of pericytes in angiogenesis and tissue remodeling rather than homeostasis (Murfee et al. 2006). Interestingly, Rock et al. found that a FoxJ1-CreER transgene also marks NG2+ pericytes in the lung (Rock et al. 2011), although there have been no further reports in the literature using this transgenic mouse for pericyte fate mapping. Our group investigated NG2 and CD146 expression in human pericytes. We found that PDGFR β + human lung pericytes have low CD146 expression unlike mouse lung pericytes (Hung et al. 2017a, b). Taken together, the studies suggest that the lung pericyte population is heterogeneous. Understanding functional differences in lung pericyte subpopulations is an area of ongoing investigation.

Cre-loxP technology can also induce specific gene deletions in pericyte-lineage lung cells. A cross of mice with loxP-flanked Yap1 and Wwtr1 (encoding TAZ protein) alleles to PDGFRβ-CreER mice generated pericyte-specific inducible deletions of these genes in postnatal lung (Kato et al. 2018). The disruptions in YAP1 and TAZ signaling in pericytes altered postnatal lung morphogenesis. Another novel application of Cre-loxP technology involves targeted ablation of pericytes within the lung. Mice are inherently insensitive to diphtheria toxin (DT) as they lack its receptor (DTR). We crossed ROSA26iDTR mice, in which the expression of the simian diphtheria toxin receptor (iDTR) is Cre inducible, to FoxD1-Cre mice to generate the double transgenic FoxD1-Cre;ROSA26iDTR model. In this mouse model, iDTR is expressed in FoxD1-derived cells, rendering them sensitive to ablation upon exposure to DT. Conventional delivery of DT by intraperitoneal injection resulted in neurologic side effects such as seizures within 72 hours of DT administration (unpublished data). This observation reflected the critical role of brain pericytes in the regulation of blood-brain barrier (Hung et al. 2017b). To circumvent this limitation, we administered low-dose DT by oropharyngeal aspiration. Using this method, we achieved approximately 40% ablation of PDGFR β + stromal

cells in the lung at 7 days after DT delivery (Hung et al. 2017b). Long-term ablation, however, remains elusive as progenitor populations replenish ablated cells.

3.3 Pericytes During Lung Homeostasis and Repair

The exact roles of pericytes in lung homeostasis remain largely uncharacterized. Functional studies that disrupt the pericyte-endothelial signaling axis (e.g., PDGF-PDGFRß) result in early embryonic lethality due to abnormal vasculogenesis. Most models that induce pericyte loss focus on developing vessels rather than fully mature pericyte-endothelial units. In one study, pericytes were depleted by administering a PDGFR β -blocking antibody in postnatal pups, which caused abnormal retinal capillary formation (Ogura et al. 2017) and demonstrated a critical role of pericytes in retinal angiogenesis. However, administration of the same antibody in adult mice did not result in pericyte coverage loss, suggesting the PDGF-PDGFR β signaling axis is dispensable in the developed microvascular unit. Akt/Jagged1 signaling maintains perivascular stromal cell coverage in homeostasis in the heart and retina as disruption of endothelial Akt production led to pericyte apoptosis and breakdown of perivascular matrix (Kerr et al. 2016). Whether blockade of the Akt/ Jagged1/Notch signaling axis results in similar findings in the lung remains unknown. When retinal pericytes were ablated with DT in adult mice, microangiopathy developed, suggesting that maintenance of vascular integrity is a critical function of retinal pericytes (Valdez et al. 2014). In our model of lung pericyte ablation with DT, we did not observe changes in lung permeability (Hung et al. 2017b), suggesting that lung pericytes may not be as critical to normal barrier function as in other organs. Thus, our understanding of pericyte biology in mature lungs under homeostatic conditions is limited.

The lung has limited ability to regenerate compared to skin and gut epithelium. Acute lung injury from a variety of insults leads to denudement of damaged alveolar epithelium and a concurrent local inflammatory response. This is normally followed by resolution of inflammation, transient scarring, and repopulation of the lost epithelial barrier. In some instances, a pathological response results in persistent scarring or fibrosis, leading to distortion of normal architecture and impairment of lung function. The precise cellular mechanisms that control regenerative versus pathological responses in the lung remain an area of intense interest.

Accumulating evidence suggests pericytes are important in regulating lung repair as progenitors of myofibroblasts and mesenchymal progenitor cells. The multidrug resistance transporter ATP-binding cassette G (ABCG2) was identified as a marker in lineage-tracing experiments that labeled mesenchymal progenitor cells (MPCs) that give rise to pericytes (Jun et al. 2011; Marriott et al. 2014; Chow et al. 2013; Gaskill et al. 2017). Differentiation of ABCG2-lineage cells to mature pericytes was important in attenuation of bleomycin-induced lung fibrosis and restoration of normal vascular function following injury (Gaskill et al. 2017). Overexpression of the Wnt/β-catenin pathway in ABCG2-lineage cells led to increased pericyte specification without maturation. These mice developed worse lung fibrosis and increased microvascular dysfunction, suggesting MPC differentiation into mature, functional pericytes is integral to normal repair in the lung. There may be other pools of progenitors that give rise to renewal of pericytes in different physiologic contexts such as aging and apoptosis. Identification of the progenitor pool and understanding the molecular signals that direct regeneration will greatly advance the field's understanding of normal and abnormal repair in the lung interstitium, with relevance to many chronic pulmonary diseases such as COPD and interstitial lung diseases where effective medical therapy continues to be lacking.

One aspect of the regenerative response that has garnered significant attention is the identity of adult progenitor cells that are capable of self-renewal or even renewal of other cell lineages (multipotency). These elusive adult progenitor cells are thought to be of mesenchymal origin and are often referred as mesenchymal stem cells (MSCs). Pericytes have been postulated to be a source of MSCs in multiple organs (Crisan et al. 2008). MSCs are marked by expression of the transcription factor Gli1 and ABCG2 and comprise a small subset of the PDGFR_{β+} cells in the lung (Marriott et al. 2014; Chow et al. 2013; Kramann et al. 2015). Although these MSCs have been called "pericytes," this term primarily reflects their anatomical location, as they do not express other markers associated with mature pericytes in the mouse, such as NG2 and CD146. Using a genetic tracing approach to isolate ABCG2+ cells, Chow et al. showed that lung MSCs can differentiate into NG2+ pericytes and endothelial cells in vitro (Chow et al. 2013). In contrast, a study using the transcription factor Tbx18 as a marker of pericytes found that Tbx18-lineage cells did not exhibit multipotency in vivo (Guimaraes-Camboa et al. 2017). Likewise, we did not detect expression of MSC markers on human lung pericytes (defined by NG2+ PDGFRB+) in vitro (Wilson et al. 2018). One possibility to account for the conflicting reports on pericyte multipotency is that cell culture environments often introduce non-physiologic cues that may induce phenotypic changes in pericytes, cues that are not representative of the native tissue environment where pericytes reside. To date, there is no evidence to suggest lung pericytes possess multipotent cell fate plasticity in vivo.

3.4 Pericytes in Lung Disease

Lung Inflammation and Injury Historically, focus on pericytes has been limited to their functions as structural mural cells that support vascular maturation and endothelial homeostasis. Accumulating evidence, however, suggests these specialized cells may have broader biological functions. One area that has captured the interest of investigators is the potential role of pericytes in immunity. Much of the evidence for pericytes in inflammation comes from studies in the central nervous system where pericytes elaborate chemoattractants, adhesion molecules, and paracrine signaling to amplify local inflammation (Jansson et al. 2014; Rustenhoven et al. 2017).

3 Pericytes in the Lung

Similar to findings in other organs, our group has shown that mouse lung pericytes respond to pro-inflammatory signaling. Murine lung pericytes possess multiple functional TLRs and elaborate cytokines in response to specific TLR agonists in vitro (Table 3.3) (Hung et al. 2017a). Similarly, cultured human lung pericytes respond to inflammatory cues and upregulate cytokine expression. Compared to mouse lung pericytes, human lung pericytes exhibited a narrower range of TLR responses, with TLR 2/6 and TLR 4 signaling leading to the most robust proinflammatory responses (Table 3.3). We showed that depletion of pericytes by DT exposure attenuated the acute inflammatory response in a sterile lung injury model (Hung et al. 2017a, b). How lung pericyte ablation affects the inflammatory profile in other models of sterile lung injury and infectious models is yet to be defined. Based on our experience, we speculate that pericytes play an important supportive role in mediating local lung inflammation. Their perivascular position in the alveoli suggests they may play important roles in the activation of the endothelium through paracrine signaling and direct contact during inflammation. Furthermore, they reside in a prime location to sense pro-inflammatory alveolar components and may be one of the very first responders to alveolar damage. Beyond the production of inflammatory cytokines, pericytes may also direct trafficking of inflammatory cells that exit systemic circulation through upregulation of adhesion molecules as well as modification of the extracellular matrix in the perivascular space and the lung interstitium.

Pulmonary Fibrosis During pulmonary fibrosis, the main effector cell for matrix production is the lung myofibroblast. However, the origin of lung myofibroblasts remains controversial. In our transgenic mouse model work, we found that FoxD1-

Species	Stimulus	Inflammatory cytokines and adhesion molecules	
Mouse	IL-1r	CXCL1, CXCL2, CXCL10, CCL2, ICAM1	
	TLR2/1	CXCL1, CXCL2, CXCL10, CCL2, TNFα, ICAM1	
	TLR2/6	CXCL1, CXCL2, CXCL10, CCL2, TNFα, ICAM1	
	TLR4	CXCL1, CXCL2, CXCL10, CCL2, TNFα, ICAM1	
	TLR5	ICAM1	
	TLR7	CXCL1, CXCL2, CXCL10, CCL2, TNFα, ICAM1	
	TLR9	CXCL2, TNFα	
Human	TLR2/6	CXCL1, CXCL2, CXCL8, CCL2, ICAM1	
	TLR4	CXCL1, CXCL2, CXCL8, CCL2, ICAM1	

Table 3.3 Inflammatory response of lung pericytes^a

^aPericytes were selected based on PDGFRβ positivity

derived cells express common markers used to identify pericytes such as PDGFRß, NG2, and CD146, while they lack expression of endothelial-, epithelial-, or hematopoietic-specific markers. In addition, FoxD1-derived cells are located adjacent to endothelial cells, suggesting they are indeed pericytes (Fig. 3.2) (Hung et al. 2013). Importantly, they contributed to >50% of α -smooth muscle actin (α SMA)-positive myofibroblasts in the bleomycin model of lung fibrosis (Hung et al. 2013) (Fig. 3.2). Our study and Rock et al. (Rock et al. 2011) found other cell types contribute significantly to the myofibroblast pool in the lung. In contrast, in both kidney and liver models of fibrosis, pericytes were the predominant source of myofibroblasts (Lin et al. 2008; Humphreys et al. 2010; Mederacke et al. 2013). These findings establish the novel concept that pericytes are key effectors and potential therapeutic targets in pulmonary fibrosis.

Pulmonary Arterial Hypertension Pulmonary Arterial Hypertension (PAH), defined by elevated mean arterial pressure > 25 mmHg at rest, is characterized by progressive remodeling of the distal pulmonary arterials with resultant increase in pulmonary vascular resistance, leading to right heart failure and ultimately death. Pulmonary endothelial dysfunction is a key feature of PAH pathogenesis. The pulmonary artery wall includes a secondary layer of vascular smooth muscle cells (SMCs) or smooth muscle-like pericytes (Hemnes and Humbert 2017). Pericytes isolated from PAH lungs had impaired association with endothelial cells (Yuan et al. 2015). Another study showed increased number of pericytes (defined by 3G5 staining) surrounding pulmonary vessels of all sizes in explanted human PAH lungs and in rodent models of pulmonary hypertension (Ricard et al. 2014). Furthermore, the increased number of pericytes was detected before changes in arterial pressures were detected, suggesting the changes in pericyte were not secondary to hemodynamic derangements. Their data suggested that dysregulated FGF2 and IL-6 signaling from endothelial cells drive pericyte proliferation during PAH and contribute to pathogenesis.

Interestingly, there were two case reports of infants with Adams-Oliver syndrome, a rare genetic disorder characterized by congenital scalp defects and limb defects of unknown pathogenesis, who developed severe infantile pulmonary hypertension, intracranial bleeding, and cutis marmorata telangiectatica congenita (Patel et al. 2004). At autopsy, lack of pericyte coverage was found areas of vascular dilatation, while increased pericyte coverage and proliferation were found in association with vessel stenosis. They hypothesized that aberrant pericyte recruitment caused pulmonary hypertension in this syndrome (Patel et al. 2004). These studies support the role of pericyte recruitment and proliferation in the pathogenesis of pulmonary arterial hypertension.

Hereditary Hemorrhagic Telangiectasia Hereditary Hemorrhagic Telangiectasia (HHT) also known as Osler-Weber-Rendu syndrome is an autosomal dominant disorder characterized by arteriovenous malformations (AVM) affecting major organs, particularly the lung, liver, and brain. Lung AVMs are more commonly seen in HHT1 patients. Most HHT1 patients have mutations in *ENG* encoding endoglin

(McAllister et al. 1994), a receptor for transforming growth factor- β (TGF β)/bone morphogenetic protein (BMP) expressed primarily in endothelial cells and pericytes. Impaired communication between endothelial cell and pericyte, including loss of normal TGF β activation and signaling, is postulated to lead to impaired pericyte differentiation and vessel maturation in HHT (Thalgott and Lebrin 2015). One group reported that thalidomide increased pericyte number, α -SMA expression, and their recruitment to blood vessels in a mouse model of HHT, leading to vasculature stabilization (Thalgott and Lebrin 2015). A speculated mechanism was a thalidomide-induced increase of PDGF-B expression by endothelial cells.

Pericytes and Asthma Asthma is a common disease characterized by recurrent inflammatory episodes with airway and vascular remodeling. The airway remodeling includes myofibroblast accumulation, collagen deposition, and increased smooth muscle mass leading to subepithelial fibrosis and airway narrowing. Our understanding of the contributions of pericytes in asthma is limited. In a murine model of chronic house dust mite (HDM) exposure, investigators noted decreased capillary-associated pericyte coverage (defined by NG2 positivity) and increased subepithelial (peribronchial) pericytes. These findings were exaggerated when mice were treated with a PDFGR β inhibitor and resulted in worsened airway hyperresponsiveness and airway smooth muscle thickening (Johnson et al. 2015). Given evidence supporting pericyte transition to myofibroblast in other conditions, it is interesting to speculate that pericytes likewise contribute to subepithelial fibrosis in asthma. However, more studies are needed to define a role of pericytes in asthma pathogenesis.

3.5 Conclusion

We are only beginning to appreciate the multiple roles pericytes play in lung disease pathogenesis. Studies in animal models suggest lung pericytes exhibit a degree of biological plasticity that was previously underappreciated. They participate in inflammation and fibrosis, and they also regulate microvascular permeability and stability (Fig. 3.3). Clinically, some disorders such as pulmonary hypertension and HHT are associated with changes in pericyte coverage. So are pericytes beneficial or harmful in disease? To date, there is not enough information on lung pericytes to answer this question. The timing of pericyte activation during disease, the interaction of pericytes with their cellular neighbors and their microenvironmental niche when homeostasis is disturbed, and the environmental cues that activate pericytes are some of the important knowledge gaps in lung pericyte biology that require further study. Refining methods to identify, isolate, and manipulate lung pericytes in the laboratory will be essential to advancing knowledge on these cells in pulmonary health and disease.



Fig. 3.3 Schematic of potential roles of pericytes in the lung

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