

Dendritic Cell Trafficking and Function in Rare Lung Diseases

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Abstract

Dendritic cells (DCs) are highly specialized immune cells that capture antigens and then migrate to lymphoid tissue and present antigen to T cells. This critical function of DCs is well defined, and recent studies further demonstrate that DCs are also key regulators of several innate immune responses. Studies focused on the roles of DCs in the pathogenesis of common lung diseases, such as asthma, infection, and cancer, have traditionally driven our mechanistic understanding of pulmonary DC biology. The emerging development of novel DC reagents, techniques, and genetically modified animal models has provided abundant data revealing distinct populations of DCs in the lung, and allow us to examine mechanisms of DC development,

migration, and function in pulmonary disease with unprecedented detail. This enhanced understanding of DCs permits the examination of the potential role of DCs in diseases with known or suspected immunological underpinnings. Recent advances in the study of rare lung diseases, including pulmonary Langerhans cell histiocytosis, sarcoidosis, hypersensitivity pneumonitis, and pulmonary fibrosis, reveal expanding potential pathogenic roles for DCs. Here, we provide a review of DC development, trafficking, and effector functions in the lung, and discuss how alterations in these DC pathways contribute to the pathogenesis of rare lung diseases.

Keywords: dendritic cells; histiocytosis; sarcoidosis; fibrosis; hypersensitivity pneumonitis

Dendritic Cells

Dendritic cells (DCs) were first described by Ralph Steinman and Zanvil Cohn in 1973 (1) as cells with branching, extended cellular processes that distinguish them from other adherent myeloid cells, such as monocytes and macrophages. DCs are distributed throughout the body and are the “professional” antigen-presenting cells of the immune system. Most notably, they are known to acquire antigen in tissues, migrate to draining lymph nodes (LNs), and initiate T cell–mediated immunity. Recently, our understanding of the origins, development, and effector functions of DCs

has greatly expanded with the advent of DC-specific reagents and genetically engineered mice. These newly developed tools and their functions are summarized in Table 1 (2–9). Human DCs are notoriously difficult to isolate, maintain, and study. Therefore, most of our understanding of DC biology is derived from studies performed in mice. We focus on DC biology based on mouse DCs, but cite relevant human data to the extent that it is available.

DCs originate in the bone marrow, circulate in the blood, and either enter the LNs via high endothelial venules (HEV) to give rise to lymphoid DCs or enter

peripheral tissues to give rise to nonlymphoid DCs (10). Novel reporter mice reveal that DCs arise from monocyte–DC progenitors derived from hematopoietic stem cells. As illustrated in Figure 1, hematopoietic stem cells give rise to common myeloid progenitors, including a subset of FMS-related tyrosine kinase 3–expressing cells, which differentiate into more restricted macrophage and DC progenitors (MDPs) in the bone marrow. The FMS-related tyrosine kinase 3–expressing MDPs are the direct precursors to common DC progenitors, which give rise to precursor DCs (pre-DCs) and plasmacytoid DCs

(Received in original form February 9, 2017; accepted in final form June 6, 2017)

This work was supported in part by the support from National Institutes of Health grants HL119538 (M.T.B.), HL115334 (C.J.), and U54HL127672 (F.X.M.), and Veteran's Administration grant I01BX002347 (M.T.B.).

Author Contributions: Conception and design—M.T.B. and F.X.M.; drafting the manuscript for important intellectual content—H.L., C.J., A.R.O., R.L.N., N.G., F.X.M., and M.T.B.

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Am J Respir Cell Mol Biol Vol 57, Iss 4, pp 393–402, Oct 2017

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Originally Published in Press as DOI: 10.1165/rcmb.2017-0051PS on June 6, 2017

Internet address: www.atsjournals.org

Table 1. Currently Available Advanced Tools in Dendritic Cell Area, Their Applications, and Beneficial Areas

Tools	Application	Beneficial Area	Reference
Immortalized DC line	DC gene modification, <i>in vitro</i> responsiveness	DC activation and signaling	2
Multichannel flow cytometry and monoclonal antibodies	DC surface marker measurement, intracellular staining, DC tracking	DC biology and characterization	3
Reporter genes	DC trafficking	DC migration	4, 5
Magnetic bead-based DC isolation/fluorescence-activated cell sorting	DC isolation	DC biology	6
Cre-Loxp/Crispr-Cas gene modification	Mouse model development, induce specific mutations in DC	Disease models, define DC role in disease pathogenesis	7
RNAseq/epigenetic analyses	DC gene expression assay	Subpopulation delineation	8, 9

Definition of abbreviations: Cas, CRISPR associated protein; Cre, Cre recombinase; Crispr, clustered regularly interspaced short palindromic repeats; DC, dendritic cell; Loxp, locus of X[cross]-over in P1; RNAseq, RNA sequencing.

(pDCs) (11, 12). pre-DCs and pDCs leave the bone marrow and travel via the circulation to secondary lymphoid organs and nonlymphoid tissues. pre-DCs terminally differentiate into conventional

DC (cDC) subsets in the periphery (13). Alternatively, MDPs give rise to common monocyte progenitors, which differentiate into circulating monocytes (14). Circulating Ly6C⁺ monocytes migrate into tissue or

LN via the HEV to either give rise to macrophages, if a niche is open, or differentiate into monocyte-derived DCs (moDCs) (15, 16). moDCs are defined by their expression of major histocompatibility complex class II and CD11c, and their DC functional properties, including antigen presentation (17).

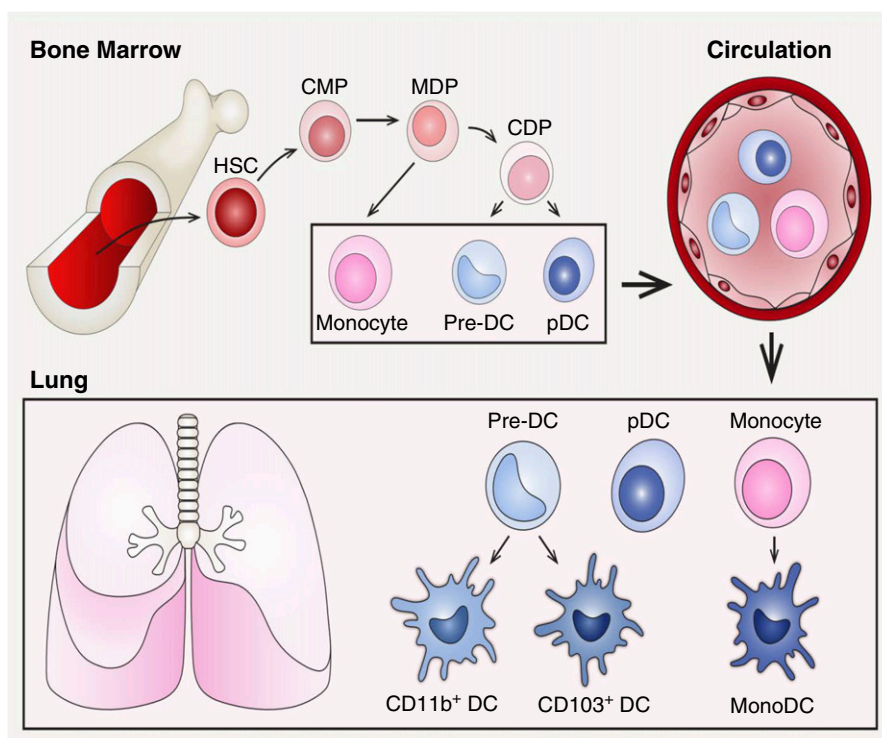


Figure 1. The origin and development of pulmonary dendritic cells (DCs) from hematopoietic stem cells (HSCs). In the bone marrow, HSCs give rise to common myeloid progenitors (CMPs), which differentiate into more restricted macrophage and DC progenitors (MDPs). MDPs give rise to common DC progenitors (CDPs), then to precursor DCs (pre-DCs) and plasmacytoid DCs (pDCs). Alternatively, MDPs can give rise to common monocyte progenitors, which then differentiate into monocytes in circulation. The pre-DCs, pDCs, and monocytes then leave the bone marrow and travel via the blood to secondary lymphoid organs and nonlymphoid tissues. After migrating into the lung, pre-DCs differentiate into CD103⁺ DC and CD11b⁺ DC subsets. Monocytes are recruited to the lungs under inflammatory stimuli and further differentiate into monocyte-derived DCs (monoDCs).

Pulmonary DC Populations

DCs are present throughout the epithelium and interstitium, where they are ideally positioned to monitor the luminal microenvironment. Flow cytometry is a powerful tool for studying the immune system, and DCs are most commonly distinguished from other cells by the expression of various combinations of surface markers. These markers include the presence and relative expression levels of adhesion molecules, chemokine and cytokine receptors, and Toll-like receptors (TLRs) as summarized in Table 2 (18–21). In mice, there are two major cDC subsets, CD103⁺ DCs and CD11b⁺ DCs, which are developmentally regulated by transcription factors basic leucine zipper transcription factor ATF-like 3 (Batf3) and interferon regulatory factor 4 (Irf4), respectively (22–25). CD103⁺ DCs and CD11b⁺ DCs have nonlymphoid and lymphoid counterparts based on function and origin. Nonlymphoid CD103⁺ DCs are thought to be the counterparts of lymphoid CD8⁺ DCs and nonlymphoid CD11b⁺ DCs of lymphoid CD8⁻CD11b⁺ DCs (15). Another major subset is pDCs, which are important in maintaining self-tolerance and are responsible for

Table 2. Cell Surface Phenotype of Human and Mouse Dendritic Cells

Species	Subpopulation	Subsets	Cell Surface Marker	Residence in Lung under Steady State	Toll-Like Receptors	CCRs on Immature DCs	CCRs on Mature DCs
Mouse	cDC	CD11b ⁺ DC	CD11c ⁺ , CD8α ⁻ , CD11b ^{hi} , CD103 ⁻ , MHC class II ⁺ , Langerin ⁻	Yes	1, 2, 4, 6, 7, 8, 9, 13	CCR1, CCR2, CCR4, CCR5, CXCR3, CXCR4	CCR7, CXCR4
		CD103 ⁺ DC	CD11c ⁺ , CD8α ⁻ , CD11b ^{lo/-} , CD103 ⁺ , MHC class II ⁺ , Langerin ⁺	Yes	2, 3, 4, 6, 9, 11, 12, 13		
	pDC	pDC	CD11c ^{int} , CD11b ^{lo/-} , B220 ⁺ , Ly6c ⁺ , MHC class II ^{-/lo} , Siglech ⁺	Yes	7, 9, 12		
	moDC	moDC	CD11c ⁺ , CD64 ⁺ , CD11b ^{hi} , CD103 ⁻ , MHC class II ⁺ , Langerin ⁻ , Ly6C ⁺	No	3, 7, 8		
Human	cDC	CD1c ⁺ DC	CD1c ⁺ , CD11b ⁺ , CD11c ⁺ , CD13 ⁺ , HLA-DR ⁺ , BDCA-1 ⁺	Yes	1, 2, 3, 4, 5, 6, 8, 10	CCR1, CCR2, CCR4, CCR5, CCR6, CXCR1, CXCR4	CCR7, CXCR4
		CD141 ⁺ DC	CD141 ⁺ , XCR1 ⁺ , CLEC9A ⁺ , BDCA-3 ⁺	Yes	2, 3, 8		
	pDC	pDC	CD11c ^{dim} , BDCA2 ⁺ , BDCA4 ⁺ , CD123 ⁺ , L-selectin ⁺ , IL-3R ⁺ , HLA-DR ^{-/lo}	Yes	7, 9		
	moDC	moDC	CD14 ⁺ , HLA-DR ⁺ , CD1c ⁻ , CD141 ⁻ , DC-SIGN ⁺ , CD163 ⁺	No	3, 7, 8		

Definition of abbreviations: CCR, chemokine receptor; cDC, conventional DC; CXCR, C-X-C chemokine receptor; DC, dendritic cell; HLA-DR, human leukocyte antigen-antigen D related; MHC, major histocompatibility complex; moDC, monocyte-derived DC; pDC, plasmacytoid DC.

the production of large amounts of type I IFN- α (26, 27). In addition, the moDC population is a subset of DCs recruited from circulation into the lung in response to infection or injury (28).

Compared with mouse DCs, there is no clear consensus regarding the classification of human pulmonary DC subsets. Human DCs and mouse DCs share basic similarities, and can be divided into cDC and pDC populations (29, 30). Genomic and functional studies indicate human epithelial-associated DCs can also be divided into four major subpopulations, which are: pDCs, CD1c⁺ DCs, CD141⁺ DCs, and moDCs (10, 31). The specific surface markers that facilitate discrimination between these subpopulations are detailed in Table 2. However, this classification has been challenged by a recent study that identified five different DC subsets in human lung based on differential expression of Langerin, CD1c, and CD14 (8). Clearly, it is important to obtain and collate additional

transcriptional and functional data to definitively classify human pulmonary DCs and other mononuclear phagocytes.

DC Localization and Migration

In mice, all DC subtypes are found in the lung under steady-state conditions (32). However, subsets of lung DCs are differentially distributed. CD103⁺ DCs are closely associated with the respiratory epithelium and extend processes into the airway lumen, whereas CD11b⁺ DCs mainly reside beneath the airway basement membrane (Figure 2) (33–35). Under steady-state conditions, a limited number of DCs reside in lung tissue and patrol the environment, whereas circulating pre-DCs migrate into the lung at a constant rate to replenish the resident DC pool, as it turns over every 10–14 days (13, 36, 37). In mice, DCs constitute up to 0.5–2% of total lung leukocytes at steady state (6). After

exposure to antigens, pathogens, or proinflammatory cytokines, different subsets of lung DCs are rapidly recruited to the lung, and comprise up to 5% of total lung leukocytes (18). However, the number of DCs in the lung is difficult to estimate, given their relatively short lifespan and their migratory behavior. For example, after DCs encounter antigens, they become activated, deploy innate immune defenses, and migrate to draining mediastinal LNs, where they initiate adaptive immune responses and facilitate peripheral tolerance (38). Moreover, during inflammation, monocytes are rapidly recruited into the lung, differentiate into moDCs, and participate in the inflammatory response by secreting cytokines and chemokines, which, in turn, recruit and activate additional leukocytes (Figure 2) (28, 39).

DC migration is tightly regulated by specific chemokines and adhesion molecules under both physiological and inflammatory conditions (32). DC migration from the blood into the inflamed tissues is controlled

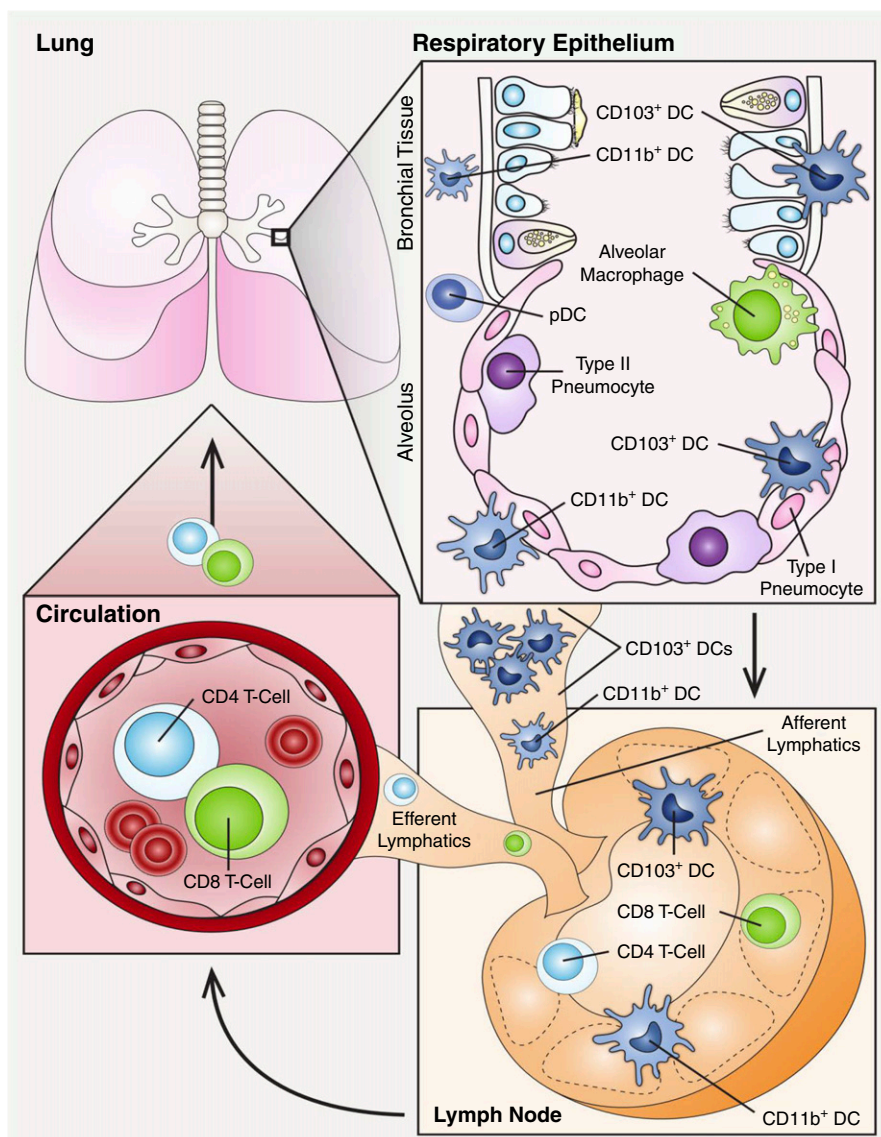


Figure 2. Distribution and migration of pulmonary DCs. Subsets of DCs are widely distributed throughout the lung, and segregate into unique niches that vary by lung compartment. In the upper respiratory tract, CD103⁺ DCs mainly reside in the mucosal wall and extend processes into the airway lumen in between epithelial cells. CD11b⁺ DCs and pDCs are mainly located underneath the basement membrane. After maturation, both CD103⁺ DCs and CD11b⁺ DCs can migrate to lymph nodes (LNs) via lymphatics and present antigens to T cells. CD103⁺ DCs are the migratory subsets that populate LNs.

by several chemokine receptors (CCRs), including CCR1, CCR2, CCR5, and CCR6 (40–42). CCR6 on immature DCs and its ligand, CCL20, is the most important chemokine axis for recruitment of DCs to the lung from circulation (32, 43). Lung epithelial cells express a basal level of CCL20 to maintain DC homeostasis. However, CCL20 expression is rapidly induced after encountering pathogenic and environmental stimuli (43). Lung DC

recruitment is also mediated by additional CCRs, such as CCR2, as well as other factors that facilitate DC migration, including E- and P-selectins, adhesion molecule L1, and integrins CD11b/CD18 (44–47).

DC trafficking from the lung to the draining LNs rapidly increases during inflammation and infection (48, 49). Lymphatic channels provide important routes for cell migration and are critical for

DC trafficking between peripheral tissues and LNs (50). In the lung, DCs first migrate to bronchopulmonary LNs through the lymphatics, then drain into the mediastinal trunk (Figure 2) (51). Egress of DCs from lung to draining LNs is tightly regulated (32). After pathogenic or environmental activation, DCs undergo maturation, decrease CCR6 expression, and increase CCR7 expression (32, 52). CCR7 is the CCR that drives DC migration along gradients toward higher concentrations of ligands, CCL19 and CCL21, produced in the lymphatics and draining LNs (53, 54). CCL19 is primarily secreted by stromal cells and mature DCs in the T cell zone of LNs (55), whereas CCL21 is produced constitutively by stromal cells and endothelial cells of lymphatic vessels and of HEVs (56). DC egress can also be influenced by other mediators, such as prostaglandin E2 and sphingosine-1-phosphate (57, 58). Knowledge of how human antigen-laden DCs migrate from lung to peripheral LNs is limited. However, like mouse DCs, human DCs decrease CCR6 expression and increase CCR7 expression after maturation allowing migration toward CCR7 ligands (59).

DC Function in Pulmonary Disease

Much of our knowledge of DC function in pulmonary disease derives from the study of infectious diseases and common lung diseases. We know that DC function is tissue, pathogen, and context specific. For example, during viral infection, DCs endocytose viral antigens and migrate to the mediastinal LNs, where they activate antigen-specific naive and memory T cells (60). Mouse studies reveal that these T cells undergo multiple rounds of proliferation and migrate out of the LN into peripheral tissues, where they interact with newly recruited DCs that present viral antigens within the infected tissue. In infected tissue, cytotoxic effector T cells orchestrate the direct killing of infected cells expressing viral antigens on the cell surface and contribute to the production of proinflammatory cytokines that help in the resolution of infection (61, 62). DCs respond differently in the context of *Mycobacterium tuberculosis* lung infections. During *M. tuberculosis* infection, DCs

phagocytose the pathogen, leading to the production of high levels of inflammatory cytokines, including IL-6, TNF- α , IL-12, IL-1 α , and IL-1 β . These cytokines stimulate additional leukocytes and contribute to granuloma formation as a mechanism to control pathogen growth and distribution (63). The unique roles of DCs in asthma further exemplify the complex and plastic functional properties of DCs in lung diseases. In patients with asthma and mouse models of allergic asthma, multiple DC populations are increased in the lung that secrete lymphocyte activating cytokines, which are associated with disease severity (64). In asthma, otherwise harmless antigens modify airway epithelial barrier function and activate epithelial cells in a manner that leads to DC activation and the initiation of an allergic T cell response. For example, house dust mite feces contain allergens with proteolytic activity that costimulate TLRs on resident lung cells. These events lead to production of epithelial chemokines, including CCL20, which recruit lung DCs. Furthermore, the proteolytic activity of the allergens can promote the production of cytokines that drive immune responses in DCs (64–66).

DC Function in Rare Lung Disease

Pulmonary Langerhans Cell Histiocytosis

Pulmonary Langerhans cell histiocytosis (PLCH) is a rare interstitial lung disease characterized by the accumulation of Langerin-positive DCs, bronchiolocentric nodule formation, and cystic remodeling of the lung (67). PLCH is usually a single-system disorder, with pulmonary impairment ranging from asymptomatic disease to life-threatening respiratory failure (68). PLCH occurs almost exclusively in active and former smokers (67) with the crude prevalence estimated at 0.27 and 0.07 per 100,000 in males and females, respectively (68, 69). Historically, PLCH was considered an idiopathic reactive disease, because of large numbers of inflammatory cells found around pulmonary lesions and the presence of high levels of inflammatory cytokines (70). However, recent genetic analyses indicate that PLCH is more accurately defined as an inflammatory neoplastic disorder. This classification is based on studies that

demonstrate more than 50% of patients with PLCH have an acquired, activating mutation in the proto-oncogene rapidly accelerated fibrosarcoma B (BRAF) within the DC lineage that results in constitutive activation of the mitogen-activated protein kinase (MAPK) pathway (71, 72). The most common mutation identified is BRAF V600E, but recent studies revealed mutations in other signaling proteins in the MAPK pathway (73, 74). Interestingly, the DCs in PLCH lesions express high levels of DC maturation markers, which may contribute to the local “cytokine storm” that drives nodule formation and/or cystic remodeling (75). DCs exhibit decreased expression of CCR6 and increased CCR7 expression after maturation, which promotes DC migration toward draining LNs (32). However, Fleming and colleagues (76) showed that DCs within lesions express both CCR6 and CCR7 in the pediatric form of systemic Langerhans cell histiocytosis. Therefore, it is possible that altered regulation of CCR6 and CCR7 contributes to the increased accumulation and activation of DCs in PLCH. Alternatively, the aberrant accumulation of DCs in the lung may be a consequence of enhanced DC proliferation or viability. Indeed, MAPK pathway activation, especially BRAFV600E, has been known to be involved in increased cell proliferation and/or decreased cell apoptosis in melanoma and thyroid cancer (77, 78).

In addition to genetic mutations in the MAPK pathway, cigarette smoke is believed to be a key complementary factor in PLCH pathogenesis. Smoking is known to increase the expression of several proinflammatory mediators in the lung, such as TNF- α , granulocyte/macrophage colony-stimulating factor, transforming growth factor- β , and CCL20, which are involved in DC differentiation and function (79). The effects of smoking on DC function have been investigated in other smoking-related diseases, such as chronic obstructive pulmonary disease (COPD). Overall, the number and maturation state of pulmonary DCs is increased in COPD. However, regional lung differences in patients with COPD are present, such as increased numbers of immature DCs in small airways and decreased total numbers of DCs in large airways (80–82). Cigarette smoke increases CCL20 and recruits DCs into the lung in patients with COPD and lung cancer (83–85). In addition, DCs from

patients with COPD and mice exposed to cigarette smoke exhibit enhanced survival (86), and studies from smokers and mouse models indicate that multiple cytokines and chemokines that affect DC maturation, activation, and migration are elevated after smoking (87, 88). The facts that the majority of patients with PLCH are current smokers and that the disease sometimes regresses with smoking cessation suggest that the pulmonary microenvironment created by cigarette smoke is required for disease expression and persistence. However, the specific nature of the alterations in the pulmonary microenvironment responsible for recruiting and retaining DCs are unknown.

Sarcoidosis

Sarcoidosis is a systemic granulomatous disease of unknown etiology that causes inflammation and tissue damage in multiple organs, most commonly the lung. The incidence of sarcoidosis in the United States is approximately 10.9 and 35.5 per 100,000 persons of European and African descent, respectively (89, 90). Although the etiology is unknown, increasing evidence suggests that sarcoidosis is an antigen-driven autoimmune disease (91, 92). It is characterized by Th1 T cell polarization and exaggerated immune responses against unknown causative antigens (93–95). Although most research has focused on alveolar macrophages as the primary pathogenic antigen-presenting cells in sarcoidosis, more recent evidence indicates that DCs play a causative role. There is an increased number of DCs in the draining LNs of patients with sarcoidosis and, unlike other inflammatory lung diseases, there is an increased number of immature DCs in the lung tissue, especially the alveolar space (94). Furthermore, there is a twofold increase in cDCs in bronchoalveolar lavage (BAL) from patients with sarcoidosis, which express lower levels of the maturation marker, CD83, and the costimulatory molecule, CD86 (96). Pulmonary DCs from patients with sarcoidosis demonstrate a reduced capacity to induce T cell proliferation *ex vivo* compared with DCs isolated from healthy lungs, suggesting that the immature surface marker phenotype correlates with an observed reduction in DC function (97). IFN- γ is one of the most important cytokines that induce DC maturation and

cytokine production, including the major Th1 polarizing cytokine, IL-12. Interestingly, IFN- γ and IL-12 levels are elevated in sarcoidosis BAL fluid, suggesting a defect in the process of IFN- γ -dependent DC maturation (98, 99). Furthermore, moDCs isolated from patients with sarcoidosis display normal maturation markers, but have an enhanced ability to induce TNF- α expression when cocultured with allogeneic naive CD4⁺ T cells (93). The role of TNF- α in sarcoidosis pathogenesis and prognosis has been well studied. Although the role of DCs remains to be defined, the high abundance of TNF- α receptor on DCs suggests that DCs may be important regulators of TNF- α -mediated disease progression. Similar to another DC-involved autoimmune disease, psoriasis, TNF- α inhibitors have been clinically tested in patients with sarcoidosis with some promising preliminary outcomes in selected patient subsets (100, 101). Due to undeveloped techniques and knowledge, most earlier studies did not differentiate macrophages from DCs in BAL fluid, and additional studies are necessary to define distinct roles in sarcoidosis. Taken together, these data clearly demonstrate dysfunction within the DC population in sarcoidosis, and the enrichment of DCs in the lung and draining LNs suggests that abnormal DC tracking contributes to pathogenesis. As increasing evidence emerges, it is possible that DC-targeted therapy may become a promising clinical option.

Hypersensitivity Pneumonitis

Hypersensitivity pneumonitis (HP) is an interstitial lung disease commonly characterized by granulomatous inflammation with prominent infiltration of lymphocytes, macrophages, and fibroblasts around indigestible antigens or particles. A large variety of antigen and/or particle exposures can result in HP. Based on the rate of progression, HP can be divided into acute, subacute, and chronic forms, although clinical presentations may overlap (102). HP pathogenesis is complex, but a consensus understanding of HP involves pre-existing genetic susceptibilities and/or environmental factors, followed by exposure to specific antigens. It has been suggested that acute HP is mediated by immune complex formation, whereas enhanced Th1 responses are responsible for the subacute and chronic forms (102). Studies also implicate cytotoxic delayed

hypersensitivity in the observed abundance of Th1/Th17 cytokines and mechanisms of tissue injury (103). In addition, type III and type IV hypersensitivity have been noted to result in fewer granulomas, but more extensive fibrotic remodeling in some patients (104). Given the importance of DCs in maintaining lung immune homeostasis, the development of granuloma formation, and mediating hypersensitivity reactions, a causative role in the development and progression of HP is certain. Human data are limited, although there is a fivefold increase in the number of DCs in the lungs of patients with chronic HP compared with healthy control subjects (105). Much of our current understanding of HP pathogenesis is derived from animal models. An acute HP mouse model indicates that increased numbers of mature DCs persist in the lungs of *Saccharopolyspora rectivirgula*-challenged animals, and that these DCs play a causative role in granuloma formation via increased production of proinflammatory chemokines (106). Indeed, mice deficient in IFN- γ do not develop granulomatous lesions after exposure to *S. rectivirgula* (107). Furthermore, depletion of CD34, a cell surface receptor involved in DC migration and activation, impairs DC migration from lung to peripheral LN and renders mice resistant to the development of acute HP (108). The DCs from CD34-deficient mice show impaired cytokine secretion and fail to appropriately deliver antigen to T cells in the acute HP model. Mouse studies also reveal that DCs are critical to the development of HP pathology, as depletion of the pathogen recognition receptor, TLR9, renders DCs unable to respond to antigens. The end result is restricted Th1 cytokine and chemokine release, and attenuated lung pathology (109). Similar to patients with HP, there are increased numbers of mature DCs in the lungs of the acute HP mouse model (106). The apoptosis of granulocytes and nonhematopoietic cells are thought to contribute to HP pathogenesis by activating DCs to increase proinflammatory chemokine production (110). The local enrichment of these chemokines recruits other inflammatory cells to the lung, amplifying HP pathological changes. Together, the evidence suggests that DC maturation, migration, and interaction with other cells are critical to the pathogenesis of

HP. Unfortunately, neither the human studies nor mouse models have identified specific populations of DCs involved in the pathogenesis of HP. Identifying these populations or other mechanistic details will facilitate future targeted approaches to reduce the immune-mediated components of HP pathology.

Idiopathic Interstitial Pneumonias

Idiopathic interstitial pneumonias (IIPs) are a cluster of diseases sharing similar clinical and radiologic presentations. Based on histological features, IIPs are further divided into eight different subsets (111). The etiopathogenesis of all types of IIPs is poorly understood. In this review, we focus on idiopathic pulmonary fibrosis (IPF) and nonspecific interstitial pneumonia (NSIP), the most common members of this family of scarring lung diseases. NSIP is an important IIP with a clinical presentation that is similar to IPF, but is associated with a better prognosis. NSIP is the second most common cause of IIP, and is commonly associated with autoimmune connective tissue diseases (112). Little is known about the pathogenesis of NSIP, except that there is a robust accumulation of DCs in the lungs of patients with NSIP, which are in close proximity to CD8⁺ and CD4⁺ lymphocytes (113). In contrast, there are several lines of research that strongly implicate DC dysfunction in the pathogenesis of IPF, which is one of the most lethal fibrotic lung diseases (114, 115). Lung biopsy of patients with IPF reveals usual interstitial pneumonia, characterized by patchy, spatially, and temporally heterogeneous areas of early and completed fibrosis in the lung periphery and lymphatic structures. The lungs of patients with IPF are heavily infiltrated by immature DCs in areas of epithelial hyperplasia and fibrosis, whereas mature DCs, characterized by the expression of maturation markers, like CD40, CD86, and CD80, accumulate in well organized, lymph node-like structures (116). This finding is supported by other studies demonstrating increased numbers of immature DCs in the lavage fluid of patients with IPF (117). Moreover, fibroblasts and epithelial cells in patients with IPF express high levels of CCL19, which can lead to increased DC recruitment from the circulation (118, 119). Along these lines, Freynet and colleagues (120) have shown that coculture of DCs with lung fibroblasts from patients with IPF

diminishes the expression of DC activation markers. Together, these findings suggest that pulmonary fibroblasts may influence IPF progression by maintaining populations of immature DCs, which are unable to suppress ongoing inflammation.

The most common mouse model for IPF involves the administration of bleomycin to induce acute or subacute fibrosis in the lung. In this model, there is a significant accumulation of DCs in the lung after bleomycin challenge. However, unlike human IPF, the mouse DCs express high levels of maturation markers, including CD40, CD86, and CD83, and exist in close proximity to memory T cells (121). These findings are consistent with observations in other pulmonary diseases, which have revealed that maturation of lung DCs is followed by a secondary activation of memory T cells that may perpetuate chronic inflammation. Interestingly, experiments using antibodies to block DC

maturation or deplete mature DC CCRs attenuate the pathological hallmarks of pulmonary fibrosis in this model (121, 122). Unfortunately, the discrepancy of DC phenotypes between mouse models and patients with IPF suggest that the bleomycin-induced model does not accurately reflect the immune alterations observed in human disease. Mouse models that more authentically recapitulate the immune dysfunction observed in IPF are needed to further our understanding of IPF pathogenesis and the possible involvement of DC dysfunction.

Conclusions

The recent development of DC-specific reagents and informative mouse models reveal new insights into the development, maintenance, and function of pulmonary DC populations. These advances have

furthered our understanding of the unique roles of DCs in controlling tissue and immune homeostasis and in the initiation and progression of common and rare pulmonary diseases. Our future challenge is to develop high-fidelity animal models of rare lung disorders using newly available tools to study the contribution of DC development, trafficking, and lung-specific effector functions to disease pathogenesis. In addition, we need to conduct focused translational studies that use new DC-specific reagents to determine the causal relationship between specific alterations in DC function and pulmonary pathology. These efforts promise to reveal novel insights into rare diseases, inform our understanding of common lung diseases, and lead to the development of new treatment strategies. ■

Author disclosures are available with the text of this article at www.atsjournals.org.

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