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Yong-Xiao Wang *Editor*

Lung Inflammation in Health and Disease, Volume II

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Lung Inflammation in Health and Disease, Volume II

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Preface

As previously discussed in Volume I, inflammation is a natural cellular process occurring in virtually all types of human body tissues, organs, and systems. This process can be acute or chronic. Acute inflammation is a healthy, immediate response to protect and repair the body from harmful stimuli. Usually it occurs within a couple of hours. Chronic inflammation is a lengthier cellular process that is not conducive to natural healing and may lead to pathological states including arthritis, asthma, and pulmonary hypertension.

Normally, inflammation can also be classified as systemic or localized. The former affects the entire human body, which is a pathogenetic component in numerous acute and chronic diseases including atherosclerosis, diabetes, sepsis, trauma, and others with a significant morbidity and mortality. The latter is localized as in a specific organ. For example, inflammation caused by asthma and pulmonary hypertension are localized in the lungs.

Lung diseases are very common and can also be very severe. It is well known that lung infections are the greatest single contributor to the overall global health burden. For instance, lung diseases are the most common causes of deaths of children under 5 years of age, which occur more than 9 million annually. Indeed, pneumonia is the leading killer for children worldwide. Asthma is the most common chronic disease, affecting about 14% of children globally and continuing to rise. Likewise, COPD is recognized to be the fourth leading cause of death in the world and the numbers are growing. The lung is not only the largest internal organ in the human body, but also the only internal organ that is exposed constantly to the external environment; as such, no other organ is more vital and vulnerable than the lung. This may explain the common morbidity and mortality of lung diseases.

Systemic inflammation may induce and even exacerbate local inflammatory diseases. Likewise, local inflammation can cause systemic inflammation. Indeed, there is increasing evidence of coexistence of systemic and local inflammation in patients with asthma, COPD, and other lung diseases. Moreover, the comorbidity of two and even multiple local inflammatory diseases often occurs. For instance, rheumatoid arthritis not only frequently happens together with but also promotes the development of pulmonary hypertension. The comorbidity of local and systemic as well as two or more inflammatory diseases significantly deteriorates the quality of life and may even exacerbate death in patients.

The current treatment options for lung diseases are neither always effective nor specific at all. The development of new therapeutics is earnestly needed. Equally desperately, the molecular mechanisms and physiological significance of lung diseases are still not fully understood. Apparently, this despondent fact is a major encumberment to creating new efficacious drugs in the treatment of lung diseases. This scenario is even worse in two and more lung diseases accompanied with other inflammatory diseases due to their complexity and diversity.

Despite the current state being unsatisfactory, great progresses have been made in many aspects of lung diseases from the molecular geneses to regulatory mechanisms to signaling pathways to cellular processes to basic and clinical technologies to new drug discoveries to clinical manifestations to laboratory and clinical diagnoses to treatment options to predictive prognosis. To the best of our knowledge, however, no one, cohesive book is available to present these state-of-the-art advances in the field. Thus, as one of the major aims, we compile this timely and much-needed book to provide a high-quality platform in which well-known scientists and emerging pioneers in basic, translational, and clinical settings can present their latest, exciting findings in the studies of lung inflammation in health and disease. The contents from multiple outstanding authors with unique expertise and skills of molecular and cell biology, biochemistry, physiology, pharmacology, biophysics, biotechnology, translational biomedicine, and medicine will provide new knowledge, concepts, and discoveries in the field. The second major aim is to help direct future research in lung diseases and other inflammatory diseases. The scope of the book includes nearly all new and important findings from very recent basic, translational, and clinical research in the studies of the molecular genesis, networks, microdomains, regulation, functions, elimination, and drug discoveries of inflammation in lung health and disease, which are involved in animal and human lung epithelial cells, smooth muscle cells, *endothelial* cells, adventitial cells, fibroblasts, neutrophils, *macrophages*, *lymphocytes*, and stem/progenitor cells. Lastly but importantly, the book will offer the latest and most promising results from clinical trials in terms of exploring interventions of local and systemic inflammation in the treatments of lung diseases.

This book features contributions from numerous basic, translational, and physician scientists in the fields of pulmonary vasculature redox signaling in health and disease, and as a result offers a widespread and comprehensive overview for academic and industrial scientists, postdoctoral fellows, and graduate students who are interested in redox signaling in health and disease and/or normal and pathological functions of the pulmonary vasculature. The book may also be valuable for clinicians, medical students, and allied health professionals.

We are sincerely grateful for the overwhelming support from leading scientists who contributed their expertise. Due to their contributions, we are pleased to share Volume II now. Similar to Volume I, the current volume is composed of 17 chapters from prominent investigators and clinicians covering novel fundamental roles and molecular mechanisms of inflammatory cellular responses in the development of acute respiratory distress syndrome,

asthma, pulmonary hypertension, sarcoidosis, and other lung illnesses. Several articles principally deal with the interactions among inflammatory signaling with reactive oxygen species, calcium, sex, and other vital intracellular molecular signaling in lung diseases. We also share articles focused on the innovative diagnostic approaches and therapeutic treatment options in the aforementioned lung disorders. We are confident these reports detailing the most important basic, translational, clinical, and drug discovery studies will not only enrich our current knowledge, but will also serve to direct and promote future research in the field.

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I want to express my wholehearted gratitude to all of the authors for their dedication and diligence in contributing book chapters, particularly during the challenging and unprecedented times of the global COVID-19 pandemic. Many of the authors in this book have not only performed exceptional roles as writer but also as reviewer. Their selfless contributions are sincerely appreciated. I also want to thank Ms. Alison Ball and Mr. Arjun Narayanan at Springer Nature for their assistance, patience, and enthusiasm in seeing this book to fruition.

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Can GPCRs Be Targeted to Control Inflammation in Asthma?

1

Pawan Sharma and Raymond B. Penn

Abstract

Historically, the drugs used to manage obstructive lung diseases (OLDs), asthma, and chronic obstructive pulmonary disease (COPD) either (1) directly regulate airway contraction by blocking or relaxing airway smooth muscle (ASM) contraction or (2) indirectly regulate ASM contraction by inhibiting the principal cause of ASM contraction/bronchoconstriction and airway inflammation. To date, these tasks have been respectively assigned to two diverse drug types: agonists/antagonists of G protein-coupled receptors (GPCRs) and inhaled or systemic steroids. These two types of drugs "stay in their lane" with respect to their actions and consequently require the addition of the other drug to effectively manage both inflammation and bronchoconstriction in OLDs. Indeed, it has been speculated that safety issues historically associated with beta-agonist use (beta-agonists activate the beta-2-adrenoceptor (β_2AR) on airway smooth muscle (ASM) to provide bronchoprotection/bronchorelaxation) are a function of pro-inflammatory actions of β_2AR agonism. Recently, however, previously unappreciated roles of various GPCRs on ASM contractility and on airway inflammation have been elucidated, raising the possibility that novel GPCR ligands targeting these GPCRs can be developed as anti-inflammatory therapeutics. Moreover, we now know that many GPCRs can be "tuned" and not just turned "off" or "on" to specifically activate the beneficial therapeutic signaling a receptor can transduce while avoiding detrimental signaling. Thus, the fledging field of *biased agonism pharmacology* has the potential to turn the β_2AR into an anti-inflammatory facilitator in asthma, possibly reducing or eliminating the need for steroids.

Keywords

GPCR · Beta-2 agonists · Asthma · Inflammation · Bronchodilator · Obstructive lung disease · COPD · Biased agonism

Abbreviations

AHR	Airway hyperresponsiveness
ASM	Airway smooth muscle
AERD	Aspirin-exacerbated respiratory disease

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COPD	Chronic obstructive pulmonary disease
CaSR	Calcium-sensing receptor
CysLT	Cysteinyl leukotriene
IL	Interleukin
GPCR	G protein-coupled receptor
OLD	Obstructive lung diseases
mAChR	Muscarinic acetylcholine receptor
mPGES-1	microsomal prostaglandin E synthase-1
LABA	Long-acting beta-2 agonist
PG	Prostaglandin
LPS	Lipopolysaccharide
PAR-2	Protease-activated receptor-2
PMNT	Phenylethanolamine-N-mthyltransferase
PKA	Protein kinase A
SABA	Short-acting beta-2 agonist
TGFβ1	Transforming growth factor beta 1
TAS2R	Type II taste receptors
TNF-α	Tumor necrosis factor alpha
TRPV4	Transient receptor potential vanilloid 4
β_2AR	beta-2 adrenoceptor

The management of obstructive lung diseases (OLDs), asthma, and chronic obstructive pulmonary disease (COPD) is predicated on the importance of controlling excessive bronchoconstriction that increases airway resistance. Increased airway resistance manifests in the inability to breathe, which is not only potentially fatal but also impacts the quality of life [1–3]. Accordingly, drugs managing OLDs either directly regulate airway constriction by blocking or relaxing airway smooth muscle (ASM) contraction or indirectly regulate ASM contraction by inhibiting the principal cause of ASM contraction/bronchoconstriction and airway inflammation. To date, these tasks have been respectively assigned to two diverse drug types: agonists/antagonists of G protein-coupled receptors (GPCRs) and inhaled or systemic steroids.

Although it is important to recognize that non-allergic/nonatopic asthma is also an important health concern, this review will focus on allergic asthma, which has a rich history of research and drug discovery efforts dedicated to understanding and managing the disease. Herein, we will review the logic underlying allergic asthma management, the approaches undertaken to date to manage the two major features of the disease (bronchoconstriction and airway inflammation), and the ability of current and future GPCR-targeting drugs to go beyond their ability to directly regulate ASM contraction and manage airway inflammation [4].

1.1 Allergic Asthma Pathobiology and Attempts to Manage It

It is widely recognized that asthma is a complex disease, often labeled a syndrome, in which various factors can result in an exaggerated immune response to an allergen in the lung that results in obstruction to airflow. Although an increase in airway mucus contributes to this increased obstruction, airway narrowing caused by ASM contraction can greatly impede airflow, and the use of rapidly acting bronchodilators that work by relaxing ASM is usually sufficient to manage an acute asthmatic attack. Conceivably, preventing the *cause* of bronchoconstriction (airway inflammation) should be sufficient to manage asthma, but this is difficult to achieve in most asthmatics; thus, asthmatics are typically managed by either of the following: (1) prophylactic inhaled corticosteroids to control inflammation with the use of an inhaler of short-acting beta-agonist (SABA, acting on beta-2 adrenoceptors (β_2ARs) on ASM) bronchodilator to reverse bronchospasm when needed (mild asthmatics) or (2) daily prophylactic inhaled corticosteroids in combination with a long-acting beta-agonist (LABA) to help prevent (i.e., bronchoprotect)

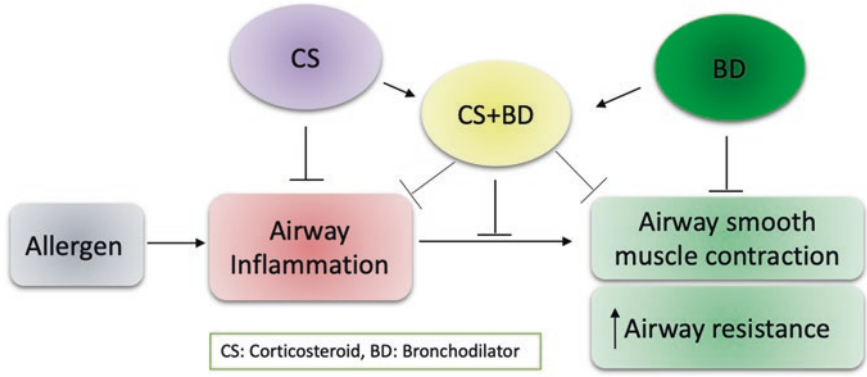

Fig. 1.1 Control of inflammation and bronchospasm in asthma. Corticosteroids (CS) when given alone can block allergic inflammation, while their effectiveness in asthma control is increased by concomitant administration of a bronchodilator (BD) such as β_2AR agonists which alone are not efficacious in controlling inflammation but are highly effective in preventing bronchospasm by targeting ASM. Of note, a modest cooperative effect in controlling inflammation and bronchospasm has been asserted by various studies

bronchospasm (mild, moderate, and some severe asthmatics). Schematic illustrating control of inflammation and bronchospasm by these drugs is depicted in Fig. 1.1.

1.2 The Relationship Between Airway Inflammation and Airway Contraction

The exaggerated immune response to allergen in the lung of asthmatics results in the production of multiple factors that cause ASM contraction. These factors include GPCR agonists that directly act on ASM to either effect contraction or sensitize the ASM to pro-contractile agents. Multiple GPCRs that can mediate ASM contraction are expressed on the plasma membrane of ASM cells [5–10]. Among the best characterized GPCRs in airway/asthma biology are the m3 muscarinic acetylcholine receptor (m3mAChR), H1 histamine receptor (H1HR), and cysteinyl leukotriene type 1 receptor (CysLT1R). Cognate ligands (acetylcholine, histamine, and CysLTs, respectively) for each of these receptors tend to be upregulated in expression in the allergen-exposed airway of asthmatics. Numerous other well-established GPCR agonists, including, but not limited to, endothelin (acting on ET-1R on ASM to induce ASM contraction), thromboxane (TP receptor), prostaglandin E2 (PGE_2; acting on EP1, EP2, EP3, and EP4 receptor with variable effects), and adenosine (acting on A1, A2a, and A2b adenosine receptors with variable effects), are induced during allergic lung inflammation and act either directly or indirectly on ASM to cause bronchoconstriction [9, 11–15]. Moreover, recent studies in human lung suggest that, whereas EP2 receptors dominate mast cell stabilizing effects of PGE_2, EP4 receptors dominate bronchodilation [16]. Recent studies have also identified (in both murine and human ASM) various GPCRs on ASM with the capacity to regulate (either contract or relax) ASM cells, ASM tissue ex vivo, or airways in vivo [17]. Numerous GPCRs have been identified as capable of mediating relaxation of contracted ASM cells, with the β_2AR being the principal GPCR targeted in asthma management for over the last 50 years [9].

Additionally, certain GPCRs that have little or limited capacity to directly stimulate pro-contractile or pro-relaxant signaling can stimulate the production of autocrine or paracrine GPCR agonists that in turn directly regulate ASM contractile state. Some GPCR agonists acting on (non-ASM) resident or infiltrating airway cells can stimulate the local release of cytokines that regulate ASM contractile state. The complexity of this intercellular communication and regula-

tion can be evidenced in a recent study by Bonvini et al., in which trypsin-activated protease-activated receptor-2 (PAR-2) on ASM cells gates *t*ransient *r*eceptor *p*otential *v*anilloid 4 (TRPV4) channels to release ATP into the extracellular space and activate P2XY purinergic channels on mast cells, which in turn release CysLT to activate CysLT1Rs on ASM and cause contraction [18].

Many of the abovementioned GPCRs, stimulated by increased endogenous levels of their cognate ligands, likely contribute in some degree to the ASM contraction and airway narrowing caused by allergic inflammation in asthma. With the exception of the m3mAChR (therapeutically targeted in asthma/COPD with the m2/m3 mAChR antagonist tiotropium [19, 20]), however, pharmacological blockade of these receptors is not sufficient to reverse acute bronchoconstriction and manage an acute asthma attack [21].

Other inflammatory agents that are typically not GPCR agonists promote increased ASM contraction by sensitizing ASM to other more direct contractile stimuli. Such agents include cytokines such as tumor necrosis factor alpha (TNF-α) and interleukin (IL)-1β, as well as transforming growth factor beta 1 (TGFβ1), IL-4, IL-13, and IL-8 [22–26]. The mechanisms by which this sensitization occurs are well established and primarily involve increasing the ASM cell's ability to contract to a given level of intracellular calcium that is released in response to contractile GPCR activation (i.e., *calcium sensitization*) [27–36].

An additional mechanism by which inflammatory agents increase ASM contraction is via their enhancement of cholinergic discharge in the airway [37–39]. Physiological contraction of ASM occurs via the release of acetylcholine from sympathetic nerves innervating ASM, to activate m3mAChRs on ASM [40, 41]. In animal models of allergic inflammation, particularly rodent models, it is clear that increased cholinergic discharge contributes significantly to the airway hyperresponsiveness (AHR) associated with allergic lung inflammation [41–43]. In human asthmatics, the relative contribution of excessive cholinergic discharge to AHR is not well understood (and is not necessary for AHR to exist) but is likely important given the therapeutic effectiveness of m3mAChR antagonists in at least a subpopulation of asthmatics [19, 20].

1.3 Current Treatment of Acute Bronchoconstriction

The life-threatening nature of an acute asthmatic attack requires rapid reversal of airway narrowing via direct regulation of ASM contraction. To date, such treatment has been almost exclusively limited to short-acting beta-agonists (SABAs) targeting the β_2AR on ASM and to a lesser extent to m3mAChR antagonists. Because multiple procontractile agonists often exist in the inflamed, asthmatic airway, specific m3mAChR antagonism may not be sufficient to reverse bronchoconstriction; thus, SABAs are the drug of choice for an asthmatic attack. Beta-agonists relax contracted airway smooth primarily by antagonizing intracellular pathways that are stimulated by contractile agonists and their cognate receptors (see [44–46] for a comprehensive review). Thus, beta-agonists tend to be effective in reversing ASM contraction caused by variable, and multiple, contractile stimuli.

1.4 Prophylactic Management of Bronchoconstriction by Controlling Inflammation

Not surprisingly, limiting or preventing the airway inflammation that causes bronchoconstriction is an excellent, and preferred, approach to manage asthma. For decades, inhaled corticosteroids have been the primary drug of choice for the management of mild asthma (with SABA inhalation when needed) [47]. However, majority of asthmatics today are managed by prophylactic, maintenance drugs consisting of an inhaled GPCR ligand (β_2AR agonist or m3mAChR antagonist) that directly targets ASM contraction, in a formulation that combines an inhaled steroid. Initially, the combination of an inhaled

long-acting beta-agonist (LABA) salmeterol along with an inhaled steroid (fluticasone) dominated the market. However, over time, other combinations of LABAs plus steroids along with long-acting muscarinic receptor antagonists (LAMAs) combined with steroids emerged, although the latter combination was and is more applicable to COPD management. The prevention/mitigation of inflammation by steroids has remained the cornerstone of the combination approaches, while the addition of more direct bronchorelaxation agents represents an additional arm of prophylactic control that could translate into better disease management including reduced exacerbations [48–50].

1.5 Control of Allergic Airway Inflammation by Steroids: Why We Keep Using the Sledgehammer Instead of a Scalpel

For the majority of asthmatics, inhaled corticosteroids are effective in controlling lung inflammation, despite the fact that they are often administered during ongoing inflammation and not necessarily prophylactically [51]. Some asthmatics, including many severe asthmatics, are *steroid-resistant* (to both inhaled and oral steroids; the cause of which is a subject of intense research and debate) and consequently have difficulty managing their disease [52–54]. Notwithstanding steroid-resistant asthmatics, steroids are powerful in suppressing allergic inflammation based on their ability to greatly suppress the pro-inflammatory function of multiple resident and infiltrating cell types in the lung and halt the progression of inflammation at multiple steps [47, 55–57]. The principal mechanism of these actions of corticosteroids involves the glucocorticoid receptor-mediated suppression of inflammatory mediator genes and to a lesser extent glucocorticoid receptor-mediated induction of other genes [47, 56, 58–65]. However, although this "sledgehammer" effect on gene regulation and multiple cell functions typically results in effective control of allergic lung inflammation, the effects of steroids are not exclusively anti-inflammatory. Numerous "off-target" effects of steroids exist, contributing to various clinical side effects associated with both inhaled and oral steroid use [53, 65]. The complement of steroid actions on inflammatory processes includes antithetical/counterproductive actions that limit therapeutic efficacy (i.e., certain anti-inflammatory processes maybe inhibited, along with pro-inflammatory processes being stimulated) [66, 67]. Ideally, a more refined approach that avoids off-target and antithetical effects would be preferable, *if* such targeting could *sufficiently* reduce inflammation to manage asthma features. Until recently, however, a more precise targeting of inflammatory mechanisms that drive asthma pathobiology did not exist. Even with the early promising results of certain biologics (typically antibodies targeting specific inflammatory mediators including IgE, IL-5, IL-5Rα, IL-4Rα, and IL-13) [68, 69], it is unclear whether targeting specific cytokines or inflammatory steps will be a superior or equivalent means of managing inflammation when compared with steroids for the majority of asthmatics. Moreover, the administration of biologics is both difficult (typically *s.c.* or *i.v.* injection) and expensive and justified only in severe asthmatics whose asthma is otherwise unmanageable [70, 71]. For now, the sledgehammer remains the most effective tool for the most asthmatics. Is there another solution?

1.6 Limitations of GPCR Ligands in the Control of Asthma and Inflammation

Arguably, the optimal asthma drug would be able to both prevent and neutralize inflammation while also directly inhibiting ASM contraction. To date, this drug does not exist, although as discussed recent studies have demonstrated the ability of certain GPCRs to regulate both ASM contraction and inflammation in murine models of asthma. CysLT1R antagonists have the capacity to both inhibit ASM contraction and airway inflammation, but their efficacy as a direct bronchodilator is minimal and as an anti-inflammatory agent is lim-

ited, perhaps being best in those patients whose lung inflammation is driven significantly by CysLT generation in the airway. Given the absence of any GPCR possessing efficacy as both a bronchodilator and anti-inflammatory, combination therapies of (GPCR ligand bronchodilator) LABAs/LAMAs and steroids are currently required for sufficient asthma control of both inflammation and bronchospasm and are overwhelming prescribed for most asthmatics.

However, this does not mean that inflammation control in asthma by GPCR pharmacology is not possible. Because multiple GPCRs participate in inflammation development, including many only recently appreciated receptors and others with but a nascent pharmacology, it is conceivable that the targeting of certain GPCRs may be sufficient to manage allergic lung inflammation. In addition, unlike biologics, GPCR agonists are small molecular drugs with inherent properties favorable for drug development, administration, and patient adherence [4, 72].

1.7 Recently Appreciated GPCRs Whose Targeting May Help in Managing Allergic Airway Inflammation

Advances in basic science capabilities in molecular and cell biology and receptor pharmacology have aided the discovery of previously unappreciated roles of various GPCRs in airway and asthma biology. Although many of these recent studies stemmed from attempts to find novel bronchodilators, a by-product of these studies has been the discovery of novel mechanisms by which GPCRs regulate allergic lung inflammation. Below, we discuss each of these GPCRs implicated in inflammation control and the potential of these receptors as asthma therapeutic targets.

1.8 Bitter Tastant Receptors

Evolutionarily bitter taste receptor signaling evolved as a mechanism to avoid potentially toxic food often bitter in taste. This function was primarily imparted by the bitter taste receptors (belonging to type II taste receptors, TAS2R), a family of seven transmembrane GPCRs expressed on the taste buds [73]. In the gastrointestinal system, these highly specialized chemosensory cells contribute to the innate host defense mechanism [74, 75]. It is now well established that TAS2Rs are expressed on variety of cell-types including ASM cells in the airways [76]. The first evidence to demonstrate the beneficial effect of bitter taste receptor signaling in providing effective bronchorelaxation was shown using human ASM cells where agonists of TAS2Rs were able to induce localized calcium and reverse airway obstruction to contractile agonists [76]. These observations were then verified in other species, and soon, it was established and recognized that TAS2R agonism may be a viable target to promote airway relaxation. Studies also demonstrated that the beneficial signaling activated by TAS2Rs in the airway smooth muscle was distinct and was not reliant on protein kinase A (PKA) activation, unlike β2 agonists [76–78]. Moreover, chronic treatment with TAS2R ligands does not lead to receptor desensitization in ASM, thereby preserving the beneficial bronchorelaxation effect [79]. Since the original characterization of bitter tastant receptors in the lung and ASM, it has been established that bitter tastants can provide effective bronchodilatory effects by promoting relaxation of ASM in multiple species and in animal models of asthma [76, 79–83]

It is also now apparent that bitter tastant receptor ligands can also mitigate other pathological features of asthma such as airway inflammation and airway remodeling, thereby providing a comprehensive asthma control [83]. The beneficial effects of bitter ligands have been shown in both prophylactic and treatment models where these agents acted on multiple levels in asthma pathology and prevented allergen-induced influx of immune cells into the airways and blocked key inflammatory cytokines that drive asthma pathogenesis that leads to airway remodeling and AHR [83]. Though bitter tastants are potentially an effective alternative to beta-agonists in terms of their bronchodilatory effects, it still remains to be seen whether these agents will be safe and equally

effective in the clinic as the biggest challenge in their development is the identification of a specific TAS2R subtype that is highly relevant in asthma and translation of preclinical studies to humans [84].

1.9 Calcium-Sensing Receptor

The calcium-sensing receptor (CaSR) is best known for its role in regulating calcium homeostasis in the body. CaSRs on the parathyroid gland survey circulating calcium levels, which involves calcium binding to and activating the CaSR which initiates intracellular signals that suppress the release of parathyroid hormone. Interestingly, the CaSR can be activated by numerous other molecules, including polyvalent cations, amino acids, and virus elements, and is expressed on multiple cell types, including those in the lung. In Yarova et al., a prominent role of CaSRs in mediating the development of the asthma phenotype was revealed. The capacity of CaSRs to promote ASM contraction was demonstrated by a loss of CaSR-stimulated contraction in ASM cells and tissue in which the CaSR gene was ablated and by pretreatment with CaSR antagonists known as calcilytics. Importantly, calcilytics could also reverse the hyperresponsiveness and inflammation induced in vivo in a mixed allergen model of murine asthma. Relevance of CaSRs to human asthma was suggested by data demonstrating expression of CaSR in human ASM, with greater levels observed in ASM from asthmatics. The ability of CaSRs to regulate inflammation is likely due to its expression on invading inflammatory cells (eosinophils, macrophages). Interestingly, inflammation was shown to increase CaSR expression in both human and mouse tissues [85].

One of the most intriguing aspects of CaSR in asthma is that (CaSR antagonists) calcilytics have real potential as asthma drugs. They are small molecules that are readily deliverable by inhalation, and their efficacy is favored by the ability to target multiple cell types and mechanisms that contribute to the asthma phenotype. Moreover, various calcilytics have already undergone clinical trials for safety and efficacy in diseases such as osteoporosis and autosomal dominant hypocalcemia (reviewed in [86]). Thus, despite the promiscuous nature of the CaSR, it might ultimately prove to be a useful asthma therapeutic target.

1.10 EP Receptors

The EP receptor family is activated by the ubiquitous inflammatory agent prostaglandin E2 and to a lesser extent other prostanoids [87]. The four members of the EP receptor family (EP1, EP2, EP3, and EP4) couple to different G proteins, signal to different pathways, and have variable expression in multiple cell types in the lung. With respect to allergic lung inflammation and asthma, PGE_2 through EP receptors thus regulates multiple cellular functions that serve different and often competing functions that control both inflammation and ASM contraction. For example, in humans, EP3 receptors in ASM cause contraction, whereas EP4 receptors mediate ASM relaxation [88]. Control of inflammation by EP receptors is complex. The net effect on PGE_2 activating multiple EP receptor subtypes in the allergen-challenged mice demonstrated that EP2, EP3, and EP4 agonists all could inhibit certain indices of allergen-induced inflammation in mice lacking mPGES [89]. In another study, employing three different airway disease models (including a more chronic ovalbumin (OVA) sensitization/challenge), in each of the EP knockout mice, demonstrated that the EP4R (and not EP1–EP3) was responsible for the anti-inflammatory effect of PGE_2 in each model [90]. Collectively, studies to date suggest that PGE_2 is largely beneficial, with the capacity to inhibit many pathological features of asthma. In both animal models and cell-based assays, PGE_2 inhibits multiple indices of allergic inflammation [89–93], inhibits proliferation of cultured ASM cells [94–99], and relaxes contracted airways ex vivo [100–103] while promoting bronchoprotection/bronchorelaxation in vivo [101, 103]. Moreover, these effects are conserved across

species and most importantly are evident in human subjects.

The *potential* of PGE_2 as an asthma therapeutic, at least with respect to its bronchorelaxant properties, has been recognized for years. The bronchodilator effects of PGE_2 have been demonstrated in a range of patients (normal, asthmatic, and chronic bronchitis) [104]. This effect has been shown in other studies using healthy and asthmatic subjects, respectively [105, 106]. PGE_2 also protects against exercise-induced [105] and aspirin-induced bronchoconstriction in subjects with aspirin-exacerbated respiratory disease (AERD) [107, 108]. PGE_2 also prevents early and late allergen-induced bronchoconstrictor responses when given before allergen challenge [109, 110] and is protective against bronchoconstrictors such as histamine and methacholine [106, 111]. With respect to inflammation, PGE_2 also blocks the recruitment of eosinophils and basophils to the bronchial mucosa during allergen-induced late-phase responses and attenuates the release of mast cell-derived products. Thus, PGE_2 has validated functions as an anti-inflammatory and bronchoprotective agent in asthmatics [110, 112] In that regard, it is most established among potential asthma therapeutics for its ability to directly bronchodilate and to suppress inflammation.

However, despite these benefits of inhaled PGE_2, the development of prostanoid agonists for the treatment of asthma has been hindered as inhaled PGE_2 has repeatedly been shown to produce reflex cough in humans [104, 112, 113]. PGE_2 has been shown to excite airway afferent nerves [114], which concurs with the cough seen in both healthy and asthmatic patients during studies with inhaled PGE_2. Recent studies using cell, tissue, and in vivo models strongly implicate the EP3 receptor subtype in mediating cough induced by PGE_2 across all species tested, including human [115–120].

Clearly, the answer to harnessing the pro-relaxant and anti-inflammatory properties of PGE_2 as an asthma treatment or prophylaxis relies on specific targeting of EP receptor subtypes, with a primary goal of avoiding EP3 receptor agonism. Unfortunately, the development of ligands with sufficiently high specificity for each of the EP subtypes has been difficult to date. Moreover, this solution first requires a clear understanding of the role of EP receptor subtypes in the many cell types participating in airway inflammation and pathobiology in asthma. In airway epithelial cells, PGE_2 modulates many functions including an increase in ciliary beat frequency [121] and Cl^- channel conductance [122], whereas both induction [123] and inhibition [124] of mucin production have been reported. In vivo administration of EP agonists has been shown to inhibit LPS- (EP2) and allergen-induced (EP2/EP3/EP4) mucous cell metaplasia in rat nasal epithelium [124, 125]. EP receptors also play an immunomodulatory role in the epithelium; EP2/EP4 agonists increase IL-6 release [126], whereas EP4 inhibits IL-8 release [127]. A recent report shows that human airway epithelial (HAE) cell migration is promoted by PGE_2 and selective EP agonists (EP1–EP4), but upon undergoing TGFβ-induced Epithelial mesenchymal transition (EMT), the response to PGE_2 and EP2 and EP4 agonists becomes inhibitory, indicating adaptation of EP responses to remodeling in the lung [128].

Human mast cells have been shown to express EP2, EP3, and EP4 receptors. PGE_2 suppressed the generation of cytokines and cysteinyl leukotrienes primarily by eliciting signaling through EP2 receptors (although a suppressive effect was evident at high doses) [91]. Others have noted regulatory effects of PGE_2 on other inflammatory cell types including eosinophils [129], T cells [130], T regs [131], alveolar macrophages [132], and neutrophils [133] using cells from various species. Whereas some of these studies have suggested that EP2 and EP4 are the principal EP subtypes capable of inhibiting the inflammatory functions of these cells, definitive insight has been limited [134] due the limitations of subtype selective ligands.

Collectively, the above studies all point to a high potential of EP receptor subtype targeting for regulating both bronchospasm and airway inflammation in asthma. One caveat is that most of our understanding of EP receptor subtype function in the lung and lung cells during allergic inflammation comes from animal studies, and (1) the nature of, and control of, of allergen-induced

inflammation in animals (particularly mice) differs (often significantly) from that of humans, and (2) species differences in cellular EP receptor subtype function have been identified, one striking difference being in the control of ASM contraction/relaxation [118]. However, the current pace of research in this area is encouraging, supported by ongoing industry efforts in EP subtype-selective drug discovery [135] aided by the increasing ability of both structural biology and receptor modeling science to enhance these efforts.

1.11 Protease-Activated Receptor 2 (PAR2)

PAR2 signaling in the lung has complex effects reflecting the diverse functions of the various lung cell types that express PAR2. Initial studies demonstrated that airway delivery of anti-PAR2 antibodies, or a cell permeable peptide inhibitor of PAR2 signaling, prevented allergen-induced AHR and airway inflammation in mice [136]. Moreover, using a mouse OVA model for PAR(2)-modulated airway inflammation, genetic ablation of β-arrestin2 (βarr2) decreased leukocyte recruitment, cytokine production, and mucin production in OVA-treated mice, yet PAR(2)-mediated PGE_2 production and the associated and decreased baseline airway resistance were unaffected by βarr2 knockout. Subsequent studies using OVA, cockroach extract, or *Alternaria alternata* to induce lung inflammation further confirmed a protective effect of PAR2 activity acting via PGE_2-mediated relaxation of ASM and a pathogenic effect of PAR2 mediated through PAR2 activation (and dependent on β-arrestin2) most likely on inflammatory cells [137, 138]. Collectively, these studies suggest that PAR2 is a potential useful GPCR target for controlling allergic lung inflammation, and a strategy enabling specific targeting of PAR2-β-arrestin2 signaling would be optimal, enabling the protective effect of PAR2-PGE_2 signaling axis to be retained.

1.12 Any Finally … the β_2AR? How Biased Agonism Pharmacology May Turn a Problem into a Solution

The inability of current beta-agonists to control inflammation almost certainly underlies the need to treat asthmatics with steroids. Although a handful of studies examining the effects in cell-based models have attributed anti-inflammatory properties to beta-agonists [139–145], there is little if any evidence that beta-agonist use reduces allergic inflammation in the lung [146, 147]. The cooperative effect of LABA and steroids in managing asthma is likely a function of each drug addressing an individual disease feature: LABA prophylactic inhibition of airway constriction (bronchoprotection) and steroid prophylactic inhibition of inflammation. Certain studies have identified some interesting cooperative mechanisms at the cellular level [48, 58, 148–150], but the predominate means by which these two drugs work together well appears to be that beta-agonists directly manages ASM contraction, while steroids limit inflammation. Both the cause (inflammation) and the effect (bronchoconstriction) are addressed to the extent that synergy at the cellular level is probably not required for this combination to be effective in most asthmatics.

A long history of safety issues also suggests that beta-agonists alone are inadequate to manage the disease in many asthmatics, perhaps due to the inability to control inflammation. "Epidemics" in which beta-agonist use was associated with high levels of asthma mortality occurred in the 1960s with high dose of inhaled isoproterenol (a nonspecific beta-agonist) use in the United Kingdom, followed by the use of a potent SABA, fenoterol, which also increased asthma-related mortality in New Zealand [151–157]. In the USA, a statistically insignificant increase in asthma-related deaths and safety concerns were reported with the use of LABAs. It was later noted that these life-threatening adverse events with the use of LABA therapy were limited by suboptimal study designs. Follow-up prospective clinical trials and meta-analyses consistently demonstrated their effectiveness and safety, although these trials did not contain suffi-

cient power to address these safety concerns definitively [158, 159]. Moreover, clinical data further suggest that chronic beta-agonist use is associated with a reduction in bronchoprotective effect [160, 161], increase in AHR [162], and loss of asthma control [162–164]; whether this is due to a loss of effectiveness of beta-agonists caused by receptor desensitization or a failure to address the underlying cause (inflammation) of the disease is unclear. However, when the most recent (and highly publicized) beta-agonist safety issue arose during the SMART trial examining the efficacy of salmeterol monotherapy, it was widely speculated that the significant ability of salmeterol to relax ASM *masked* its inability to control airway inflammation [165, 166], thus leaving patients significantly at risk.

1.13 Evidence that Beta-Agonists and the β_2AR Actually Promote Inflammation and Asthma Development

There is a paucity of meaningful clinical data assessing the effects of beta-agonist use on inflammation in asthma. A handful of underpowered clinical studies suggest limited anti-inflammatory effects of beta-agonists in reducing IL-8, eosinophils, mast cells in Bronchoalveolar lavage (BAL), and airway mucosa samples after LABA therapy [167–169]. In contrast, a considerable amount of research into the effects of beta-agonists and the β_2AR in murine models of allergic lung inflammation exists. These studies were pioneered by the Bond lab, who initially proposed that, as in heart failure, a "βAR paradox" exists for asthma. With heart failure, a loss of pump function occurs as cardiac myocytes and their β_1ARs become less responsive to endogenous norepinephrine. Although, theoretically, the use of exogenous beta-agonists as therapy might help stimulate the hypodynamic heart, it turns out that βAR *blockers* are the more effective treatment. This is because, as ultimately determined, β_1AR activation is actually a pathogenic driver of heart failure, and preventing this β_1AR-driven pathogenesis with β_1AR antagonism proved to be therapeutically beneficial [170].

In a series of elegant studies, Bond and colleagues demonstrated (highlights summarized in Fig. 1.2) that pharmacological blockade, or genetic ablation of the β_2AR or systemic epinephrine (the only endogenous ligand for the β_2AR), improved the asthma phenotype and that agonist-induced activation of the β_2AR was necessary for full development of the lung inflammation and the asthma phenotype [171–177]. Moreover, results from a pilot clinical trial determined that, in 8 out of 10 mild asthmatics, 9 weeks of treatment with the "beta-blocker" nadolol produced a significant, dose-dependent increase in PC20 as well as a significant reduction in FEV1 [178, 179].

1.14 Was It as Simple as β_2AR Signaling Was Actually Bad and Fostered Asthma Development?

Not exactly. During this time, the GPCR biology field discovered that certain GPCRs, including β_2ARs, were capable of stimulating diverse and sometimes functionally antithetical signaling pathways, and most of these signaling events were dependent on arrestin proteins [180, 181]. Arrestins were originally identified as regulatory proteins that promote β_2AR desensitization but were subsequently found capable of mediated G protein-independent signaling by binding the β_2AR and helping form a distinct signalosome. Strategies that inhibited the ability of arrestin proteins to bind to the β_2AR (e.g., arrestin knockdown) could inhibit specific signaling (e.g., ERK1/ERK2 signaling) while preserving other signaling (cAMP/PKA) [182]. In addition, drugs classically known as βAR antagonists, based on their ability to block βAR-stimulated cAMP production, could cause arrestin recruitment to βARs and stimulate signals that appeared independent of G proteins [182, 183]. These studies ushered in the exciting new age of "biased ligand pharmacology," and the race was on to develop new drugs that could "tune" receptors to preferen-

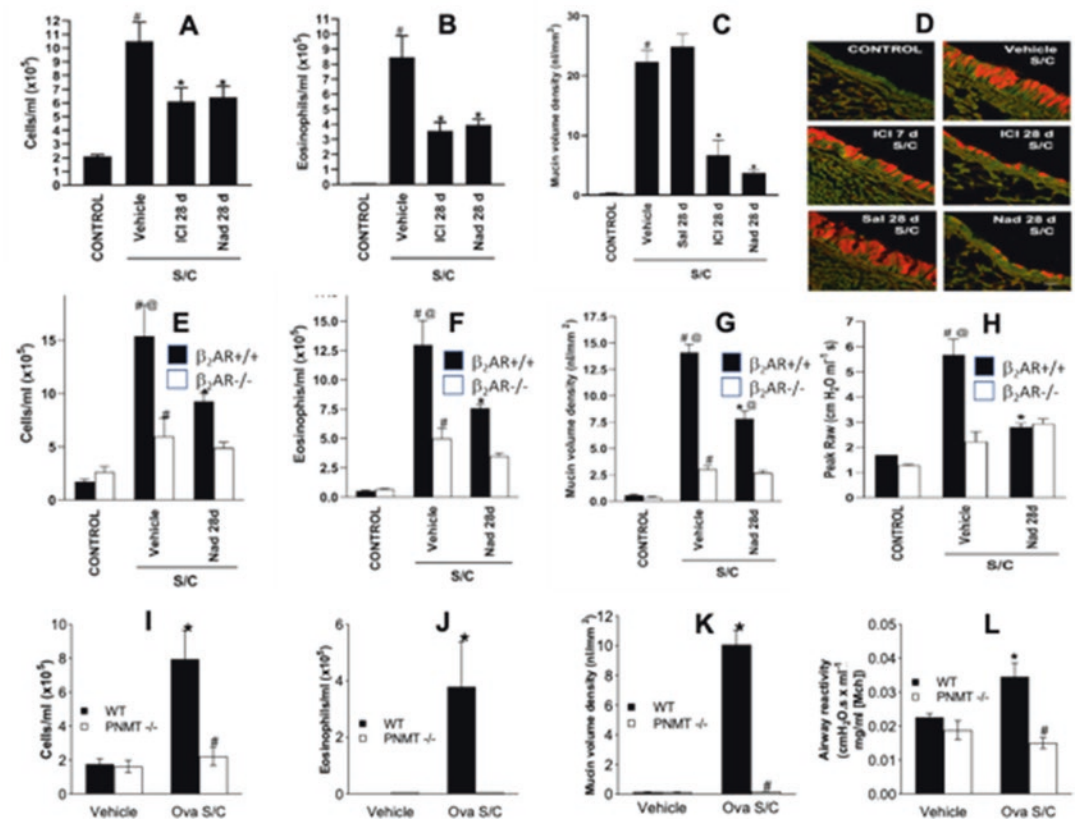

Fig. 1.2 Pharmacological, genetic inhibition of β_2AR signaling improves the asthma phenotype. *A-D*. In the classic ovalbumin (OVA) model of murine allergic lung inflammation, chronic co-administration of inverse agonists ICI118551 and nadolol, both of which block both canonical β_2AR signaling as well as arrestin binding to β_2AR, inhibits the OVA-induced increases in BALF total cellularity (**a**), eosinophils (**b**), and mucin (**c**). Moreover, chronic salbutamol treatment augments OVA-induced mucin (**c**). *D*. Periodic Acid-Schiff-stained airways from mice treated as per (**c**). *E-F*. Genetic ablation of the β_2AR similarly inhibits OVA-induced increases in lung cellularity (**e**), eosinophils (**f**), and mucin (**g**), as well as increases in methacholine-stimulated airway resistance (**h**). *I-J*. Genetic ablation of phenylethanolamine N-phenylethanolamine N-methyltransferase (PMNT, the enzyme catalyzing the final step in the synthesis of epinephrine) similarly inhibits OVA-induced increases in lung cellularity (**i**), eosinophils (**j**), and mucin (**k**), and methacholine-stimulated airway resistance (**h**). Data from Nguyen et al. *Am J Respir Cell Mol Biol* 2006 (**a**–**d**), Nguyen et al. Proc Natl Acad Sci USA 2009 (**e**–**h**), and Thanawala et al. *Am J Respir Cell Mol Biol* 2013 (**i**–**j**)

tially activate specific pathways, instead of simply turning receptors on or off.

Intrigued by this fledgling field of biased ligand pharmacology, Bond and colleagues considered whether the permissive effect of beta-agonists on asthma pathobiology was linked to arrestin effects on β_2ARs and possible arrestin-dependent signaling. The modest albeit encouraging effect of nadolol in the clinical pilot study led them to consider whether the use of nadolol, which blocks both G protein and arrestin-dependent signaling by the β_2AR, might be to some extent "throwing the baby out with the bath water." *Might a better strategy be to preserve the β_2AR-Gs-cAMP-PKA signaling while blocking arrestin-dependent effects?* They therefore launched a series of studies that demonstrated that certain "beta-blockers" (e.g., carvedilol, propranolol) that blocked β_2AR-Gs signaling yet failed to inhibit β_2AR-arrestin binding (and stimulated

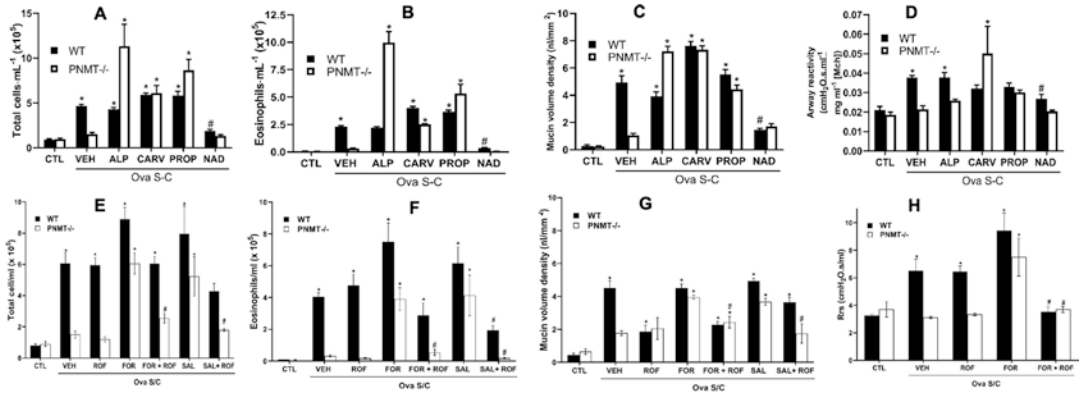

Fig. 1.3 Asthma pathology is influenced by the nature, degree of biased β_2AR signaling. *A-D*. Systemic depletion of epinephrine caused by PMNT deletion inhibits OVA-induced BALF total cellularity (**a**), eosinophils (**b**), mucin (**c**), and airway hyperresponsiveness (AHR) (**d**), while replacement of systemic epinephrine with a balanced β_2AR partial agonist alprenolol (ALP) or arrestin-biased carvedilol (CAR) or propranolol (PROP) helps restore each of these features of asthma. Conversely, nadolol (NAD), which blocks both β_2AR-Gs signaling as well as arrestin binding to the β_2AR does not. *E-F*. Replacement of systemic epinephrine with balanced β_2AR agonists formoterol (FOR) or salmeterol (SAL) in PMNT −/− mice restores OVA-induced increases in lung cellularity (**e**), eosinophils (**f**), and mucin (**g**), as well as increases in methacholine-stimulated airway resistance (**h**). Moreover, co-treatment with the PDE4 inhibitor roflumilast (ROF), which increases β_2AR-Gs-stimulated cAMP accumulation, partially reverses the deleterious effects of chronic treatment with balanced agonists formoterol and salmeterol on total lung cellularity, eosinophils, mucin, and AHR. Data from Thanawala et al. *Br J Pharmacol* 2015 (**a**–**d**) and Forkuo et al. *Am J Respir Cell Mel Biol* 2016 (**e**, **f**)

ERK1/ERK2 signaling in 293 cells as per [182]) (i.e., arrestin-biased ligands) were not effective in mitigating allergen-induced inflammation and AHR and in fact exacerbated the condition, especially in PMNT−/− (epinephrine-deficient) mice [177] (Fig. 1.3a–d). Without a Gs-biased β_2AR ligand in hand, Bond and colleagues biased signaling toward the Gs/cAMP/PKA pathway through use of phosphodiesterase (PDE) inhibitors which specifically increased intracellular cAMP in lung cells. Both PDE4 inhibitors rolipram (not shown) and roflumilast (Fig. 1.3e–h) significantly reversed the adverse effects of formoterol and salmeterol on allergen-induced bronchoalveolar lavage fluid (BALF) cellularity and eosinophils, mucin, and AHR in both wild-type and PMNT−/− mice [173].

Additional studies demonstrated that the loss of IL-13-induced asthma phenotype caused by global genetic ablation of β_2AR was rescued by transgenic expression of the β_2AR in only airway epithelia [184], suggesting that β_2AR-arrestin signaling regulates the immunomodulatory function of airway epithelia and is critical to the development of the asthma phenotype. Should future studies clarify this as true, the two critical questions that remain are as follows: (1) is this the case with human asthma and (2) can Gs-biased β_2AR agonists or allosteric modulators that are both effective and safe in asthmatics be developed? To date (unlike arrestin-biased β_2AR ligands), identifying or developing such drugs has been a challenge, but with the rapid advances in structural biology and computer modeling that enable drug development, it is only matter of time before such drugs are known or developed.

1.15 What the Future Holds: The Promise of Biased Agonism Pharmacology

To date, the failure to identify a GPCR target, and a therapeutic ligand for it, capable of successfully managing allergic lung inflammation in human stems from the limitations of GPCR biology and pharmacology in basic research and the limitations of drug discovery. GPCR biology and phar-

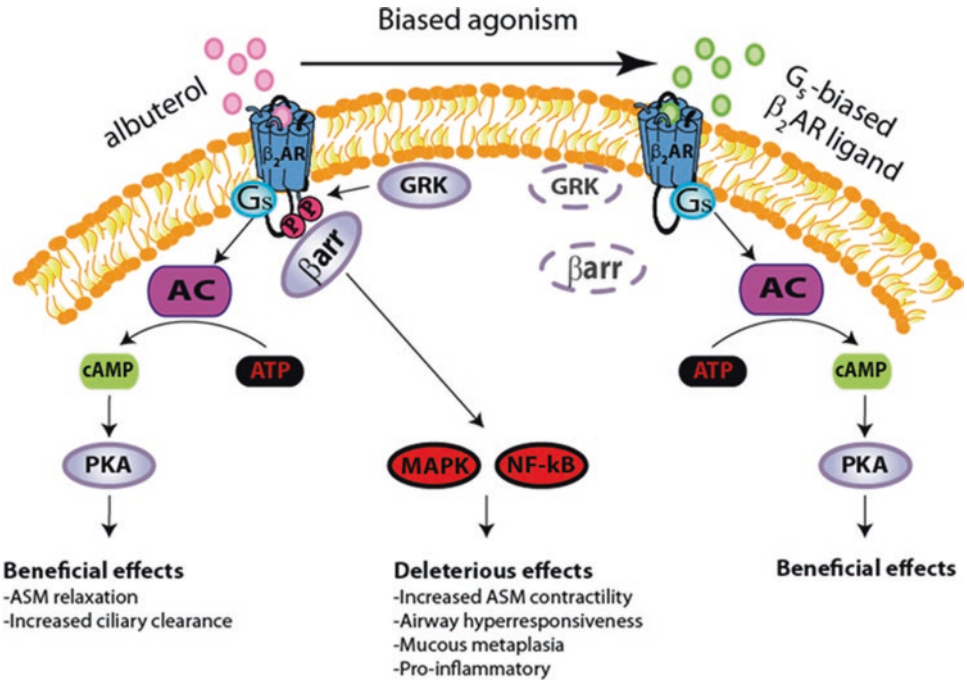

Fig. 1.4 Biased agonism pharmacology in ASM. Illustration of signaling mechanisms using principles of biased agonism to promote beneficial therapeutic effects in asthma

macology research in asthma is currently exploding, aided by increasing powerful genetic, molecular, cell biology, and computational tools and by the increasing rate of drug discovery, itself aided by advances in structural biology, computer modeling, and better screening tools and strategies. Moreover, the recent appreciation of qualitative signaling properties by GPCRs, and the realization that receptors can be "tuned" and not just turned "off" or "on" to specifically activate the beneficial therapeutic signaling a receptor can transduce, suggests that biased agonism pharmacology will develop the drugs we need to optimally control airway inflammation and asthma, as shown in Fig. 1.4 [185]. In addition, because GPCR ligands are small molecules and can be continuously refined to improve specificity of targeting while minimizing off-target effects, we should ultimately have an asthma therapy that supplants steroids and has a superior efficacy and safety profile.

1.16 Why Do We Care About Developing GPCR Ligands Capable of Managing Allergic Lung Inflammation?

As mentioned above, the properties of small-molecule GPCR ligands make them attractive therapies. In addition, it would be advantageous to control inflammation without the numerous side effects associated with corticosteroid treatment. The major issue remains whether control of inflammation by such drugs is truly sufficient to manage allergic inflammation and whether such a scalpel can do the job currently performed by a sledgehammer.

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Cellular and Molecular Processes in Pulmonary Hypertension

2

Vic Maietta, Jorge Reyes-García, Vishal R. Yadav, Yun-Min Zheng, Xu Peng, and Yong-Xiao Wang

Abstract

Pulmonary hypertension (PH) is a progressive lung disease characterized by persistent pulmonary vasoconstriction. Another well-recognized characteristic of PH is the muscularization of peripheral pulmonary arteries. This pulmonary vasoremodeling manifests in medial hypertrophy/hyperplasia of smooth muscle cells (SMCs) with possible neointimal formation. The underlying molecular processes for these two major vascular responses remain not fully understood. On the other hand, a series of very recent studies have shown that the increased reactive oxygen species (ROS) seems to be an important player in mediating pulmonary vasoconstriction and vasoremodeling, thereby leading to PH. Mitochondria are a primary site for ROS production in pulmonary artery (PA) SMCs, which subsequently activate NADPH oxidase to induce further ROS generation, i.e., ROS-induced ROS generation. ROS control the activity of multiple ion channels to induce intracellular Ca^{2+} release and extracellular Ca^{2+} influx (ROS-induced Ca^{2+} release and influx) to cause PH. ROS and Ca^{2+} signaling may synergistically trigger an inflammatory cascade to implicate in PH. Accordingly, this paper explores the important roles of ROS, Ca^{2+}, and inflammatory signaling in the development of PH, including their reciprocal interactions, key molecules, and possible therapeutic targets.

Keywords

Pulmonary hypertension · Vascular hypertrophy · Vascular remodeling · Mitochondria · Reactive oxygen species · Calcium signaling · Ion channel

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Abbreviations

ACE	Angiotensin-converting enzyme
Ang II	Angiotensin II
Apaf1	Apoptotic protease-activating factor 1
AT_1	Angiotensin II type 1 receptor
ATP	Adenosine triphosphate
Bax	Bcl-2-like protein
CaMKII	Calcium/calmodulin kinase II
CaSR	Calcium sensing receptor
Ca_v	Voltage-dependent Ca^{2+} channel
c-MYC	Proto-oncogene encoding bHLH transcription factor protein
Coenzyme Q	Ubiquinol-cytochrome c reductase
Cyt	Cytochrome
DAG	1,2-Diacylglycerol
DNA	Deoxyribonucleic acid
DRP1	Dynamin-related protein 1
Duox	Dual oxidase
ER	Endoplasmic reticulum
ETC	Electron transport chain
FAD	Flavin adenine dinucleotide
Gpx1	Glutathione peroxidase 1
HIF-1	Hypoxia-inducible factor 1
HUVEC	Human umbilical vein endothelial cells
ICAM-1	Intercellular adhesion molecule 1
IP_3(R)	Inositol 1,4,5-trisphosphate (receptor)
K_V	Voltage-dependent potassium channel
LDL	Low-density lipoprotein
MCP-1	Monocyte chemoattractant protein
mPTP	Mitochondrial permeability transition pore
mRNA	Messenger ribonucleic acid
NADH	Nicotinamide adenine dinucleotide
NADPH	Nicotinamide adenine dinucleotide phosphate
NOX	NADPH oxidase
PASMCs	Pulmonary artery smooth muscle cells
PDK1	Gene coding for pyruvate dehydrogenase kinase 1
PH	Pulmonary hypertension
PHD	Prolyl hydroxylase
PKCε	Protein kinase C epsilon
PLC	Phospholipase C
RISP	Rieske iron-sulfur protein
RNAi	RNA interference
ROS	Reactive oxygen species
RyR	Ryanodine receptor
siRNA	Small interfering RNA
Smad3	Gene coding for Smad protein, transducers for TGF-β
SOD	Superoxide dismutase
SR	Sarcoplasmic reticulum
TGF-β	Transforming growth factor beta
TRPC	Transient receptor potential cation channels
VEGF(R)	Vascular endothelial growth factor (receptor)

2.1 Introduction

Pulmonary hypertension (PH) is a progressive and multifactorial disease which remains mostly undiagnosed with a poor prognosis and a 5-year mean survival rate under 70 percent in affected population [1]. This ailment is characterized by persistent pulmonary vasoconstriction progressing to proliferation of endothelial and smooth muscle cells that lines the arteries and arterioles of the pulmonary vasculature. This pulmonary vascular remodeling (PVR) results in elevated pulmonary vascular resistance and pressure leading to right ventricular hypertrophy and failure and ultimately death [2]. Mean pulmonary arterial pressure greater than 25 mmHg at rest or greater than 30 mmHg during exercise is indicative of pulmonary hypertension [3]. A histological view denotes muscularization of peripheral pulmonary arteries involving hypertrophy and hyperplasia, loss of small pre-capillary arteries, and neointimal formation [3]. Moreover, plexiform lesions (complex vascular lesions are aberrant channels in the obliterated vessel lumen and in the adventitia) form/arise at later stages of the disease due to either the clonal expansion of apoptosis-resistant endothelial cells (ECs) or the deposition of circulating endothelial progenitor

cells at injury sites [3]. Untreated PH can eventually lead to right heart failure [4, 5]. Potential causes are linked to mitochondrial dysfunction. For instance, alterations in reactive oxygen species (ROS) homeostasis in pulmonary artery smooth muscle cells (PASMCS) and ECs are involved in the development of PVR seen in pulmonary arterial hypertension [6]. Moreover, changes in ROS intracellular concentration ($[ROS]_i$) may influence the vascular reactivity dependent on the intracellular Ca^{2+} concentration ($[Ca^{2+}]_i$) [7]. Cross-talk among these forces may initiate and enhance PH [3]. This article aims to review and discuss the molecular mechanisms underlying PH, primarily the role of ROS in the development of this lung disease and their cross-talk with several intermediate Ca^{2+} signaling molecules.

2.2 ROS

Growing evidence suggests that changes in $[ROS]_i$ mainly from mitochondrial dysfunction in pulmonary artery ECs (PAECs) and PASMCs contribute to the development of PH. Mitochondrial function plays a critical role in cell Ca^{2+}homeostasis, ATP and ROS generation, inflammation, progression of the cell cycle, and apoptosis [8]. ROS are reactive chemical entities, including oxygen-based free radicals (superoxide [$\cdot O_2^-$] and hydroxyl [OH·]) and non-radical derivatives of molecular oxygen (H_2O_2) [9]. Free radicals are species or molecules containing one or more unpaired electrons and are capable of independent existence. The number of unpaired electrons renders them unstable and short-lived by imparting the reactive capabilities. Nonradical derivatives are less reactive and more stable [10]. The different sites of O_2^- and H_2O_2 distribution activate distinctive signaling pathways and functional responses in cells [11, 12]. In the mitochondria, ROS are the byproducts of chemical reactions along the electron transport chain (ETC). Electrons are transferred from NADH dehydrogenase enzymatic complex to other protein complexes in the process of reducing molecular oxygen to produce ATP. In the process, the formation of reduced and highly reactive metabolites occurs, as is simplified in Fig. 2.1 [13]. These chemicals are normally considered as toxic byproducts of aerobic metabolism causing damage to lipids, proteins, and DNA [13, 14]. Cells contain antioxidant enzymes, like superoxide dismutase (SOD), catalase, and glutathione peroxidase, that turn ROS into less reactive forms, thereby preventing subsequent oxidative damage. The dismutation of $\cdot O_2^-$ in mitochondria, cytosol, and extracellular matrix is the main source of H_2O_2, a diffusible signaling molecule [13, 14]. Oxidative stress occurs when the overproduction of oxidants overwhelms the antioxidant capacity of the cell [14]. There is increasing evidence that ROS serve as signaling molecules in addition to being toxic oxidants. It is understood that nitric oxide (NO·) acts as a potent vasodilator when produced by the endothelial NO synthase (eNOS) [15]. NO· is also known for being a toxic oxidant in macrophages targeting bacteria [16].This dual characteristic is surely not limited to this chemical species. It has been proposed that the mitochondrion acts as a hypoxic sensor that initiates ROS generation [17]. Furthermore, the hypoxic environment is responsible for elevated reactive oxygen species in PASMCs [1, 17, 18]. ROS are produced along the mitochondrial electron transport chain, both enzymatically and non-enzymatically [19]. The enzymatic pathway involves the action of mitochondrial complexes I (NADH: ubiquinone oxidoreductase), II (succinate dehydrogenase), and III (cytochrome bc_1 complex) as denoted in Fig. 2.1. NADH dehydrogenase in complex I, succinate dehydrogenase in complex II, and ubiquinol-cytochrome c reductase (coenzyme Q) in complex III have been found to leak electrons that produce superoxide anions, the precursors of most reactive oxygen species [19]. Experiments using inhibitor molecules to block key components of each mitochondrial respiratory chain complex provide evidence that ROS generation in the mitochondria arises from these proteins [17]. In this context, some researchers, like Archer and colleagues, showed that rotenone and antimycin A, the complex I inhibitor and complex III postubisemiquinone site inhibitor, respectively, mimic and eventually block the decrease in ROS generation induced by acute

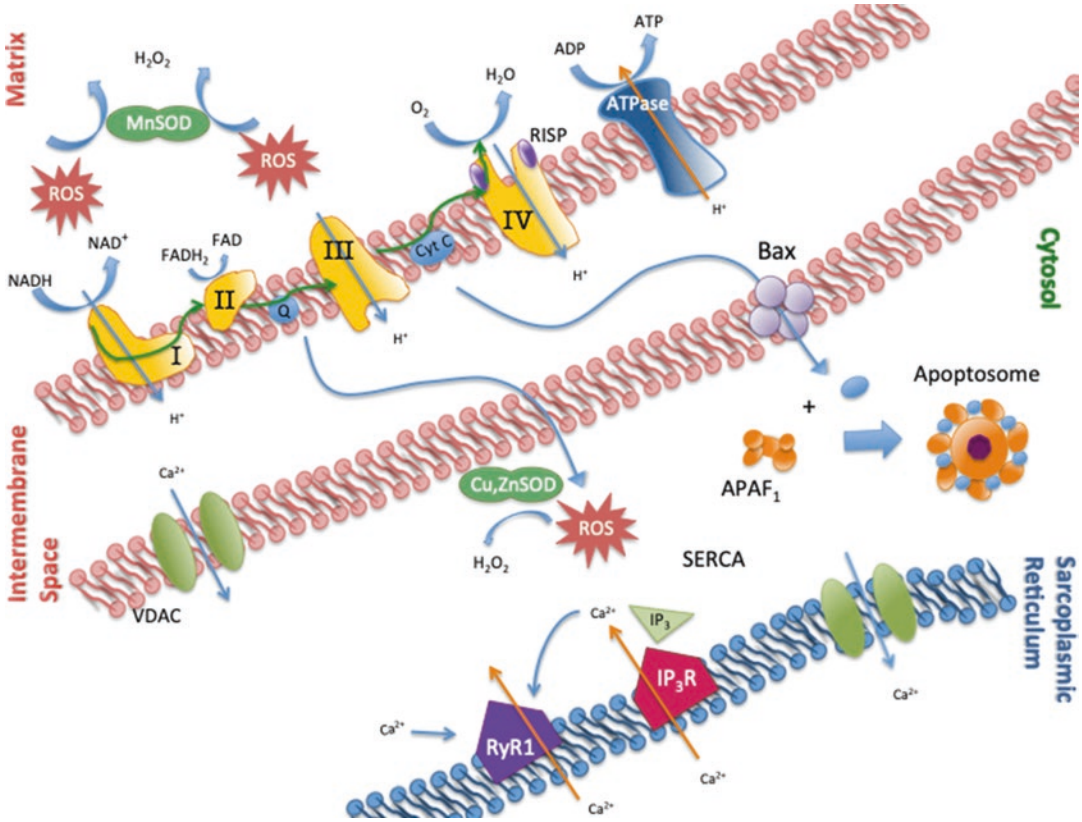

Fig. 2.1 A schematic diagram of the reactive oxygen species (ROS) leakage from various stages of the mitochondrial electron transport chain (ETC) in a vascular smooth muscle cell. Superoxide dismutase enzymes (SOD) convert these species into less reactive hydrogen peroxide molecules (H_2O_2) that can escape the mitochondria as signaling molecules, which interact with several cell proteins. Factors leading to Ca^{2+} accumulation in the cytosol, cell stress, or mitochondrial membrane depolarization trigger formation of the permeability transition pore (mPTP, not shown) between the inner and outer membranes. Bax and the voltage-dependent anion channels (VDACs) are the primary regulators of the mPTP. Loss of cytochrome *c* (Cyt c) from the ETC combined with apoptotic protease-activating factor 1 ($APAF_1$) complexes in the cytosol forming apoptosomes, a commitment to cell death. Inositol 1,4,5-trisphosphate (IP_3) will then trigger Ca^{2+} release from the sarcoplasmic reticulum, which in turn triggers a phenomenon known as Ca^{2+}-induced Ca^{2+} release from ryanodine receptor 1 (RyR1). Finally, Ca^{2+} will trigger contraction and other responses of the cell

hypoxia in isolated lungs and PASMCs from rats [18, 20]. Nevertheless, other works using rat PASMCs as well proved that rotenone and myxothiazol, a complex III preubisemiquinone site inhibitor, block, but do not mimic, the responses to hypoxic stimuli [21–23]. Correspondingly, studies made by our research group elucidated that the inhibitor actions of rotenone and methylphenylpyridinium iodide on complex I, nitropropionic acid and thenoyltrifluoroacetone on complex II, and myxothiazol on complex III block ROS generation in freshly isolated mouse PASMC [7, 17, 24]. Furthermore, the inhibition of complex III postubisemiquinone site and complex IV failed to block a hypoxic-elicited ROS response. These insights provide strong evidence that mitochondrial ETC complexes I and II and preubisemiquinone site in complex III operate as a functional unit, which is responsible for ROS production in PASMCs.

Hypertension and metabolic syndrome are related ailments sharing an oxidative stress component. Zhang and colleagues found in isolated A10 cells (under metabolic syndrome conditions,

i.e., incubated with 10 nmol/l insulin or 1 μmol/l dexamethasone) that ROS activity of complex I increased at 24 and 48 h with a decrease after 72 h, while the ROS activity of complex III declined across the full 72 h of the experiment . Moreover, they confirmed that complex I is essential for ROS overproduction since ROS generation is highly decreased by rotenone, whereas Apo, the NADPH oxidase (Nox) inhibitor, and AMA, the complex III inhibitor, failed to abolish ROS production [25]. Regardless of which complex contributes the most to $[ROS]_i$ increase, the use of MitoTracker and ROS-sensitive fluorescent dye H_2DCF indicates that mitochondria-dense areas of isolated mouse PASMCs show acute hypoxic increases in ROS concentrations ahead of nonmitochondrial areas of the cells [17]. This evidence points to the mitochondria as the intracellular source of ROS in response to hypoxic conditions.

ROS may act as a preconditioning adaptive response to brief episodes of ischemia that lower necrosis in myocardiocytes during subsequent extended periods of ischemia [26]. Vanden Hoek and colleagues demonstrated that 10 minutes of hypoxia prior to simulated ischemia and reperfusion challenge reduced cell death and potentiated the return of contraction in cultured chick myocardiocytes. In the same work, the use of NOS inhibitor (N-nitro-L-arginine) and NADPH oxidase inhibitor (diphenyleneiodonium, DPI), reported to eliminate superoxide formation from NOS, failed to attenuate the ROS generation during hypoxic preconditioning, excluding NOS as a source of superoxide. Conversely, myxothiazol diminished the ROS generation during hypoxic preconditioning, pointing mitochondrial complex III as the responsible of ROS production. During univalent electron transfer to O_2, usually at the ubisemiquinone site, the resulting superoxide may subsequently be converted to H_2O_2 in the cytosol by copper, zinc-SOD (Cu, Zn-SOD) [19, 26]. This assumption led to Vanden Hoek and coworkers to treat the cells with exogenous H_2O_2, which evokes preconditioning-like protection and markedly lowers apoptosis. Moreover, SOD inhibition which augments superoxide generation relative to H_2O_2 formation annuls the protective effects of preconditioning. Collectively, the hydrogen peroxide is more directly responsible for the protective effects during ischemia, and complex III is the main source of superoxide. In this context, Adesina and colleagues elegantly demonstrated that targeting mitochondrial H_2O_2 in pulmonary artery endothelial cells ameliorates pulmonary hypertension pathogenesis [2]. Altogether, these studies point out that reducing mitochondrial H_2O_2 may prevent hypoxia-induced pulmonary hypertension.

It has been found that more H_2O_2 is produced by PASMC mitochondria than systemic arterial SMC mitochondria. These mitochondria have lowered respiratory rates, are more depolarized, and contain more mitochondrial SOD [20]. Furthermore, the H_2O_2 is able to activate voltage-dependent potassium (K_v) channels.

2.3 Role of NADPH Oxidase

Another source of ROS is the NAD(P)H oxidase family of enzymes located in the outer membrane of cells and inner mitochondrial membranes. These enzymes are implicated in the regulation of vascular tone through the production of H_2O_2 and reducing the availability of NO by $\cdot O_2^-$ quenching (through $ONOO^-$ formation) [27, 28]. Nicotinamide adenine dinucleotide (NADH) and nicotinamide adenine dinucleotide phosphate (NAD(P)H) oxidase (Nox) are responsive to different cytokines, angiotensin II (Ang II), mechanical forces (e.g., shear stress), and metabolic factors [15, 29]. Hypertensive patients and normotensive subjects with a family history of hypertension (genetic risk) exhibit elevated H_2O_2 in plasma compared with blood pressure-matched normotensive subjects [30]. This suggests a genetic basis for hypertension, which is linked to ROS generation.

The Nox family of proteins includes Nox1–5 and Duox 1 and 2. The phagocyte Nox (Nox2) was the first characterized isoform comprised of six subunits that interact to form the active enzyme. The two integral membrane proteins, p22phox and gp91phox (α and β subunits, respectively), form the heterodimer flavocytochrome

b558 (Cyt b558). The cytosolic regulatory complex is comprised of the three subunits $p40^{phox}$, $p47^{phox}$, and $p67^{phox}$.[22] Only upon stimulation and phosphorylation of $p47^{phox}$ will the cytosolic complex associate with Cyt b558 to form the active enzyme. Complete formation of the active oxidase requires Rac2 and Rap1 guanine nucleotide-binding proteins [31]. Once completed, electrons from the substrate make their way to oxygen forming O_2^- which is quickly converted to peroxide.

Nox4 was identified in kidney in 2000 by Geiszt and coworkers [32]. Primary expression of Nox4 was displayed in the medial layer of pulmonary blood vessels of mice and humans using anti-Nox4 antibodies and in situ hybridization by Mittal and coworkers [33]. Nox4 mRNA is the most abundant transcript in blood vessels (1000 times greater than Nox1 and Nox2) [34]. This enzyme is constitutively active in cardiovascular tissues and is involved in oxygen sensing, vasomotor control, cellular proliferation, differentiation, migration, apoptosis, senescence, fibrosis, and angiogenesis [35]. Unlike Nox1–3, Nox4 does not depend on cytosolic protein binding for ROS generation [36]. Transfer of electrons from NADPH to FAD occurs continuously due to the unique C-terminus [37].

Nox4 is expressed primarily in the mitochondria of cardiac myocytes. Ago and colleagues determined that the expression of Nox4 is upregulated in response to hypertrophic stimuli, e.g., pressure overload by imposing transverse aortic constrictions in mice, leading to oxidative stress in mitochondria of the heart and subsequently mitochondrial dysfunction and cardiac cell death [38]. Later on, Kuroda and colleagues showed that increases in Nox4 expression and O_2 production in mitochondria are blocked in cardiac-specific deletion of *Nox4* (c-*Nox4* $^{-/-}$) mice. Moreover, c-*Nox4* $^{-/-}$ displayed decreased fibrosis, cardiac hypertrophy, and apoptosis and improved cardiac function compared with wild-type (WT) mice. The authors also found that increased expression of Nox4 enhances oxidative stress and cardiac dysfunction [39]. These findings point to ROS generated by Nox4, as well as other areas of the ETC, which contribute to mitochondrial permeability transition-matrix swelling, outer membrane rupture, and the release of cytochrome *c* (CytC) into the cellular matrix [39, 40]. These insights point out Nox4 as the main contributor to oxidative stress in mitochondria of cardiomyocytes, driving mitochondrial and heart dysfunction during pressure overload.

Factors that have upregulated Nox4 activity include transforming growth factor beta (TGF-β), Ang II, tumor necrosis factor alpha (TNF-α), ER stress, shear stress, hypoxia, and ischemia [41–47]. It has been found that Nox4 expression is elevated in the intimal lesions of coronary arteries underlying atherosclerosis in humans [48]. Both shear stress and Ang II promote ROS generation from Nox1/NADPH located in the plasma membrane of cells along arterial bends, which oxidizes low-density lipoproteins (LDL) [35, 45]. The minimally modified LDL will induce monocyte chemoattractant protein (MCP-1), thereby eliciting an immune response and recruiting leukocytes to the area [45].

Nox4 mediates the growth of hypoxia-induced growth of PASMCs and induces vascular endothelial growth factor (VEGF) secretion and angiogenesis [49, 50]. Nox4 activity may be lowered by inhibitory agents of ROS generation, as well as the processes that are triggered by hypoxic activity, as shown in Fig. 2.2. PKCε translocation peptide inhibitor and glutathione peroxidase 1 (Gpx1) overexpression may be used to disrupt PKCε activation of Nox4 and lower intracellular ROS concentrations, respectively, in order to further reduce ROS [7]. Directly targeting Nox4 with apocynin effectively lowers ROS generation and additionally reduces the intracellular Ca^{2+} concentration in the cells that promote vasoconstriction and proliferation (to be discussed later) [7].

2.4 Hypoxia-Inducible Factor 1

During hypoxia, the transcription of several gene products is induced in order to supply O_2 to cells and tissues [51]. Most of the cellular responses to the hypoxic environment are regulated by hypoxia-inducible factors (HIFs), a family of

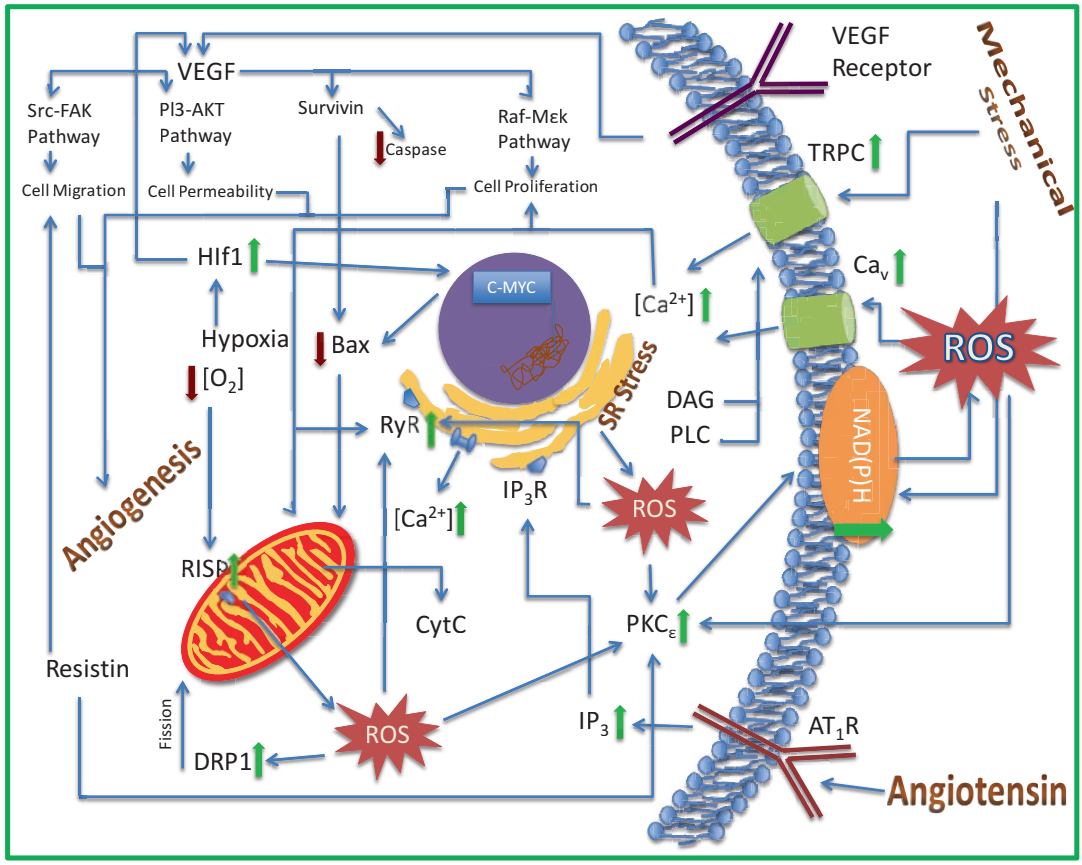

Fig. 2.2 A diagram of the underlying processes implicated in pulmonary hypertension. Plummeting O_2 concentrations in the cytoplasm can activate the hypoxia-inducible factor 1 (HIF-1), which can activate the fetal gene program and alter cellular metabolism. ROS generated by NADPH and the mitochondrial ETC are important signaling molecules that contribute to myocyte dysfunction and respiratory illnesses. ROS can activate proteins and channels that release Ca^{2+} into the cell, which elicits proliferation responses as well as apoptosis. Vascular endothelial growth factor (VEGF) and angiotensin may trigger and promote proliferation, migration, or permeability responses

DNA binding proteins. These transcription factors mediate the induction of genes related to the formation of new blood vessels guaranteeing the O_2 delivery and promoting cell survival [51]. Interestingly, the cellular adaptation to hypoxic conditions allows the growth and rapid development of certain cells such as embryos and solid tumors [52]. Moreover, HIFs have been associated with the pathogenesis of pulmonary arterial hypertension [53, 54]. HIFs are heterodimers formed by an O_2-regulated α subunit and a hydrocarbon receptor nuclear translocator (ARNT) β subunit [55, 56]. Studies about the synthesis of erythropoietin (EPO) as response to hypoxia led to the characterization of HIF-1 [56]. EPO is a peptide hormone that triggers erythropoiesis, subsequently increasing O_2 supply [52]. HIF-1α subunit is a master transcriptional regulator that is constitutively expressed and under normoxic conditions is rapidly degraded by the ubiquitin-proteasome system [51]. Under hypoxic conditions, whereby ROS generated in the mitochondria escape as H_2O_2, prolyl hydroxylase (PHD) is inhibited, which is normally responsible for HIF-1α degradation. PHD under normal conditions hydroxylates HIF-1 in proline and asparagine residues, targeting it for protein degradation. Once PHD is inhibited, the HIF-1 α-ARNT het-

erodimer is formed and binds to hypoxia-responsive element of several genes in the nucleus of the cell [57, 58].

HIF-1 can regulate O_2 mitochondrial homeostasis and biogenesis [59, 60]. This transcription factor facilitates the transition from aerobically derived ATP to anaerobically derived ATP by inducing glycolytic enzymes, pyruvate kinase M, and glucose transporters, helping cells to produce energy in hypoxic conditions [61, 62]. More specifically, HIF-1 upregulates pyruvate dehydrogenase kinase 1 (PDK1), which is the kinase responsible for inactivating pyruvate dehydrogenase (PDH). This process prevents the oxidative decarboxylation of pyruvate to acetyl-CoA, thereby interfering with pyruvate metabolism via the tricarboxylic acid (TCA) cycle [63, 64]. Furthermore, HIF-1 regulates cytochrome *c* oxidase (COX, complex IV) in hypoxic cells. This complex in the inner mitochondrial membrane is a dimer comprising 13 subunits each (COX1–COX13). Fukuda and coworkers showed in mammalian cells that HIF-1 switches the COX4–1 isoform to COX4–2 which optimizes COX activity under hypoxic conditions, exhibiting higher metabolic rates and ATP production as compared to cells without the COX4–1 isoform [65].

HIF-1 has also been implicated in the metabolic reprogramming and tumorigenesis in renal carcinoma by inhibition and degradation of c-MYC (a regulator of biogenesis and O_2 consumption). The inhibition of c-MYC leads to a decrease in respiration [66]. Moreover, c-MYC is involved in the downregulation of anti-apoptotic Bcl-2 family members such as Bax (Bcl-2-like protein 4) [67]. Bax, a channel-forming protein in the outer mitochondrial membrane, facilitates the release of cytochrome *c* to the cytosol [68]. The release of cytochrome *c* is illustrated in Fig. 2.1 through the Bax association with the mitochondrial outer membrane. That in itself is a commitment to cell apoptosis. Furthermore, the loss of cytochrome *c* and the Rieske iron-sulfur protein (RISP) center of complex III terminates the ROS signal from the mitochondria [69]. This downregulation mechanism may involve the reduced activity of Bax in order to protect the mitochondria and the cell from apoptosis (Fig. 2.2).

2.5 Vascular Endothelial Growth Factor

As stated before, HIF-1 is activated within hypoxic microenvironments, i.e., surrounding tumors, which eventually leads to vascular endothelial cell proliferation and angiogenesis in order to restore normoxic conditions to a specific location [70, 71]. During angiogenesis, the sprouting of new blood vessels from pre-existing vasculature is mediated by regulator factors such as fibroblast growth factor (FGF), platelet-derived growth factor (PDGF), epidermal growth factor (EGF), angiopoietins, and the vascular endothelial growth factor (VEGF), which is particularly upregulated as the result of HIF-1 activation [72]. During hypoxia, HIF-1 binds the regulatory region of the VEGF gene, inducing its transcription and protein synthesis in ECs. These cells contribute to the formation of new blood vessels, supplying oxygenated blood to deprived tissues and restoring the normoxic state [62].

VEGF exerts its biological actions through two receptors, the VEGF receptor 1 (VEGFR1) and the VEGF receptor 2 (VEGFR2), both members of the family of receptor tyrosine kinases (RTKs). VEGF and VEGFR2 are abundant in lung tissue and are essential for its development and maintenance [73]. In fact, patients suffering from severe PH show elevated levels of VEGF and soluble VEGFR2 in their blood plasma as well as in plexiform lesions [74]. The structural similarity between VEGFR and other RTKs makes its biology complex and involved. Angiogenesis is highly regulated and controlled by its own expression levels as well as by multiple proteins that can interact with the endogenous ligand. Positive regulators of VEGF mRNA expression include FGF, transforming growth factor alpha (TGF-α) and beta (TGF-β), and PDGF [75]. Moreover, it has been proposed that VEGFR1 is capable of binding placenta growth factor (PLGF) and VEGFB, but does not bind VEGFR2 [76, 77]. The overall ratio of these different ligands competing for the VEGFR binding site may potentiate the effects of VEGF. Currently, it is well accepted that VEGFR2 is the principal mediator of mitogenic and angiogenic effects of

VEGF, as well as microvascular permeability. Additionally, several isoforms of VEGF display different properties such as diffusibility and mitogenic activity [75]. Interestingly, some VEGF isoforms can bind to numerous proteins in the extracellular cell matrix (ECM), promoting integrin-dependent cell spreading, migration, and cell survival [78–80]. Additionally, VEGF also interact with the Notch signaling to regulate the formation of new vessels. Notch is a key signaling pathway that mediates the development of several cell types including ECs [81, 82].

VEGFR2 stimulation may activate several different signaling pathways, as illustrated in Fig. 2.2, including PI3K (phosphatidylinositol 3-kinase)-Akt (protein kinase B) pathway, PI3K-mTORC2 (mammalian target of rapamycin complex 2) pathway, Raf-MEK (mitogen-activated or extracellular signal-regulated protein kinase kinase)-MAPK (mitogen-activated protein kinase) pathway, and the Src-FAK (focal adhesion kinase) pathway. The mTORC2 pathway promotes cell survival and vascular permeability while inhibiting the Bcl-2-associated death promoter and caspases [83]. The Raf-MEK-MAPK pathway activates cell proliferation and the Src-FAK pathway elevates cell motility [84]. The relationship between mitochondrial function and VEGF was explored by Guo and colleagues. They found in human umbilical endothelial vein cells (HUVECs) that ROS generation decreased upon VEGF treatment. They also showed that oxidative phosphorylation and ATP levels increased, as well as catalase and Gpx1 expression levels, both part of the ROS defense system. VEGF was also able to activate mTOR through phosphorylation of the ribosomal S6 protein. The cells stimulated with VEGF accumulated in the S and G_2 phases, forming tube-like structures, and this phenomenon was abolished with the use of rapamycin (the mTOR inhibitor). The authors concluded that VEGF protects the ECs by enhancing mitochondrial function [85].

The evidence points out that hypoxia triggers the upregulation of VEGF and its receptors, leading to angiogenesis. In this context, the role of VEGF in PH has been widely explored in animal models through pharmacological and genetic approaches. It was found through experimental overexpression of VEGFA (the most abundant isoform) that the development of hypoxia-induced PH was blunted [86]. Then Farkas and colleagues demonstrated in experimental lung fibrosis rats that VEGF ameliorated PH via inhibition of endothelial apoptosis, while obstructing VEGF worsened it [87]. Endothelial cell survival is mainly regulated by VEGFR1, while VEGFR2 signaling cascade is involved in vascular differentiation and capillary-like tube formation [88]. VEGF induces production of the anti-apoptotic protein survivin (Fig. 2.2), which is transcriptionally regulated by mTOR, PI3K-Akt, and Bcl-2/ERK pathways [72, 89]. Survivin has been found in the pulmonary arteries of patients with PH and is associated with plexiform lesions [90, 91]. The inhibition of surviving expression elicits pulmonary vascular apoptosis and reverses PH, suggesting a novel therapeutic strategy [90]. Pharmacological inhibition of VEGFR1 and VEGFR2 by the small-molecular RTK inhibitor SU5416 in combination with chronic hypoxia in a murine model evokes angio-obliterative PH (by cell death-dependent pulmonary endothelial cell proliferation), vascular remodeling, and right ventricular hypertrophy and failure [92, 93]. It is well understood that, in the Su5416/hypoxia model, the triggering signal is the inhibition of VEGFR kinase activity. However, there is no conclusive evidence implicating the blockade of VEGF signaling as the modulator of PH in humans [92]. A possible exception is the PH displayed in patients suffering from chronic myelogenous leukemia and treated with the tyrosine kinase inhibitor dasatinib [94]. The existence of an endogenous molecule capable of inhibiting the VEGFR activity and subsequently triggering PH should be further explored.

Angio-obliterative PH may be described as vascular wound healing runaway train. Alterations in O_2 levels induce neointimal lesions and subsequent right ventricular remodeling. In order to accomplish angiogenesis in Su5416/hypoxia PH models or human PH, apoptosis-resistant cells resulting from the pharmacological or the autocrine VEGF2 blockade lead to a proliferate response via elevated levels of other growth fac-

tors such as FGF and PDGF. Moreover, VEGF signaling may continue uninhibited by the action of VEGFR3 or to the integrin αvβ3 (expressed in the membrane of activated ECs) [92].

PH is a usual hemodynamic impediment in heart failure. In several pathophysiological circumstances such as ischemia, hypertrophy, and hypoxia, the postnatal heart activates the fetal gene program, which in turn affects protein synthesis, excitation-contraction coupling, intracellular Ca^{2+} signaling, and apoptosis [95]. The fetal gene program involves the activation of the PI3K-Akt pathway, which raises glycogen levels and protects against ischemic damage [95–97].

2.6 Other Proteins Involved in ROS Signaling

VSMCs contribute to hypertension development through the increase in vascular resistance via SMC growth and contraction. The renin-angiotensin system, mainly by the action of Ang II, increases arterial blood pressure through Ang II type 1 (AT_1) receptors [98]. An elevated protein expression and signaling of AT_1 in the pulmonary vasculature of patients with PH has been shown [99]. Ang II is produced in lung and endothelial cells by angiotensin-converting enzyme (ACE) acting on angiotensin I [98, 100]. Schelling and colleagues observed that Ang II activated the phospholipase C (PLC)-β1 isoform, which is consistent with other signaling cascades induced by vasoconstrictor hormones [101]. Moreover, it has been demonstrated that PLC can interact with transient receptor potential canonical (TRPC) channels in the plasma membrane [102, 103], as depicted in Fig. 2.2. PLC principally hydrolyzes phosphatidylinositol 4,5-biphosphate (PIP_2) into the secondary messenger inositol 1,4,5-trisphosphate (IP_3) and diacylglycerol (DAG) [101]. DAG remains in the plasma membrane where it can activate TRPCs which allow Ca^{2+} entry into the cell [104]. IP_3 diffuses across the cytosol to bind the IP_3 receptors (IP_3Rs) on the surface of the sarcoplasmic reticulum (SR) [105]. Ca^{2+} flooding the cytoplasm triggers secondary cascade events wherein additional protein kinase C (PKC) and Ca^{2+}/calmodulin kinase II (CaMKII) are activated [106]. Ca^{2+} influx also activates ryanodine receptors (RyRs) on the SR membrane, which in turn release more stored Ca^{2+}, a process known as Ca^{2+}-induced Ca^{2+} release (CICR) (shown in Fig. 2.1) [107]. Ca^{2+} is essential in smooth muscle contraction, elevating blood pressure, and in some cases provoking apoptosis. As portrayed in Fig. 2.2, Ang II can increase Nox1 activity and ROS generation in VSMCs, thereby mediating the development and progression of cardiovascular diseases [35, 108]. In addition, Matsuno and colleagues demonstrated using Nox1-deficient mice that ROS derived from Nox1/NADPH are critical for the pressor response to Ang II by reducing the availability of NO [34].

The dynamin-related protein 1 (DRP1) activity in mitochondrial fission may contribute to the quasi-malignancy of ECs and hyperproliferation of VSMCs involved in PH [35, 109]. DRP1 is a GTPase that mediates mitochondrial fission and autophagy. As can be seen in Fig. 2.2, this protein is located in the cytosol, but may be recruited to the outer mitochondrial membrane with calcium in response to stress and ROS [8, 110]. DRP1-dependent autophagy is triggered to remove damaged mitochondria during ischemia events [111]. In this regard, Zhang and colleagues showed how the non-specific ROS inhibitor, N-acetylcysteine (NAC), decreased DRP1 activity. Moreover, TEMPO, the mitochondrial ROS inhibitor, significantly lowered hypoxia-induced DRP1 expression. The genomic inhibition of DRP1 by siRNA also decreased ROS, while overexpression of DRP1 increased them. Furthermore, silencing DRP1 led to elevated rates of mitochondria fragmentation in cultured PASMCs, while overexpression of DRP1 partly inhibited fragmentation [8]. These findings point out that ROS are generated principally in mitochondria, mediating the fission of this organelle in PASMCs contributing to pulmonary vascular remodeling. Studies have found suppression of DRP1 to positively affected myocardiocytes and other cell types during ischemia-reperfusion events by preserving mitochondrial structure and distribution, lowering oxygen consumption, and reducing

apoptosis rates [111]. However, Shirakabe and colleagues found that mitochondrial dysfunction, hypertrophy, and heart failure developed rapidly in DRP1 KO mice, suggesting a protective role of this protein [112]. The complexity of DRP1 may not be completely understood to fully map its involvement in mitochondrial dysfunction as it relates to PH.

In another study, glioblastoma U251 cells under hypoxia showed elevated expression of DRP1 through either ROS action or upregulation of HIF-1α. HIF-1α was inhibited using echinomycin, which reduced DRP1 expression and attenuated mitochondrial fission [113]. It was found that blocking the FIS1 fission protein and DRP1 prevented the fragmentation of mitochondria and abated the loss of CytC, which effectively protected cells from apoptosis [114]. Cytochrome *c* oxidase is the transmembrane protein imbedded in the cardiolipin of complex IV of the ETC. When elevated, ROS, the cardiolipin-cytochrome *c* complex, undergoes a peroxidase function, thereby releasing the heme protein. Zhang and colleagues were able to visualize the release of CytC through COX IV staining microscopy [8]. CytC is extruded through pores and eventually makes its way to the cytoplasm, as shown in Fig. 2.1.

Cytochrome *c* interacts with IP_3 on ER causing Ca^{2+} release [115]. Higher rates of CytC release from the mitochondria into the cytoplasm were observed in cells treated with siDRP1 (opposite to DRP1 overexpression). Knockdown of DRP1 even prevented mitochondrial fragmentation and CytC loss despite the translocation of Bax to the outer mitochondrial membrane [116]. Bax resides in the cytosol until apoptotic signaling (H_2O_2, heat, changes in pH, and mitochondrial membrane remodeling) causes it to bind to the outer mitochondrial membrane [117]. It is likely that Bax interacts with voltage-dependent anion channels and fission/fusion machinery in order to imbed itself into the outer membrane of the mitochondria [118]. CytC is then lost through voltage-dependent anion channels. Figure 2.1 displays how CytC binds to the apoptotic protease-activating factor 1 (Apaf1) forming the apoptosome and initiates programmed cell death [118]. In support, Thomas and Jacobson found delayed CytC release in A549 lung epithelial cells. These cells had impaired Drp1 mitochondrial recruitment and decreased Drp1-dependent fission. Consequently, the authors observed less mitochondrial fission and a resistance to apoptosis [119].

Finally, it is understood that Rac is an important signaling molecule in cardiovascular systems. Rac is a cytosolic low-molecular-weight guanine nucleotide-binding protein, which is a member of the Rho family of small GTPases. It was found that this GTPase promotes hypercholesterolemia in mice, which includes NADH-derived ROS, impaired vasorelaxation, elevated macrophage infiltration, and enhanced plaque rupture [120]. Rac1-Nox-mediated ROS have been shown to inhibit NO production and promote low-density lipoprotein (LDL) production as well as the production of inflammatory mediators like intracellular adhesion molecule 1 (ICAM-1) and vascular cell adhesion molecule 1 (VCAM-1), therefore progressing atherosclerotic lesions [121].

2.7 Ca^{2+} Signaling

There is cross-talk between cellular Ca^{2+} and ROS [122]. Extracellular ROS from NADPH oxidase and endogenous H_2O_2 were shown to stimulate the L (long-lasting)- and T (transient)-type voltage-dependent Ca^{2+}channels which favor the entry of this ion into vascular smooth muscle cells [123, 124]. The opening of these channels may be influenced by phosphorylation processes via protein kinases activated by ROS [123]. PLC pathway is known to activate TRPCs, in association with DAG (Fig. 2.2). TRPC1, TRPC3, and TRPC6 genes are upregulated in models of cardiovascular disease, which mediates smooth muscle proliferation, and thus contribute to hypertrophy. Also, the inhibition of these channels mitigates the associated pathophysiology [125]. Ca^{2+} influx through voltage-dependent Ca^{2+} channels (VDCC, Ca_v) is implicated in the proliferation of PASMCs [126]. Pharmacological blockade and genomic interference of the $Ca_v3.1$

subtype have been proved to inhibit PASMC proliferation and the entry to cell cycle [127]. Moreover, a G protein-coupled receptor (GPCR), the Ca^{2+} sensing receptor (CaSR), along with the PI3K and the MEK1/ERK1/2 pathways is involved in the hypoxia-evoked proliferation of PASMCs [128]. Additionally, Yamamura and colleagues found in a murine model of pulmonary hypertension induced by the exposure to hypoxia that NPS2143 (an antagonist of CaSR) prevented right ventricular hypertrophy and vascular remodeling [129].

Ca^{2+} is crucial to cell homeostasis and the maintenance of a proper vascular tone. A vascular smooth muscle cell at rest maintains an intracellular Ca^{2+} concentration ($[Ca^{2+}]_i$) around 100 nM. An agonist-stimulated VSMC displays an elevated $[Ca^{2+}]_i$ that oscillates between 500 nM and 1 mM [130]. One of the biggest Ca^{2+} stores in SMCs is the sarcoplasmic reticulum (SR), which contains roughly between 2 and 5 mM of Ca^{2+} [131]. The SR uptakes Ca^{2+} using sarco−/endoplasmic reticulum Ca^{2+} ATPases (SERCAs). It is in turn released through RyRs and IP_3Rs (Fig. 2.1). It is well known that the RyR can be stimulated by mitochondria-derived ROS, which oxidize the thiol groups present in the receptor [132, 133], as seen in Fig. 2.2. This modification enhances the channel activity and increases cytosolic Ca^{2+}. It is no surprise that mice with hypoxia-induced pulmonary hypertension also display increased activity of RyR in PASMCs [134]. Furthermore, RyR2 knockout mice do not show RyR activity or the associated elevation of intracellular Ca^{2+} and do not develop pulmonary hypertension followed by hypoxic exposure. The endogenous inhibitor molecule, FK506 binding protein 12.6 (FKBP12.6), forms a complex with RyR2 in a closed conformation. Disruption of this complex is proposed to underlie increased channel activity and elevated Ca^{2+} release into the cytosol [135]. Additionally, it has been remarkably proposed that alterations in $[ROS]_i$ in PASMCs can modify the activity of ion channels, evoking a large increase in $[Ca^{2+}]_i$. In this regard, hypoxia-induced changes in $[ROS]_i$ have been shown to inhibit K^+ currents (mediated by K_V channels) [18, 20, 136]. Moreover, the blockade of these channels lead to membrane depolarization and the opening of Ca_V channels with the subsequent large increase in $[Ca^{2+}]_i$. Furthermore, PH patients with downregulated K_v proteins exhibit elevated Ca^{2+} influx via L-type voltage-dependent Ca^{2+} channels (L-VDCCs), which promote vasoconstriction and cell proliferation [20].

Appropriate Ca^{2+} uptake into the mitochondria supports metabolic processes, such as dehydrogenase activity. However, overwhelming Ca^{2+} stimulus may initiate apoptosis. Ca^{2+} efflux and influx across the mitochondria are regulated by distinctive proteins. The mitochondrial permeability transition pore (mPTP) is sensitive to voltage and Ca^{2+} and mediates the mitochondrial permeability transition (MPT). MPT is elicited by a Ca^{2+} overload in matrix Ca^{2+} concentration that results in organelle swelling. Interestingly, this process seems to play a critical role in cell death. On the other hand, Ca^{2+} import across the mitochondria occurs through the voltage-dependent anion channel (VDAC) (simplified in Fig. 2.1a). A portion of the outer mitochondrial membrane of this protein associates with other proteins (NADH, metabolic enzymes, chaperones) occurring in the inner mitochondrial membrane which modulate VDAC gating properties. The opening of this channel, usually initiated by fast or elevated Ca^{2+} ion uptake, causes depolarization, ETC inhibition and ROS generation, and loss of antioxidants like glutathione [25, 137]. Under ischemia, the opening of mPTP assists the cell by reducing Ca^{2+} overload in the cytosol, but this causes the mitochondria to swell [138]. Reperfusion causes additional ionic imbalances by reactivating energy transduction, contractions, and ROS generation [139]. Protein overload events in the SR may lead to excessive ROS generations and hyperoxidation in the SR. Accumulation of mis−/unfolded polypeptides give rise to ER stress and initiate Ca^{2+} release through RyRs and IP_3Rs into the cytosol [140].

Protein kinase C epsilon (PKCε) is abundantly expressed in adult cardiomyocytes. It regulates muscle contraction at a sarcomeric protein level, modulates intracellular metabolism through interactions with mitochondria, and plays a key role in protecting cells against ischemic injury through its involvement in hypertrophy. Acute hypoxia has

been shown to activate PKCε by 3.2-fold in PASMC [24]. Through use of ETC inhibitors as well as Gpx1 overexpression mouse models, Rathore and colleagues demonstrated how ROS subsequently increases PKCε activity. Exogenous H_2O_2 was able to elevate PKCε activity even with blockaded ETC. By inhibiting PKCε, hypoxia-induced intracellular Ca^{2+} increases were shown reduced by 40 percent [24].

It has been found that ROS generated from the mitochondria elevate the activity of PKCε as well as Nox and propagate ROS generation [141]. Recent studies implicate more specifically the RISP of complex III as the key player for mitochondrial ROS production. Isolated mitochondria that were siRNA treated to silence the RISP activity had no hypoxic ROS generation, while those with RISP overexpression produced a greater ROS response [142].The inhibition of the RISP activity has been shown to abolish the increase in $[Ca^{2+}]_i$ in PASMCs and hypoxic vasoconstriction in isolated PAs [142] .

PKCε is also an upstream modulator of resistin-evoked VSMC migration [143]. Resistin is an adipokine mainly expressed in cells of monocyte/macrophage lineage in humans [144]. Elevated serum levels of resistin promote vascular cell dysfunction and are linked to inflammation associated with atherosclerosis and myocardial infarction [145]. Interestingly, this adipokine upregulates the expression of Nox*4* and *p22phox*, but only with active PKCε as the mediator. ROS may be halted through blockading PKCε. PKCε involvement in cardiovascular diseases is further demonstrated by its role in facilitating neointimal hyperplasia and luminal narrowing in mouse models. Moreover, resistin-treated mice only showed neointimal formations with unrestrained PKCε, while blocking PKCε showed no change [145].

2.8 MicroRNAs

Non-coding genomic transcripts are also regulators of biological and pathological processes. Evaluating the role microRNAs play in heart disease is essential for developing therapeutic targets and treatment. Reddy and coworkers found that miR-99a were associated with cardiomyocyte survival and growth at preliminary stages of pulmonary hypertension, while miR-208b was activated later [146]. The miR-208 is associated with the fetal gene program. There is an asymmetry of microRNA alterations between left and right ventricular remodeling. MicroRNAs 34a, 28, 148a, and 93 were upregulated in right ventricle remodeling and downregulated in left ventricle remodeling. In the right ventricle, there was downregulation in HIF-1α, a target of miR-199a. This microRNA also targets Smad3 and may impact Ca^{2+} concentration and NO release. There is a pathogenic role of miR-126. Lowered levels of miR-126 in right ventricular remodeling led to lowered activation of the Raf-Mek-MAPK pathway. This has been experimentally treated using miR-126 mimics that resulted in better cardiac vascular density and function [147]. With laser-assisted microdissection using microRNA analysis, it was found that plexiform lesions displayed an upregulation of miR-126 and mir-21 and a downregulation of miR-204 [148].

The loss of miR-145 (genetically and pharmacologically) in PH mouse models reduced right ventricle systolic pressure [149]. MicroRNA expression has been found to be significantly different in isolated pulmonary arteries than from normal arteries in PH patients [150]. Whether the expression is altered in several microRNAs in the right heart under hypoxia [151], further research is imperative to elucidate the role of miRNAs in the initiation and development of PH.

2.9 Conclusion

PH is a widespread lung disease affecting millions of people throughout the world. The underlying causes are multifaceted and interconnected. Progressively, we and other researchers are unraveling and piecing together the interplay of ROS with intracellular Ca^{2+} and inflammatory signaling in mediating complex pathophysiological processes in PA involved by numerous proteins and genes. Abnormal function in mitochondria as a result of cellular stress

triggers multiple signaling cascades that may eventually lead to alteration in cellular homeostasis and apoptosis. Particularly, RISP in mitochondria acts as a primary hypoxia sensor in the pulmonary artery. Moreover, hypoxic environments promote ROS generation mainly from mitochondria leading to the activation of important signaling molecules such as PKCε and Nox. Both pathways result in the increase of $[Ca^{2+}]_i$ and the subsequent SMC contraction. Collectively, these mechanisms contribute to the development and progress of PH. Researchers are increasingly able to identify specific molecules in pathogenic processes in PH and thus create novel therapeutic targets to better treat this devastating illness.

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Inflammatory Pathways in Sarcoidosis

3

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Abstract

Concepts regarding etiology and pathophysiology of sarcoidosis have changed remarkably within the past 5 years. Sarcoidosis is now viewed as a complex multi-causation disease related to a diverse collection of external environmental or infectious signals. It is generally accepted that the cause of sarcoidosis is unknown. Moreover, concepts of the inflammatory pathway have been modified by the realization that intrinsic genetic factors and innate immunity may modify adaptive immune responses to external triggers. With those potential regulatory pathways in mind, we will attempt to discuss the current understanding of the inflammatory response in sarcoidosis with emphasis on development of pulmonary granulomatous pathology. In that context, we will emphasize that both macrophages and T lymphocytes play key roles, with sometimes overlapping cytokine production (i.e., TNFα and IFN-γ) but also with unique mediators that influence the pathologic picture. Numerous studies have shown that in a sizable number of sarcoidosis patients, granulomas spontaneously resolve, usually within 3 years. Other sarcoidosis patients, however, may develop a chronic granulomatous disease which may subsequently lead to fibrosis. This chapter will outline our current understanding of inflammatory pathways in sarcoidosis which initiate and mediate granulomatous changes or onset of pulmonary fibrosis.

Keywords

Alveolar macrophages · Lymphocytes · Innate immunity · Granuloma mediators · Th17 · PPARγ

Abbreviations

ABCA1	ATP-binding cassette lipid transporter-A1
ABCG1	ATP-binding cassette lipid transporter-G1
CCL	C-C motif chemokine ligand
CCR	C-C chemokine receptor
CXCL	C-X-C motif ligand
DAMPs	danger-associated molecular patterns
GWAS	genome-wide association studies
HLA	human leukocyte antigen
IFN-γ	interferon gamma
IL	interleukin

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IL-23R interleukin-23 receptor
MMP12 matrix metalloproteinase 12
mTOR mammalian target of rapamycin
NLRs NOD-like receptors
PAMPs pathogen-associated molecular patterns
PBMC peripheral blood mononuclear cells
PD-1 programmed cell death-1
PPARγ peroxisome proliferator-activated receptor gamma
PRRs pattern recognition receptors
RORγt retinoic acid receptor-related orphan nuclear receptor γt
SAA serum amyloid A
sIL-2R soluble interleukin 2 receptor
STAT signal transducer and activator of transcription
TGFβ transforming growth factor beta
Th17 T-helper 17
TLRs Toll-like receptors
TNFα tumor necrosis factor alpha
Tregs regulatory T cells
TSC2 tuberous sclerosis 2

3.1 Introduction

Concepts regarding etiology and pathophysiology of sarcoidosis have changed remarkably within the past 5 years [1]. Sarcoidosis is now viewed as a complex multi-causation disease related to a diverse collection of external environmental or infectious signals [2, 3]. It is generally accepted that the cause of sarcoidosis is unknown. Moreover, concepts of the inflammatory pathway have been modified by the realization that intrinsic genetic factors and innate immunity may modify adaptive immune responses to external triggers. With those potential regulatory pathways in mind, we will attempt to discuss the current understanding of the inflammatory response in sarcoidosis with emphasis on development of pulmonary granulomatous pathology. In that context, we will emphasize that both macrophages and T lymphocytes play key roles, with sometimes overlapping cytokine production (i.e., TNFα and IFN-γ) but also with unique mediators that influence the pathologic picture. Numerous studies have shown that in a sizable number of sarcoidosis patients, granulomas spontaneously resolve, usually within 3 years [4]. Other sarcoidosis patients, however, may develop a chronic granulomatous disease which may subsequently lead to fibrosis. This chapter will outline our current understanding of inflammatory pathways in sarcoidosis which initiate and mediate granulomatous changes or onset of pulmonary fibrosis.

3.2 Induction of Inflammation

3.2.1 Environmental Factors

Inorganic Materials Pulmonary Inflammation associated with sarcoidosis has been linked to multiple environmental factors including inorganic and organic substances. Some of the putative organic substances are antigens of infectious agents although the disease itself is not infectious. Inorganic factors may include particulate matter such as dusts and silicates, as were observed in the "sarcoid-like" granulomatous pulmonary disease found in responders to the World Trade Center disaster [5]. Sarcoidosis cases have also been associated with occupational exposures to various inorganic agents such as encountered in firefighting, construction, and machining (reviewed in [3]).

Infectious Agents The possibility of an infectious origin for sarcoidosis has been suggested by its similarity to tuberculosis. Infectious organisms associated with sarcoidosis include mycobacteria and *Cutibacterium acnes* (formerly named *Propionibacterium acnes*). DNA residues from both agents have been reported in sarcoidosis granulomas, but no live bacteria have been found (reviewed in [2]). Moreover, in both cases, related proteins (mycobacterial catalase-peroxidase and *C. acnes* catalase) were found to elicit elevated T lymphocyte responses in sarcoidosis patients, suggesting that sarcoidosis might represent an immune-mediated disease to bacterial components [2]. The concept of sarcoidosis-associated immune reactivity stems

from early studies in which intradermal injection of a pasteurized suspension of sarcoid lymphoid tissue was utilized by Kveim, a Norwegian pathologist, as a diagnostic test for sarcoidosis (reviewed in [6]). This "Kveim test" found that after 4–6 weeks, granulomatous responses were elicited in the skin from sarcoidosis patients but not from controls. Later proteonomic analyses of Kveim "antigen" reported that the presence of the mycobacterial catalase-peroxidase protein [7] has been shown to trigger elevated interferon gamma (IFN-γ) responses in sarcoidosis patients [8]. Currently, association of prior mycobacterial infection is present in many sarcoidosis cases, but there is no direct evidence for an infection-initiated etiology (reviewed in [9]).

3.2.2 Intrinsic Factors

Genetic Profiles and Autoimmunity Autoimmune mechanisms have been considered in sarcoidosis because of its complex diversity of symptoms. Proteonomic studies have identified numerous sarcoidosis-related proteins in Kveim preparations and have shown that one of them (vimentin) can elicit elevated IFN-γ responses in peripheral blood mononuclear cells (PBMC) of sarcoidosis patients but not healthy controls [6]. Vimentin is an intermediate filament protein secreted by alveolar macrophages and is important to cellular interactions (reviewed in [10]). Antibodies specific to vimentin have been detected in bronchoalveolar lavage fluid (BALF) from sarcoidosis patients [11]. Immune reactivity to vimentin is not specific to sarcoidosis, however, and antibodies to vimentin have been found in autoimmune conditions such as systemic lupus erythematosus (SLE) and rheumatoid arthritis (RA) [10]. In addition, low levels have been detected in BALF from healthy individuals [11]. In sarcoidosis, additional studies are needed to define the role of vimentin as it is unclear whether it is a cause or effect of inflammation.

Analysis of gene markers in sarcoidosis has focused on CD4+ T lymphocytes which accumulate in the lungs prior to granuloma formation (reviewed in [12]). Characterization of these cells indicates the presence of adaptive immune responses in sarcoidosis, with antigen-driven activation involving antigen-presenting cells such as macrophages. Several human leukocyte antigen (HLA) gene patterns have emerged from sarcoidosis analyses, with HLA-DRB1*01 and HLA-DRB1*04 appearing to be protective in Caucasian populations, while risk factors for sarcoidosis are represented by HLA-DRB1*03, HLA-DRB1*11, HLA-DRB1*12, HLA-DRB1*14, and HLA-DRB1*15 [12]. Interestingly, HLA-DRB1*03 is also present in patients with Lofgren's syndrome, a self-limiting form of sarcoidosis characterized by acute onset, fever, and clinical symptomology such as bilateral hilar lymphadenopathy [11] (reviewed in [2]). Clinical disease course in Lofgren's syndrome correlates with DRB1*03 presence: disease resolution occurs in 95% of DRB1*03 positives but in only 49% of DRB1*03 negatives [12]. With respect to vimentin antibodies in BALF, higher titers have been found in HLA-DRB1*03-positive sarcoidosis patients compared to HLA-DRB1*03 negatives [11]. The significance of these findings requires further study.

Genetic studies in sarcoidosis have also analyzed candidate genes associated with sarcoidosis such as the immune-related genes, tumor necrosis factor (TNF), and the interleukin-23 receptor (IL-23R) [12]. TNF meta-analysis studies revealed a significant association of the −308 polymorphism with sarcoidosis compared to controls, while other studies also found a −307 haplotype associated with good prognosis and a −857T containing one associated with persistent disease (reviewed in [12]). Studies of IL-23R variants have noted an association with Crohn's disease (CD) as well as sarcoidosis. The IL-23R gene codes for a subunit of the IL-23 receptor which is important to T-helper 17 (Th17)-mediated processes, and several alleles have been found with significant associations to sarcoidosis (reviewed in [12]). More recent approaches to the genetics of sarcoidosis have utilized genome-wide association studies

(GWAS) (reviewed in [13]). The major findings from these studies have confirmed the role of TH1 adaptive immune responses in sarcoidosis with emphasis on IFN-γ functions and signaling pathways. The authors concluded that future GWAS studies in sarcoidosis need to utilize more cutting-edge approaches to allow analyses of single-cell subpopulations as well as sequential monitoring of patients for changes in disease status [13].

Innate Immunity: Overview This section will consider several avenues of innate immune reactivity that have been reported in sarcoidosis. Innate immune responses are considered to be direct contributors to granulomatous inflammation in sarcoidosis (reviewed in [14]). Relevant innate immune factors to be discussed include the following: (a) pattern recognition receptors (PRRs); (b) the NOD-like receptor NLRP3 inflammasome network [15]; (c) the mTOR signaling pathway; (d) serum amyloid A (SAA), an acute-phase protein; and (e) chitotriosidase, an enzyme involved in pathogen defense [16] (Table 3.1).

Innate Immunity: Pattern Recognition Receptors (PRRs) Within the lung, PRRs represent an innate defense against infections within the alveolus and are expressed on alveolar macrophages, epithelial cells, endothelial cells, and other cell types (reviewed in [17]). PRRs sense microbial invaders by recognition of conserved microbial molecules classically defined as "pathogen-associated molecular patterns" (PAMPs). PRR encounter activates cellular production of inflammatory cytokines and chemokines which in turn recruit and activate macrophages and neutrophils. In the case of noninfectious injury elicited by large, inert particles such as silica crystals, some PRRs may also become active. In addition, release of endogenous intracellular molecules from injured cells, defined as "danger-associated molecular patterns" (DAMPs), also mediates further cellular inflammatory responses to noninfectious injuries [17].

Among the PRRs are Toll-like receptors (TLRs) and the cytosolic NOD-like receptors (NLRs) which include NLRP3. These molecules are expressed in alveolar macrophages, lung epithelial cells, and dendritic cells as well as on lymphocytes

Table 3.1 Mediators of innate immunity in sarcoidosis lung

Innate immune mediators	Role in pathophysiology	Pulmonary location
Pattern recognition receptors (PRRs) [17]	Host defense against pathogens; mediate inflammatory responses	Expressed on alveolar macrophages, epithelial cells, endothelial cells, and others
Pathogen-associated molecular patterns (PAMPs) [17]	Conserved microbial molecules recognized by PRRs; activate release of inflammatory cytokines	Responders to PAMPs include alveolar macrophages, epithelial cells, and endothelial cells
Danger-associated molecular patterns (DAMPs) [17]	Endogenous intracellular molecules from injured cells; mediate inflammatory responses	Responders to DAMPs include alveolar macrophages, epithelial cells, and endothelial cells
Toll-like receptors (TLRs) [14, 17]	Bind both microbial and endogenous ligands; mediate inflammatory responses	Expressed on lymphocytes, alveolar macrophages, epithelial cells, and dendritic cells
NLRP3 inflammasome network [15, 18, 19, 20]	Host defense against pathogens; initiates pyroptosis and release of pro-inflammatory cytokines	Granuloma tissues
MTOR signaling pathway [21, 22]	Regulates rapid responses of innate immune cells; involved in initiation and progression of granulomas	Granuloma tissues
Serum amyloid A (SAA) [23–25]	Acute-phase reactant; constituent of granulomas	Macrophages and giant cells within granuloma tissues
Chitotriosidase [16–26]	Host defense against chitin-containing fungi and protozoa	Produced by activated macrophages; detectable in sarcoidosis sera

(reviewed in [17]). There are ten members of the human TLR family located either at the cell surface (TLR2, TLR4–6, TLR10) or in lysosomal/endosomal membranes (TLR3, TLR7–9). Ligands include both microbial and endogenous factors which can induce production of antimicrobial peptides and pro-inflammatory mediators such as TNFα, IL-8, and proIL-1β. Further processing of proIL-1β is required by caspase activation via NLRP3 (discussed below). Mycobacterial ligands may recognize TLR2 and TLR9, and polymorphisms in both have been associated with susceptibility to mycobacterial infection and granulomatous pathobiology (reviewed in [14]). In sarcoidosis, enhanced TNFα responses to TLR2 stimulation have been found in cells from both blood and the lungs [14]. A positive feedback loop has been suggested by the capacities of TNFα and IFN-γ to enhance TLR2 expression on pulmonary epithelial cells [14].

Innate Immunity: The NLR Inflammasome Network NLRs comprise another innate immune receptor family of 22 members (in humans), but few of these have been functionally characterized. Five of these NLRs have been shown to assemble "inflammasomes" which are high-molecular-weight protein complexes present in the cytosol of stimulated immune cells (reviewed in [18]). These complexes have a critical role in host defense against pathogens and can be triggered by diverse stimuli. Basic functions of the NLRP3 inflammasome (which has been more intensely studied than other NLRs) are to initiate an inflammatory form of cell death (pyroptosis) and to release pro-inflammatory cytokines IL-1β and IL-18 (reviewed in [19]). In macrophages, NLRP3 activity begins with a priming signal which can be supplied by TLR4 agonists that induce expression of NLRP3 and proIL-1β. Next, an activation signal may be triggered by the above-described PAMPs and DAMPs, which promote inflammasome assembly, caspase-1-mediated IL-1β and IL-18 secretion, and pyroptosis. Interestingly, the priming step alone has been found to be sufficient for human monocytes to mediate caspase-1 activation and IL-1β release [19]. In sarcoidosis, the NLRP3 inflammasome network has been shown to be constitutively activated and involved in granuloma formation [20]. Upregulation of NLRP3 components including cleaved caspase-1 and IL-1β has been found in sarcoid pulmonary granulomas, and NLRP3 mRNA was elevated in cell-sorted sarcoid alveolar macrophages compared to controls [20]. Of interest were findings in a mouse granuloma model which showed that NLRP3 KO mice exhibited decreased granuloma formation compared to wild type. Additional murine studies also showed that microRNA miR-223 acted as a downregulator of NLRP3, and in miR-223 KO mice, granulomas were increased in size [20]. In sarcoidosis alveolar macrophages, miR-223 levels were decreased in contrast to the elevation of NLRP3. These findings illustrate the importance of NLRP3 inflammasomes as an active component of innate immunity in sarcoidosis pathogenesis.

Innate Immunity: The mTOR Pathway The mammalian target of rapamycin (mTOR) is a serine/threonine kinase regulatory-associated protein which acts as a central regulator of cellular metabolism (reviewed in [21]). MTOR forms a part of two complexes: mTOR complex 1 (mTORC1) and mTOR complex 2 (mTORC2) which primarily shape rapid responses of innate immune cells represented by monocytes, macrophages, dendritic cells, neutrophils, mast cells, and innate-like NK cells. Rapamycin inhibits these mTOR complexes and has been used as an immunosuppressive drug to prevent kidney allograft rejection [21]. MTOR pathways become activated by various extracellular signals such as growth factors, TLR ligands, and cytokines. Activation controls a wide range of cellular functions including translation, protein synthesis, cell growth, metabolism, and anabolic processes. Studies in mice have shown that mTORC1 can also become activated by deletion of the gene encoding tuberous sclerosis 2 (TSC2) resulting in induced hypertrophy and proliferation culminating in excessive pulmonary granuloma formation in vivo [22]. Inhibition of mTORC1 induced apoptosis and completely resolved granulomas in

TSC2-deficient mice [22]. In studies of sarcoidosis patients, clinical disease progression was found to correlate with mTORC1 activation, macrophage proliferation, and glycolysis [22]. Findings support a role for the innate immune mTOR pathway in initiation and progression of granuloma pathophysiology.

Innate Immunity: Serum Amyloid A Serum amyloid A (SAA) is a highly conserved acute-phase reactant primarily synthesized by the liver. Circulating SAA levels can increase by as much as 1000-fold during inflammation (reviewed in [23]). In sarcoidosis, staining for SAA revealed high levels of expression in granulomatous tissues compared to tissues from patients with other granulomatous disorders [24, 25]. SAA is not specific to sarcoidosis, however, and statistical analyses indicate SAA staining is not sensitive enough for use in diagnostic testing [25]. SAA expression in sarcoid granulomas localizes to macrophages and giant cells and was found to correlate with numbers of CD3+ T cells within granulomas, suggesting an SAA linkage to local Th1 immune responses [24]. Findings from a murine granuloma model indicated that SAA regulated granuloma size, in part via TLR2 signaling, with production of IFN-γ, TNF, and IL-10 accompanying increased granuloma size [24]. Anti-TLR2 antibodies attenuated these effects [24]. Authors suggest that data points to SAA as a constituent and innate regulator of chronic granulomatous inflammation in sarcoidosis [24].

Innate Immunity: Chitotriosidase Chitotriosidase is the major active chitinase enzyme in humans and is produced mainly by activated macrophages (reviewed in [26]). The enzyme is an innate immune defense against chitin-containing pathogens such as fungi and protozoa. In several human diseases, including sarcoidosis, chitotriosidase is elevated in serum and is a marker of disease severity [26]. A recent study of 694 sarcoidosis patients and 101 healthy controls confirmed the presence of significantly elevated values for serum chitotriosidase in sarcoidosis [16]. Values were also found to be increased in patients with extrapulmonary involvement and in patients requiring increased steroid dosage [16]. The mechanisms by which chitotriosidase is implicated in sarcoidosis granulomatous pathophysiology, however, remain to be determined.

3.3 Inflammatory Granuloma Formation

Initiation of Granuloma Structure Granuloma structure is the product of coordinated responses from both innate and adaptive immunity to poorly degradable antigens (reviewed in [27]). Foreign antigenic materials deposited in the lungs are acquired by macrophages which release many pro-inflammatory cytokines (TNFα, IL-1β, IL-6) that persistently stimulate immune response pathways. Dendritic cells pick up the degraded antigens and migrate to regional lymph nodes where antigens are presented to naïve CD4+ T cells. Clonal T cell differentiation and proliferation occur in the nodes, and activated CD4+ T cells, via chemokines, migrate back to inflammatory sites within the lung. Both induction and maintenance of granuloma formation in sarcoidosis require CD4+ cell activation (reviewed in [28]). Once in the lungs, CD4+ T cells release cytokines (IFN-γ, TNFα, IL-12, and IL-18) which stimulate macrophages to organize into giant cells and granulomas. Evidence from sarcoidosis studies suggests that mediastinal lymph nodes constitute the initial site of granuloma formation prior to pulmonary granuloma development (reviewed in [29]). Unlike granulomas of infectious origin, sarcoid granulomas rarely have significant necrotic areas. A mature sarcoid granuloma is composed of both epithelioid and multinucleated giant cells in a tight configuration surrounded mainly by CD4+ T-helper cells. Historically, sarcoidosis granulomas have been considered to be driven by Th1 lymphocytes, but recent data suggest Th-17 cells have major roles in granuloma formation and persistence (reviewed in [2, 30]).

Granuloma Mediators Macrophages are one of the major producers of the enzyme matrix metalloproteinase 12 (MMP12) [31]. MMP12 is one of a family of proteolytic enzymes that degrades extracellular matrix elastin and enables infiltration of immune cells responsible for inflammation and granuloma formation. In sarcoidosis, MMP12 has been found to be one of the most highly expressed (>25-fold) enzymes in lung tissues, and MMP12 protein is elevated in BAL fluids [32]. Strikingly, MMP12 expression was highest near areas of active granulomatous inflammation, and MMP12 levels in BALF correlated with disease severity. Inhibition studies with a global MMP inhibitor (Marimastat) have reported reduced granuloma formation in lung tissue models of mycobacterial infection [33]. More recently, a comparative study of *mmp12* KO and wild-type mice was carried out in a carbon-nanotube-induced granuloma model [34]. Results indicated that granulomas formed in wild-type mice were detected as early as 10 days post instillation. These early granulomas were poorly formed, but by 60 days post instillation, granulomas appeared to be well defined. Surprisingly, no histological differences in granuloma formation were noted acutely in *mmp12* KO mice compared to wild type at day 10, but by 60 days, the granulomas were smaller and less well formed. These results suggest that MMP12 is required to maintain chronic granuloma pathology [34]. Currently, pursuit of novel MMP inhibitors continues with efforts to define MMP roles in specific disease-related immunological responses and inflammation [35].

Serum Markers of Inflammation in Sarcoidosis: Chemokines Inflammatory chemokines CXCL9, CXCL10, and CXCL11 are produced in the sarcoid granulomatous lung by several cell types, including macrophages, endothelial cells, and fibroblasts (reviewed in [36]). The primary induction signal for these chemokines is IFN-γ produced by activated CD4+ T-helper lymphocytes (reviewed in [37]). The major effect of these chemokines is to promote an influx of T cells into inflammatory tissues by binding and signaling through the CXCR3 receptor present on activated T cells [37]. Analyses of IFN-γ-inducible chemokines in sarcoidosis patients have shown that serum levels are higher than those of healthy controls and correlate with each other [36, 38]. Additional analyses in sarcoidosis have shown that CXCL9 levels correlate best with systemic organ involvement, and both CXCL10 and CXCL11 levels correlate with pulmonary function decline.

Serum Markers of Inflammation in Sarcoidosis: sIL-2R Quantitation of serum levels of the soluble interleukin 2 receptor (sIL-2R) represents a standardized clinical assay for assessment of T lymphocyte activation in various immune disorders [39]. T cells express the receptor for IL-2 and, during activation, begin to secrete the receptor in soluble form (reviewed in [40]). As in other immune-related disorders, elevated blood sIL-2R levels correlate with disease activity in sarcoidosis patients and have been shown to be predictive of spontaneous remission [41]. In a recent study of undiagnosed patients whose sIL-2R results were available before a definitive diagnosis had been made, sensitivity and specificity of serum sIL-2R for detection of sarcoidosis were 88% and 85%, respectively. Additional analyses revealed that the sIL-2R assay was superior to serum angiotensin-converting enzyme (ACE) measurement used previously in diagnosis of sarcoidosis cases (62% sensitivity and 76% specificity) [40].

Serum Markers of Inflammation in Sarcoidosis: Chitotriosidase As reviewed previously above, chitotriosidase, a component of innate immunity, has been shown to be elevated in sera from sarcoidosis patients with active disease [26]. In a study population of some 232 sarcoidosis patients, sensitivity and specificity of serum chitotriosidase for detection of sarcoidosis compared to healthy controls were calculated to be 88.6% and 92.8%, respectively [42].

Granuloma Components: Macrophages

Macrophages represent the basic building blocks of granulomas. Early events in granuloma construction involve aggregation of macrophages for transformation into epithelioid cells (reviewed in [27]). The influence of CD4-driven inflammatory cytokines (IFN-γ, TNFα, IL-12, IL-18) further promotes cell-cell fusion between macrophages and dendritic cells or monocytes, creating multinucleated giant cells which form a large portion of mature granuloma core structure [43]. Outer portions of granulomas contain large numbers of T lymphocytes and a few B lymphocytes.

Alveolar Macrophages: Lipid Homeostasis and Inflammation

Alveolar macrophages exhibit unique lipid metabolic properties compared to other tissue macrophages because of the complex lung microenvironment [43, 44]. The lung is constantly bombarded with foreign material and, further, is coated with a lipid-rich surfactant that serves to prevent pulmonary collapse [45]. The lung is the most active lipid-secreting organ because of surfactant production [46]. Alveolar macrophages represent an essential component of surfactant clearance and lipid homeostasis within the lung [47]. Surfactant contains phospholipids and neutral lipids, the bulk of which is cholesterol [48]. Alveolar macrophage ATP-binding cassette (ABC) lipid transporters ABCA1 and ABCG1 participate in clearance of cholesterol [49]. Deficiencies of lipid transporters result in increased intracellular cholesterol together with overproduction of pro-inflammatory cytokines and chemokines (reviewed in [50]). Overloading macrophages with cholesterol has been shown to activate inflammasome pathways and cytokine production (reviewed [51]).

The transcription factor PPARγ directly or indirectly regulates many genes involved in cholesterol metabolism and transport, including the ATP lipid transporters (reviewed in [43]). PPARγ also antagonizes transcription of many pro-inflammatory genes via mechanisms that may include direct association with coactivators or transrepression of transcription factors [43]. Healthy alveolar macrophages, unlike other tissue macrophages, display high levels of PPARγ (reviewed in [44]). Alveolar macrophages from macrophage-specific PPARγ KO mice exhibit impaired surfactant lipid metabolism characterized by accumulation of intracellular neutral lipids, dysregulated lipid transporters, and elevated inflammatory cytokines [52, 53]. In addition, PPARγ deficiency also resulted in dysregulation of alveolar macrophage liver X receptor pathways which are critical to the promotion of cellular cholesterol export [54]. Dysregulation of PPARγ, ABCA1/ABCG1 lipid transporters, and pro-inflammatory cytokines are significant findings in alveolar macrophages from sarcoid patients [55].

In addition to cholesterol regulation in the lung, lipid transporters play key roles in host innate immunity; deficiencies lead to impaired immune cell homeostasis, further aggravating pulmonary inflammation [51].

Macrophage Profiles in the Lung

Studies of macrophage activation have led to a concept of classic and alternative activation termed M1 and M2, analogous to that of Th1 and Th2 cells (reviewed in [56]). More recently, however, it has become clear that whereas M1 and M2 phenotypes were derived from in vitro studies, tissue macrophages in vivo may display mixed responses [57].

Macrophage plasticity allows participation in both promotion and resolution of inflammation (reviewed in [58]). Generally, sarcoidosis data illustrate a model of persistent inflammation with macrophages exhibiting an M1 profile induced by pro-inflammatory cytokines such as IFN-γ [28]. Alveolar macrophages from pulmonary sarcoidosis patients have also been shown to produce IFN-γ which may provide further stimulation for granuloma formation [59]. The M1 or "classical activation" phenotype renders macrophages efficient killers of bacteria as well as transmitters of pro-inflammatory cytokines (IL-1β, IL-12, TNFα) (reviewed in [60]). An M2 or "alternative activation" phenotype, in contrast, allows macrophages to promote tissue repair which is a necessary function for the later resolution phase of inflammation (reviewed in [60]). Inducers of the

M2 macrophage phenotype include cytokines IL-4, IL-13, IL-10, and TGFβ [60]. The participation of M2 macrophages in fibrosis is still poorly understood, but M2 macrophages and giant cells have been noted within fibrotic areas of muscle specimens from sarcoidosis patients [61]. Additional studies are needed to more specifically define macrophage functions in sarcoidosis, particularly with respect to changes from a chronic granulomatous status to fibrosis.

Granuloma Components: Lymphocytes

Lymphocytes infiltrating sarcoid granulomas were once considered to be mostly Th1-polarized CD4+ cells, but current findings have established the presence of elevated Th17 phenotype lymphocytes in sarcoid granulomas and lymph nodes [62, 63] (Table 3.2). Th17 cells are a subgroup of CD4+ T lymphocytes that secrete IL-17A, a cytokine which can induce IFN-γ and TNFα production in macrophages (reviewed in [2, 30]). These Th17 products stimulate macrophages and promote both giant cell and granuloma formation. Th17 cells are not found in all granulomatous diseases; for example, they are not present in chronic beryllium disease [64]. IL-17A itself, however, can be produced in the lung by other cells such as NK cells and has an important role in mucosal immunity, including the respiratory tract [65]. Th17 cells are generated from CD4+ T cells exposed to TGFβ and IL-6 via a signaling cascade which culminates in tyrosine phosphorylation of STAT3 and STAT1 (reviewed in [66]). STAT3 induces Th17-related genes such as IL-17A and IL-23R as well as transcription factor retinoic acid receptor-related orphan nuclear receptor γt (RORγt) which is a negative regulator of alternative lineage phenotypes.

Th17 cells are remarkable for their plasticity in adopting pro-inflammatory or regulatory functions depending upon the microenvironment. Exposure to IL-1β, IL-12, and IL-23 transforms Th17 cells into a dual phenotype of Th1/Th17 which further drives inflammation with secretion of IFN-γ in addition to IL-17A. Further exposure of Th1/Th17 cells to Th1 cytokines IFN-γ and IL-12 can induce a Th17.1 phenotype which secretes mainly IFN-γ. Expression of the transcription factor T-bet has also been detected on some Th17 cells and thought to represent a transition state leading to the Th17.1 phenotype [38]. Chemokine receptors CCR6, CXCR3, and CCR4 have been helpful in differentiating among these CD4+ T-helper cells with (1) Th1 expressing CXCR3+, (2) Th17 expressing CCR6+ and CCR4 +, and (3) Th17.1 expressing CCR6+ and CXCR3+ [62] (Table 3.2). Studies indicate that CCR6-expressing Th17 cells are recruited to the lungs in pulmonary sarcoidosis by the macrophage chemokine CCL20. Newly diagnosed sarcoidosis patients with stage 2 pulmonary disease display elevated serum levels of IL-6, CCL20,

Table 3.2 T lymphocytes present in sarcoidosis lung

Initial phenotype	Inducing molecules	Induced phenotype	Secreted cytokines	Role in pathophysiology
CD4+	TGFβ, IL-6	**Th17** (CCR6+, CCR4+, CXCR3-, RORγt+)	IL-17A, IL-22, IL-23	Maintains mucosal surfaces [74]; stimulates granuloma-forming cells [2]
Th17	IL-1β, IL-12, IL-23	**Th1/Th17** (RORγt+, T-bet+)	IFN-γ, IL-17A	Promotes granuloma formation [30]
Th1/Th17	IFN-γ, IL-12	**Th17.1** (CCR6+, CCR4-, CXCR3+)	IFN-γ	Possible drivers of sarcoid immune response [64]
CD4+	Antigen affinity; ICOS[a] binding to macrophage ICOS[a] ligand [30]	**Regulatory T cells (Tregs)** (CD4+/CD25+, FoxP3+, CCR6+, CTLA-4+)	IL-10, TGFβ	Immunosuppressive activity [2]
CD4+	IFN-γ, IL-1, IL-12, CCL5, others [30, 61]	**Th1** (T-bet+, CCR6-, CCR4-, CXCR3+)	IFN-γ, IL-2	Th1% < Th17.1 in sarcoid lung [64]

[a]Inducible co-stimulator

IL-17A, and TGFβ [30, 67]. Ultimately, transformed Th17.1 cells appear in the lungs and do not proliferate, but have been considered to be end-stage cells which continue involvement in chronic pulmonary sarcoidosis [62].

Conventional regulatory T cells (Tregs) (CD4+/CD25+) are also present in sarcoid granulomas, and some studies suggest that sarcoidosis disease progression or regression is determined by the balance of Th17 and Treg cells (reviewed in [2, 30]). These Tregs also express FoxP3 and secrete both IL-10 and TGFβ. Data cited from newly diagnosed sarcoidosis patients in the study mentioned above indicated an imbalance of Th17/Tregs that coincided with the diagnosis of active disease [67]. Interestingly, murine studies have shown that Th17 cells may further differentiate via TGFβ and SMAD3 signaling pathways into IL-10-secreting, Foxp3+ Treg cells which no longer produce IL-17 [30]. These CD4+ Th17 Tregs appear to suppress inflammation by direct contact with pro-inflammatory cells. The immunosuppressive ability of conventional Tregs, however, appears to be reduced in sarcoidosis patients [2].

Inflammation and Fibrosis Less than 20% of sarcoidosis patients develop fibrosis which strongly associates with non-resolving pulmonary granulomatous inflammation (reviewed in [4, 28]). More research is needed to improve our understanding of how fibrosis can begin in a sarcoidosis pulmonary milieu characterized by elevated IFN-γ which is known to inhibit collagen expression [28]. Recent studies in human patients (including sarcoidosis) and murine models have cited evidence that expression of the programmed cell death-1 (PD-1) marker on CD4+ T cells promotes pulmonary fibrosis via STAT3-mediated secretion of IL-17A and TGFβ1 [68]. PD-1, a marker of cell exhaustion, is frequently displayed by chronically activated T effector cells and has been noted in patients with chronic sarcoidosis (reviewed in [69]). Blockade of PD-1 has been shown to restore CD4+ T cell proliferative function in sarcoidosis patients [70] and to significantly reduce fibrosis in murine models [68]. Currently, there are no clinically validated biomarkers for identifying sarcoidosis patients at risk of pulmonary fibrosis.

Summary Sarcoidosis remains a heterogeneous disease of unknown cause(s). The pathophysiology of sarcoidosis granuloma formation begins when alveolar macrophages contact inhaled particulate matter that is antigenic and capable of initiating immune activation of macrophages, dendritic cells, and lymphocytes. Initial studies in sarcoidosis focused on Th1-polarized lymphocytes, but current studies have shown the vigorous presence of Th17.1 phenotypic lymphocytes in granuloma stimulation and formation [62]. Moreover, several forms of innate immune mechanisms have also been found to participate in pulmonary inflammatory changes [14]. Both lymphocytes and alveolar macrophages generate numerous inflammatory signals (chemokines, cytokines, enzymes) that organize macrophages into giant cells and granuloma structures. Many of these products can be detected in sera and provide clinically relevant data with respect to sarcoidosis disease status [36, 40]. Figure 3.1 summarizes our current understanding of mechanisms of granuloma formation in sarcoidosis. In most patients, granulomas spontaneously resolve, but questions remain regarding markers and pathways leading to fibrosis in sarcoidosis.

New Directions The interplay between macrophages and lymphocytes in granuloma formation and resolution has not been fully defined. In the last decade, advances in flow cytometry, lineage tracing systems, and single-cell transcriptomics are making it possible to define the spectrum of macrophages phenotypes in different microdomains within healthy and diseased tissue [44, 71]. Questions regarding the role of resident macrophages and monocyte-derived macrophages have not been addressed in sarcoidosis, and application of these newer techniques may provide insight into factors which drive progressive versus resolving disease. Furthermore, the varied complexity and plasticity of T effector cells currently reported in sarcoidosis have

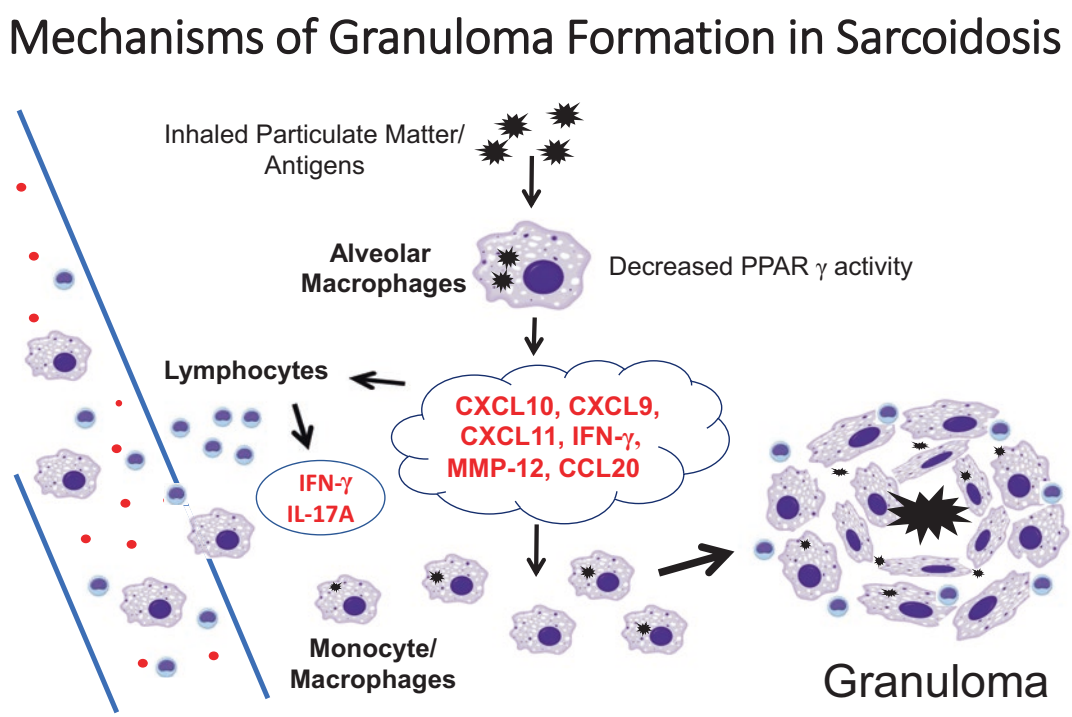

Fig. 3.1 The pathophysiology of sarcoidosis granuloma formation begins when alveolar macrophages contact inhaled particulate matter that is antigenic and capable of initiating immune activation of macrophages, dendritic cells, and lymphocytes. Lymphocytes and macrophages generate products (chemokines CXCL9, CSCL10, CSCL11, CCL20; cytokines IFN-γ, IL-17A; enzyme MMP12) that organize macrophages into giant cells and granuloma structures

opened additional questions regarding pathways of sarcoid disease progression or remission. The roles of Th1 and Th17 regulatory cells in sarcoidosis are unclear because of some confusing findings such as elevated Th17.1 in the self-limiting Lofgren's syndrome compared to non-Lofgren's patients (reviewed in [30]). It has been suggested that initial findings at diagnosis may provide clues to later sarcoidosis outcomes, and therefore, careful monitoring of patients is required in larger long-term studies. Unfortunately, current knowledge of cellular immune pathways in sarcoidosis is not yet sufficient to allow prediction of final sarcoid disease status from findings obtained at diagnosis (reviewed in [69]). Application of newer analytical technologies is needed to improve our understanding of mechanisms in disease progression or remission and, possibly, to provide better clinical treatment for sarcoidosis patients [72, 73].

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Innate Immune Responses and Pulmonary Diseases

4

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Abstract

Innate immunity is the first defense line of the host against various infectious pathogens, environmental insults, and other stimuli causing cell damages. Upon stimulation, pattern recognition receptors (PRRs) act as sensors to activate innate immune responses, containing NF-κB signaling, IFN response, and inflammasome activation. Toll-like receptors (TLRs), retinoic acid-inducible gene I-like receptors (RLRs), NOD-like receptors (NLRs), and other nucleic acid sensors are involved in innate immune responses. The activation of innate immune responses can facilitate the host to eliminate pathogens and maintain tissue homeostasis. However, the activity of innate immune responses needs to be tightly controlled to ensure the optimal intensity and duration of activation under various contexts. Uncontrolled innate immune responses can lead to various disorders associated with aberrant inflammatory response, including pulmonary diseases such as COPD, asthma, and COVID-19. In this chapter, we will have a broad overview of how innate immune responses function and the regulation and activation of innate immune response at molecular levels as well as their contribution to various pulmonary diseases. A better understanding of such association between innate immune responses and pulmonary diseases may provide potential therapeutic strategies.

Keywords

Pattern recognition receptors · NF-κB signaling · IFN response · Inflammasome · Pulmonary diseases

Abbreviations

AHR	Airway hyperresponsiveness
AIM2	Absent in melanoma 2
ALS	Amyotrophic lateral sclerosis
AnkRs	Ankyrin repeats
ASC	Apoptosis-associated speck-like protein containing a caspase recruitment domain or CARD
ATP	Adenosine triphosphate
BAF1	Barrier-to-autointegration factor 1
BAK	BCL2 antagonist/killer
BAX	BCL2-associated X
BHR	Bronchial hyperreactivity
C/EBPε	CCAAT enhancer-binding protein epsilon

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CCDC50	Coiled-coil domain-containing protein 50
cGAMP	Cyclic GMP-AMP
cGAS	Cyclic GMP-AMP synthase
CHIKV	Chikungunya virus
COPD	Chronic obstructive pulmonary disease
COVID-19	Coronavirus disease 2019
CS	Cigarette smoke
CYLD	CYLD lysine 63 deubiquitinase
DAMPs	Danger-associated molecular patterns
DDX3	DEAD (Asp-Glu-Ala-Asp)-box helicase 3
DHX15	DEAH-box helicase 15
DHX9	DExH-box helicase 9
DRAIC	Downregulated RNA in cancer, inhibitor of cell invasion and migration
eATP	Extracellular ATP
FEV1	Forced expiratory volume in 1 s
FSTL-1	Follistatin-like 1
FVC	Forced vital capacity
HCV	Hepatitis C virus
HDAC6	Histone deacetylase 6
HIV	Human immunodeficiency virus
HOPS	Hepatocyte odd protein shuttling
IFI16	Interferon-γ (IFNγ)-inducible protein 16
IFN	Interferon
IFNAR	IFN-I receptor
IFN-α	Type I interferon-alpha
IFN-β	Type I interferon-beta
IKK	IκB kinase
IL-1	Interleukin-1
IPF	Idiopathic pulmonary fibrosis
IRAKs	IL-1R-associated kinases
IRF9	IFN-regulatory factor 9
ISGF3	IFN-stimulated gene factor 3
ISGs	IFN-stimulated genes
ISREs	IFN-stimulated response elements
IκB	Inhibitor of κB
JAK1	Tyrosine kinases Janus kinase 1
JNK	Jun N-terminal kinase
LDH	Lactate dehydrogenase
LF	Lethal factor
LGP2	Laboratory of genetics and physiology 2
LPS	Lipopolysaccharide
m(6)A	N(6)-Methyladenosine
MAD5	Melanoma differentiation-associated factor 5
MAVS	Mitochondrial antiviral signaling protein
Miz1	c-Myc-interacting zinc finger protein-1
MSU	Monosodium urate
mtDNA	Mitochondrial DNA
mtROS	Mitochondrial reactive oxygen species
MyD88	Myeloid differentiation primary response 88
MYSM1	Myb-like, SWIRM, and MPN domains 1
NADPH	Nicotinamide adenine dinucleotide phosphate hydrogen
NAIPs	NLR family, apoptosis inhibitory proteins
NF-κB	Nuclear factor-κB
NLRs	NOD-like receptors
NLS	Nuclear localization sequence
NOD	Nucleotide oligomerization domain
NSP6	Nonstructural protein 6
OGT	O-GlcNAc transferase
ORF6	Open reading frame 6
OTUB1	OTU deubiquitinase, ubiquitin aldehyde binding 1
PAH	Pulmonary arterial hypertension
PAMPs	Pathogen-associated molecular patterns
PBMCs	Peripheral blood mononuclear cells
PRRs	Pattern recognition receptors
RA	Rheumatoid arthritis
RHD	Rel homology domain
RIG-I	Retinoic acid-inducible gene I
RKIP	Raf kinase inhibitor protein
RLRs	Retinoic acid-inducible gene I (RIG-I)-like receptors
ROS	Reactive oxygen species
rRNA	Ribosomal RNA
SARS-CoV-2	Severe acute respiratory syndrome coronavirus 2

SPOP	Speckle-type POZ protein
STAT	Signal transducer and activator of transcription
STING	Stimulator of interferon genes
TBK1	TANK-binding kinase 1
TIRAP	TIR domain-containing adaptor protein
TLRs	Toll-like receptors
TRAF6	Tumor necrosis factor receptor-associated factor 6
TRIF	Toll/IL-1R domain-containing adaptor-inducing IFN-β
TRIKAs	TRAF6-regulated IKK activators
TRIM14	Tripartite-motif containing 14
TYK2	Tyrosine kinase 2
USP18	Ubiquitin-specific peptidase 18
USP19	Ubiquitin-specific protease 19
VEEV	Venezuelan equine encephalitis virus
WNV	West Nile virus
YFV	Yellow fever virus
YY1	Yin Yang 1
ZBP1	Z-DNA-binding protein 1
ZCCHC3	Zinc finger CCHC-type containing 3
ZNFX1	Zinc finger NFX1-type containing 1

4.1 Introduction

The innate immune system is crucial for the host to provide a protective response to infection or tissue injury. It utilizes distinct pattern recognition receptors (PRRs) to mediate diverse sets of pathogen-associated molecular pattern (PAMP) or danger-associated molecular pattern (DAMP) recognition, leading to infection removal and maintenance of tissue homeostasis. PRRs can be categorized based on their subcellular location, including Toll-like receptors (TLRs), retinoic acid-inducible gene I (RIG-I)-like receptors (RLRs), NOD-like receptors (NLRs), and several nucleic acid sensors that detect viral DNA or RNA. Upon stimuli recognition, PRRs activate a series of intracellular signaling molecules to initiate signal transduction pathways, including the nuclear factor-κB (NF-κB) signaling, interferon (IFN) response, and inflammasome activation.

4.2 TLRs

TLRs are the earliest discovered and the best characterized PRRs. Ten TLRs (TLR1–10) had been identified for recognizing distinct PAMPs and DAMPs in humans. TLR2 forms heterodimers with TLR1 or TLR6, sensing bacterial lipoproteins and lipopeptides [1]. TLR3, TLR7, TLR8, and TLR9 recognize viral RNA and DNA in the endosome [2, 3]. TLR4 functions as a lipopolysaccharide (LPS) sensor. TLR5 specifically detects flagellins and type IV secretion system components in various bacterial pathogens, including *Salmonella*, *Vibrio*, and *Helicobacter pylori* [4]. TLR7 recognizes the GUrich miR-Let7b, secreted from rheumatoid arthritis (RA) synovial fluid macrophages, resulting in synovitis [5]. Conversely, TLR10, the unique anti-inflammatory TLR, promotes HIV-1 infection and exerts anti-inflammatory effects [6, 7]. The mouse genome encodes 13 TLRs, although humans do not harbor the gene to encode functional TLR11, TLR12, and TLR13 [8]. TLR11 and TLR12 working as heterodimers directly bind to the profilin-like molecule from the protozoan parasite *Toxoplasma gondii* [9]. TLR13 recognizes a conserved 23S ribosomal RNA (rRNA) sequence, which is crucial for binding macrolide, lincosamide, and streptogramin group antibiotics in bacteria [10].

4.3 RLRs

RLRs are a family of RNA helicases and are described as cytoplasmic sensors responsible for viral RNA sensing. Three RLRs have been well defined including retinoic acid-inducible gene I (RIG-I), melanoma differentiation-associated factor 5 (MAD5), and laboratory of genetics and physiology 2 (LGP2). RIG-I recognizes short cytosol viral RNA derived from various virus species including influenza virus, hantavirus,

reovirus, hepatitis, and rhinovirus [11, 12]. In comparison with RIG-I, MDA5 recognizes long strands of viral dsRNA following coronavirus, picornavirus, or influenza A virus infection [13, 14]. Negative regulator for this step includes LGP2, a homolog of RIG-I and MDA5, competing with RIG-I and MDA5 to interact with viral RNA, thereby inhibiting downstream signaling activation [15].

4.4 NLRs

The NLRs represent the largest and most diverse family. It is a group of evolutionarily conserved intracellular proteins that are responsible for the host against DAMPs or PAMPs. It harbors an N-terminal effector domain, a NOD domain that mediates ATP-dependent self-oligomerization, and a C-terminal LRR domain responsible for ligand recognition [16]. According to the characteristics of N-terminus, NLRs could be divided into two subgroups: the PYD domain-containing NLRP group and the CARD-containing NLRC group [17]. Most of the NLRPs, including NLRP1, NLRP2, NLRP3, NLRP6, NLRP7, and NLRP9, assemble inflammasome. NLRP1 is the first described receptor for inflammasome activation. It recognizes the stimulation of lethal factor (LF) protease secreted by *Bacillus anthracis* and is activated via proteasome-mediated degradation [18]. NLRP2 associates with the P2X7 receptor and the pannexin 1 channel to sense adenosine triphosphate (ATP) [19]. NLRP3 is activated by various stimuli, including monosodium urate (MSU), silica, asbestos, amyloid-β, alum, ATP, apolipoprotein E, nigericin, and viral RNA [12, 20–24]. NLRP6 and NLRP7 promote host defense against bacterial by detecting lipoteichoic acid and microbial acylated lipopeptides, respectively [25, 26]. NLRP9 recognizes short dsRNA from *Rotavirus* by concerting with the RNA sensor DExH-box helicase 9 (DHX9) [27]. Besides, some other NLRPs are involved in the inflammasome-independent pathway. NLRP4 inhibits double-stranded RNA or DNA-mediated type I interferon [28]. NLRP10 has significant effects on helper T-cell-driven immune responses in response to adjuvants, including lipopolysaccharide, aluminum hydroxide, and complete Freund's adjuvant [29]. NLRP11 impairs LPS-induced NF-κB activation [30]. NLRP14 promotes fertilization by blockading cytosolic nucleic acid sensing [31]. NLRCs are involved in immune responses, and they consist of six members: nucleotide oligomerization domain 1 (NOD1), NOD2, NLRC3, NLRC4, NLRC5, and NLRX1 [32]. NOD1 and NOD2 recognize peptidoglycan (PGN) fragment produced by bacteria [33]. NLRC3 binds viral DNA and other nucleic acids through its LRR domain and licenses immune responses [34]. NLRC4 is an important gatekeeper against gram-negative bacteria including *Legionella pneumophila*, *Salmonella enterica* serovar *Typhimurium* (*Salmonella*), and *Shigella flexneri* [20, 35]. NLRC5 impairs gastric inflammation and mucosal lymphoid formation in response to *Helicobacter* infection [36]. Moreover, crystal analysis of the NLRX1 C-terminal fragment indicates a role for NLRX1 in intracellular viral RNA sensing in antiviral immunity [37].

4.5 Other Nucleic Acid Sensors

Notably, several other nucleic acid sensors have been identified recently. cGAS (cyclic GMP-AMP synthase) is known to be the most important DNA sensor that generates the second messenger cyclic GMP-AMP (cGAMP) for downstream cascade activation [38, 39]. Absent in melanoma 2 (AIM2) as well as interferon-γ (IFNγ)-inducible protein 16 (IFI16) are reported to recognize intracellular DNA. Additionally, Z-DNA-binding protein 1 (ZBP1; also known as DAI or DLM-1), DEAD (Asp-Glu-Ala-Asp)-box helicase 3 (DDX3), and zinc finger NFX1-type containing 1 (ZNFX1) are involved in RNA sensing and promoting innate immune responses [40–42]. These intracellular nucleic acid sensors are widely or ubiquitously expressed in almost all cell types and responsible for viral pathogen detection as well as endogenous nucleic acid recognition.

4.6 NF-κB Signaling

NF-κB is a collective name for a transcription factor family which consists of five different DNA-binding proteins (RelA, RelB, c-Rel, p105/p50, and p100/p52) [43]. Those five family members all contain an N-terminal Rel homology domain (RHD) responsible for dimerization and cognate DNA element binding [44]. Three of them (RelA, RelB, c-Rel) are synthesized as mature proteins and harbor C-terminal transactivation domains, which are essential for transcriptional activation [45]. The other two members (p105/p50 and p100/p52) are synthesized as large precursors (p105 and p100) and partially proteolyzed by the proteasome to yield active forms (p50 and p52) for DNA binding [46, 47]. The NF-κB family members can assemble into several homodimeric and heterodimeric dimers, and two paradigmatic dimers are p50:p65 and p52:RelB [48]. Different NF-κB dimers regulate various gene expressions, which are critical for immune responses, cell proliferation, migration, and apoptosis [49].

The activation of NF-κB dimers has sophisticated controls at multiple levels. In unstimulated cells, NF-κBs are inactive and retained in the cytoplasm by the binding of its specific inhibitors called "inhibitor of κB" (IκB) family [48]. The IκB proteins contain 5–7 tandem ankyrin repeats (AnkRs) that bind to the RHD of NF-κB, thus covering its nuclear localization sequence (NLS) [48]. Upon stimulation, IκB kinase (IKK) complex, including catalytic (IKKα and IKKβ) and regulatory (NEMO, also called IKKγ) subunits, was activated. The activated IKK complex catalyzes the phosphorylation and polyubiquitination of IκB family members, leading to degradation of IκB family members via proteasome and subsequent nuclear translocation of NF-κB family members [50]. Tumor necrosis factor receptor-associated factor 6 (TRAF6), a RING domain E3 ligase, together with two TRAF6-regulated IKK activators (TRIKAs) were identified as responsible for the IKK complex activation [51]. TRIKA1 is an E2 enzyme complex containing Ubc13 and Uev1A (or the functionally equivalent Mms2). Together with TRAF6, it mediates the K63-linked ubiquitination of NEMO and TRAF6 itself. TRIKA2 is a trimeric complex composed of the protein kinase TAK1 and two other proteins as TAB1 and TAB2 [52, 53]. TAK1 is a direct kinase in TRIKA2 to phosphorylate and activate IKK in a manner that depends on TRAF6 and Ubc13-Uev1A [51]. Of note, TAK1 also activates the Jun N-terminal kinase (JNK)-p38 kinase pathway by mediating MKK6 phosphorylation [51]. Additionally, the E3 ubiquitin-ligase TRAF2 (and/or TRAF5) and the kinase RIP1 are also reported to mediate the recruitment of the TRIKA2, contributing to the downstream cascade activation [54]. Adaptors, such as myeloid differentiation primary response 88 (MyD88), TIR domain-containing adaptor protein (TIRAP), and Toll/IL-1R domain-containing adaptor-inducing IFN-β (TRIF), are reported to engage and activate TRAFs by cytoplasmic intermediate IL-1R-associated kinases (IRAKs), such as the kinase IRAK1, IRAK2, and IRAK4 [55]. Importantly, IRAK4 acts upstream of IRAK1, and the kinase activity of IRAK4 might be required for IRAK1's modification [56]. Thus, upon stimulation, PRRs (TLR1, 2, 3, 4, 6, 7, 9) mediate PAMP or DAMP recognition and subsequently recruit adaptors for TRAF and TRIKA recruitment, leading to IKK complex activation, IκB degradation, and release of NF-κB for transcription. Those stimulations include viral and bacterial infections, necrotic cell products, DNA damage, oxidative stress, and pro-inflammatory cytokines (Fig. 4.1) [57].

The regulation of NF-κB signaling has been extensively studied. Additional regulators of NF-κB signaling include OTU deubiquitinase, ubiquitin aldehyde binding 1 (OTUB1), CYLD lysine 63 deubiquitinase (CYLD), and A20 that modulates the ubiquitination of various components [58–62]. Furthermore, phosphorylation, acetylation, methylation, and palmitoylation have also been reported to fine-tune the activity of the NF-κB signaling through multiple post-translational modifications on signal proteins. Besides, Speckle-type POZ protein (SPOP) is recruited to MyD88 to inhibit the aggregation of MyD88 and recruitment of the downstream signaling kinases IRAK4, IRAK1, and IRAK2 [63]. S100A10 interacts with TLR4 and inhibits its association with adaptor proteins including

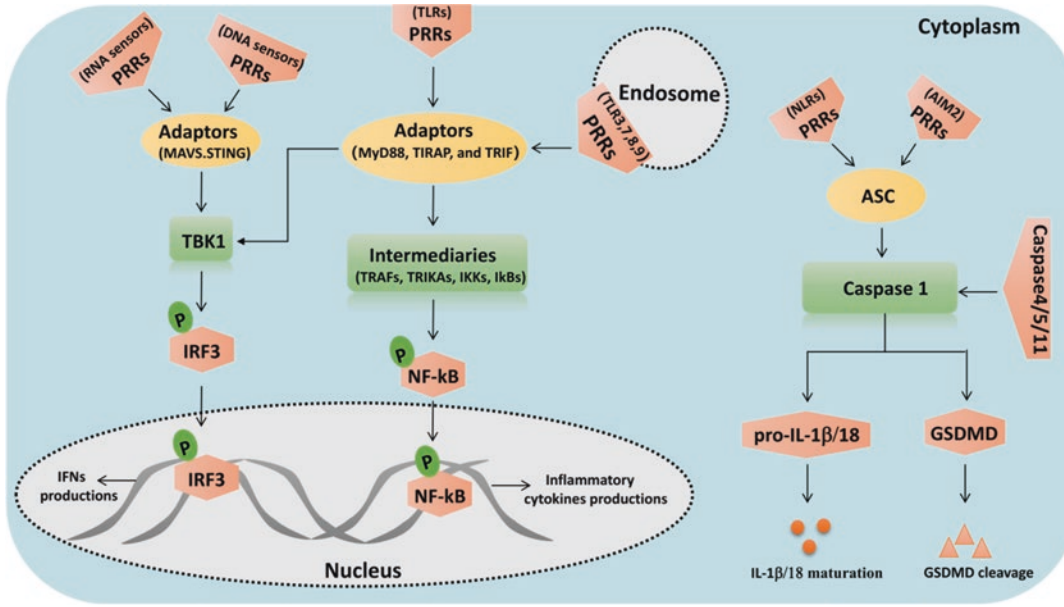

Fig. 4.1 Activation of innate immune responses. In response to distinct stimulation, different PRRs recruit various adaptors for downstream signaling cascades. In detail, cytosolic RNA or DNA sensors recruit MAVS or STING for TBK1 activation, respectively. Activated TBK1 mediates IRF3 phosphorylation, and the phosphorylated IRF3 translocates from the cytoplasm to the nucleus, promoting IFN production. TLRs on plasma or endosome membrane associate with distinct adaptors including MyD88, TIRAP, and TRIF, triggering intermediate activation and subsequent NF-κB phosphorylation. Phosphorylated NF-κBs enter into the nucleus, inducing inflammatory cytokine production. NLRs and AIM2 bind to ASC and enhance the caspase-1 activity for cleaving pro-IL-1β and pro-IL-18, leading to IL-1β/18 maturation. On the other hand, activated caspase-1 mediates the cleavage of GSDMD, and the N-terminal of GSDMD mediates membrane pore formation and pyroptosis. Also, caspase 4/5/11 directly recognize LPS and bind to caspase-1 for downstream signaling activation

MyD88 and TRIF [64]. Downregulated RNA in cancer, inhibitor of cell invasion and migration (DRAIC) impairs IKK complex assembly and inhibits the phosphorylation of IκBα and the activity of NF-κB [65]. Lamtor5 and hepatocyte odd protein shuttling (HOPS) control TRAF6 and TLR4 stability for regulating NF-κB signaling, respectively [66, 67]. A well-controlled NF-κB signaling is crucial for the maintenance of tissue homeostasis, and the dysfunction of NF-κB signaling leads to many pathological conditions such as combined immunodeficiency, type 2 diabetes, and pulmonary diseases [43, 68–70].

4.7 IFN Response

Type I interferons have long been characterized as key players in antiviral responses, inhibiting viral replication and spread by sensing PAMPs, including viral DNA and RNA [71]. Upon virus infection, PRRs promote type I interferon expression, triggering pro-inflammatory cytokine and chemokine production, as well as the expression of innate immune genes to establish an intracellular antiviral state [72]. Fourteen subtypes of type I alpha IFNs (IFN-α) in mice and thirteen in humans, and one beta (IFN-β) IFNs are engaged in that signal through the same IFN-I receptor (IFNAR) [73]. IFNAR, which is composed of IFNAR1 and IFNAR2 subunits, employs the receptor-associated protein tyrosine kinases Janus kinase 1 (JAK1) and tyrosine kinase 2 (TYK2) to phosphorylate cytoplasmic transcription factors signal transducer and activator of transcription 1 (STAT1) and STAT2. Subsequently, phosphorylated STAT1 and STAT2 assemble heterodimers and translocate to the nucleus, together with IFN-regulatory factor 9 (IRF9), to form a transcrip-

tionally active IFN-stimulated gene factor 3 (ISGF3) for directly activating the transcription of IFN-stimulated genes (ISGs) through binding IFN-stimulated response elements (ISREs; consensus sequence TTTCNNTTTC) [74, 75]. Several discovery-based screens demonstrate hundreds of ISGs for their ability to inhibit the replication of several important viruses including influenza A H1N1 virus, hepatitis C virus (HCV), yellow fever virus (YFV), West Nile virus (WNV), chikungunya virus (CHIKV), Venezuelan equine encephalitis virus (VEEV), and HIV-1 [76, 77].

Many types of PRRs can promote IFN-I production. These receptors mediate recognition of foreign and self-nucleic acids as well as a limited number of other non-nucleic acid PAMPs and recruit distinct adaptors for downstream TANK-binding kinase 1 (TBK1) phosphorylation. For example, RNA sensors including MDA5, RIG-I, and zinc finger NFX1-type containing 1 (ZNFX1) recruit mitochondrial antiviral signaling protein (MAVS) to activate and propagate antiviral response [42, 78–80]. Then, MAVS protein forms fibrils and behaves like prions to convert endogenous MAVS into functional aggregates to promote downstream signaling cascade [81]. Likely, DNA sensors including cyclic GMP-AMP synthase (cGAS) and IFI16 recruit stimulator of interferon genes (STING) for antiviral response. STING is an endoplasmic reticulum membrane protein. The cytoplasmic domain of STING undergoes a 180° rotation and unwinds around the crossover point between the proteins to form oligomers [82]. Oligomerized STING adopts a β-strand-like conformation and inserts into a groove between the kinase domain of one TBK1 through a conserved PLPLRT/SD motif within the C-terminal tail of STING [83, 84]. Activated TBK1 directly targets IRF3 for its phosphorylation and the phosphorylated IRF3 translocated from the cytosol to the nucleus for IFN production and subsequent ISG expression for the antiviral response [85]. Of note, MAVS and STING not only activate TBK1 but also recruit IRF3 to bind TBK1 to activate the IRF3 pathway [86]. In addition to MAVS and STING, TLR3 and TLR4 signaling activate TBK1 and IRF3 through the adaptor protein TRIF (Fig. 4.1) [87].

The dysfunction of IFNs results in multiple diseases. For example, activated variants in STING lead to a rare auto-inflammatory disease named STING-associated vasculopathy with onset in infancy via preventing the development of lymph nodes and Peyer's patches [88, 89]. Dysfunction of TDP-43- or C9orf72-induced STING activation causes amyotrophic lateral sclerosis (ALS) [90, 91]. Aberrant mitochondrial DNA (mtDNA)-induced cGAS-STING activation promotes lupus-like disease, acute kidney injury, renal Inflammation, and fibrosis [92–94]. Thus, the activation of the IFN response should be precisely controlled. Various regulators have been reported to modulate IFN signaling through distinct mechanisms. Myb-like, SWIRM, and MPN domains 1 (MYSM1), coiled-coil domain-containing protein 50 (CCDC50), USP15, MARCH8, OTUB1, and OTUB5 regulate IFN response through ubiquitination [95–100]. O-GlcNAc transferase (OGT), histone deacetylase 6 (HDAC6), and palmitoyltransferases modulate IFN production through O-GlcNAcylation, deacetylation, and palmitoylation, respectively [101–103]. N(6)-Methyladenosine (m(6)A) modification controls IFN response by dictating the fast turnover of IFNα and IFNβ mRNA [94]. G3BP1 and barrier-to-autointegration factor 1 (BAF) interfere DNA binding of cGAS for IFN regulation [104, 105]. Furthermore, zinc finger CCHC-type containing 3 (ZCCHC3) and DEAH-box helicase 15 (DHX15) are shown to facilitate RLR-mediated RNA recognition [106, 107].

4.8 Inflammasome Activation

Inflammasome is a molecular platform that mediates the processing of caspases, maturation, and secretion of interleukin-1 (IL-1) family members, and activation of inflammatory cell death called pyroptosis [20, 108]. It can be categorized into apoptosis-associated speck-like protein containing a caspase recruitment domain or CARD (ASC)-dependent or CARD (ASC)-independent

inflammasome activation. Upon stimulation, NLRP3 and absent in melanoma 2 (AIM2) interact with ASC for inflammasome assembly. However, NLRC4 and NLRP1 could directly activate caspase-1 for downstream cascade activation without binding to ASC. Of note, ASC binding for NLRC4 or NLRP1 could enhance its inflammasome activity, although it is dispensable for NLRC4 or NLRP1 inflammasome activation [20]. Caspase-4/5/11 are directly activated by LPS sensing and cleave GSDMD for pyroptosis independent of ASC [109]. Intriguingly, those inflammatory caspases also target NLRP3-dependent caspase-1 activation in an ASC-dependent manner [110].

NLRP1, NLRC4, AIM2, and NLRP3 inflammasomes are most widely reported. Over the past decade, numerous mechanisms have been demonstrated in those inflammasome activations. During the *Bacillus anthracis* infection, bacterial secreted lethal factor (LF) protease was reported to mediate the degradation of amino-terminal domains of NLRP1B, leading to the release of a carboxyl-terminal fragment and subsequently caspase-1 activation [18, 111]. NLRC4 is responsible for bacterial detection. However, it is not the direct sensor for its activator. NAIP (NLR family, apoptosis inhibitory protein)-mediated ligand recognition is required for NLRC4 inflammasome activation. During bacterial infection, mouse NAIP1 and NAIP2 act as cytosolic innate immune sensors for bacterial T3SS needle and rod protein recognition, respectively [112]. In comparison to NAIP1 and NAIP2, NAIP5 and NAIP6 bind to the bacterial protein flagellin for NLRC4 inflammasome activation [113, 114]. AIM2 is a direct sensor, binding double-stranded DNA and utilizes ASC to form a caspase-1-activating inflammasome. The HIN domain of AIM2 is responsible for recognizing sugar-phosphate backbone of various double-stranded DNA, including bacterial DNA, viral DNA, and radiation-induced damaged DNA [115, 116]. NLRP3 inflammasome is the most extensively characterized inflammasome. The activation of NLRP3 inflammasome involves sophisticated regulations. NF-κB signaling activation acts as the first step to mediate the priming process, including induction of both NLRP3 and pro-IL-1β. Subsequently, NLRP3 is activated. Three working models of NLRP3 activation have been proposed: (1) lysosomal rupture and release of the proteinase cathepsin B caused by crystal phagocytosis result in NLRP3 activation [117]; (2) mitochondrial reactive oxygen species (mtROS)-induced oxidized mtDNA conversion leads to NLRP3 activation [118]; and (3) ATP triggered the efflux of K+ contributing to NLRP3 activation [119]. Nonetheless, more details about NLRP3 activation need further investigation (Fig. 4.1).

Emerging evidence shows that sustained and uncontrolled inflammasome activation contributes to the development of many diseases, such as lung injury, vitiligo, very-early-onset inflammatory bowel disease, neutrophilic chronic rhinosinusitis with nasal polyps, adipose tissue inflammation, and auto-inflammatory diseases [12, 120–123]. Many regulators have been reported to regulate inflammasome activation through distinct mechanisms. Raf kinase inhibitor protein (RKIP) and synthetic vitamins K3 and K4 block inflammasome activation through interrupting inflammasome assembly [124, 125]. CCAAT enhancer-binding protein epsilon (C/EBPε), IRF4, and IRF8 modulate transcription level of inflammasome-associated genes for inflammasome regulation [126, 127]. Nicotinamide adenine dinucleotide phosphate hydrogen (NADPH) and ubiquitin-specific protease 19 (USP19) regulate inflammasome activation by reactive oxygen species (ROS) [128, 129]. Besides, various post-translational modifications were implicated in inflammasome regulation, including ubiquitination, phosphorylation, S-nitrosylation, prenylation, deglutathionylation, and ADP-ribosylation. Notably, several drugs have been developed for therapy via targeting to inflammasome activation, such as rasagiline, ticagrelor, kaempferol, and metformin [130–133]. Therefore, targeting inflammasome activation by the deployment of those drugs will shed light on inflammasome-related disease therapy.

4.9 Pulmonary Diseases

4.9.1 Role of Innate Immune Responses in COPD

NF-κB signaling and COPD Chronic obstructive pulmonary disease (COPD), a common chronic inflammatory disease of the airways, the alveoli, and the microvasculature, affects millions of people worldwide. The diagnosis of COPD is based on the reduced ratio of the post-bronchodilator forced expiratory volume in 1 s to the forced vital capacity (FEV1:FVC ratio) (<0.7) [134]. It is characterized by three pathological phenotypes including small airway obstruction due to remodeling, emphysema, and chronic bronchitis [134]. Cigarette smoking and indoor or outdoor air pollution are the most important risk factors and causes for COPD [135]. Emerging evidence indicates that innate immune responses are involved in COPD pathogenesis. The severity of COPD is reported to associate with an increased epithelial expression of NF-κB by analyzing bronchial biopsies from smokers with COPD, smokers with normal lung function, and nonsmokers with normal lung function [136]. Further analysis identified that IκB-α levels in lung tissue were significantly reduced and IKK complex activity in peripheral blood mononuclear cells (PBMCs) is dramatically enhanced in patients with COPD than in control subjects [137, 138]. Consistently, in the mouse model, cigarette smoke (CS) exposure regulates RelB by IKKa in B-lymphocytes, leading to inflammatory cytokine release [139]. Of note, loss of function of Miz1 (also known as c-Myc-interacting zinc finger protein-1 and Zbtb17) in the murine lung epithelium spontaneously develops a COPD-like phenotype via inducing sustained NF-κB signaling activation [70]. In addition, follistatin-like 1 (FSTL-1) hypomorphic mice develop spontaneous emphysema by promoting NF-κB p65 phosphorylation in a Nr4a1-dependent manner [140].

Inflammasome and COPD Except for NF-κB signaling, inflammasome activation also contributes to the onset of COPD pathogenesis. The expression levels of IL-1β and IL-18, two hallmarks of inflammasome activation, are increased in COPD patients [141, 142]. Moreover, overexpression of IL-1β or IL-18 in the lungs of mice present chronic inflammatory changes similar to COPD, and lacking IL-1R or IL-18R in mice are protected against CS-induced lung inflammation [143, 144]. Likely, elevated caspase-1 activity is also observed in the lungs from both COPD patients and the CS-treated mice model [145]. Strikingly, in the mice model, acute smoke-mediated lung inflammation is blocked by z-VAD-fmk, a pan-caspase inhibitor, or z-WEHD-fmk, a caspase-1 inhibitor [146]. Notably, high levels of two inflammasome stimulators, extracellular ATP (eATP) and ROS, are observed in patients with COPD as well as in the genetic mouse models of COPD, indicating possible inflammasome activation in COPD pathogenesis [147, 148].

IFN response and COPD The role of IFN response in COPD pathogenesis needs more investigation. Deficient IFN-β expression in the lungs and reduced sputum expression of ISGs were detected in COPD patients [149, 150]. However, acute CS exposure leads to cGAS-STING-dependent IFN response by releasing self-DNA in mice model [151]. Thus, whether CS exposure induces COPD phenotype is IFN dependent or not needs to be further explored.

4.9.2 Role of Innate Immune Responses in Asthma

NF-κB signaling and asthma Asthma, one of the major chronic non-communicable diseases, affects as many as 334 million people in the world [152]. It is defined by mucus overproduction, bronchial hyperreactivity (BHR), airway wall remodeling, and airway narrowing [153]. The symptoms of asthma include repeated periods of shortness of breath, cough, wheezing, and chest tightness [154]. Genetic susceptibility and environmental exposures as well as aberrant

immune responses contribute to the onset of disease [155]. Recent studies implicated NF-κB signaling activation as a key modulator in asthma pathogenesis. Increased activation of NF-κB was observed in asthma patients [156]. Furthermore, NF-κB activation in airway epithelial is sufficient to promote allergic sensitization to an inhaled antigen [157]. In contrast, repressed NF-κB signaling activation in airway epithelial impaired inflammation, led to decreased levels of chemokines and cytokines and circulating IgE, and ameliorated mucus cell metaplasia [158]. Notably, inhibition of NF-κB by a chimeric decoy oligodeoxynucleotide transfer prevents asthma exacerbation in a mouse model [159]. Besides, ex vivo farm dust or LPS stimulation restored anti-inflammatory TNFAIP3 gene and protein levels in asthmatic patients and shifted NF-κB signaling-associated gene expression toward an anti-inflammatory state [160]. Thus, targeting NF-κB signaling may provide a novel therapeutic approach to asthma.

Inflammasome and asthma Emerging evidence showed that inflammasome activation plays a crucial role in asthma pathogenesis. In neutrophilic asthma patients, the protein level of IL-1β was significantly higher, and sputum IL-1β protein level was associated with NLRP1, NLRP3, and NLRC4 expression [161]. Similar results with increased inflammasome components including Nlrp3, Nlrc4, caspase-1, and Il-1β were observed in eosinophilic, mixed, and neutrophilic experimental asthma in mice [162]. Lacking NLRP3 inflammasome activation in mice led to ameliorated allergic airway inflammation, reduced eosinophil infiltration, and dampened Th2 lymphocyte activation in the lung [163, 164]. Strikingly, treatment with an inhibitor of caspase-1 or NLRP3 suppresses airway hyperresponsiveness (AHR) in severe, steroid-resistant asthma [165]. Most importantly, uric acid, protein serum amyloid A, apolipoprotein E, and fatty acid exposure may contribute to inflammasome activation in allergic asthma [24, 166–168].

IFN response and asthma The role of IFN response in asthma pathogenesis is more complicated and warrants more investigation. On the one hand, increased expression of IFN-β, IFN-λ1/IL-29, OAS, and viperin in neutrophilic asthmatics and high IFN-α, IFN-β, and IFN-λ1 were detected in atopic asthmatic [169, 170]. Moreover, elevated ISG expression in epithelial in asthma is related to lung inflammation and FEV1 [171]. On the other hand, reduced IFN-α/β expression level in the bronchial epithelium in asthmatic cells was also reported [172]. Thus, how IFN response activated in asthma patients needs to be further explored.

4.9.3 Role of Innate Immune Responses in COVID-19

IFN response and COVID-19 Coronavirus disease 2019 (COVID-19), an ongoing pandemic of acute respiratory disease, affects millions of people in the world since late 2019. It is caused by a highly transmissible and pathogenic coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). A wide range of clinical features of COVID-19 patients were reported including fever, cough, myalgia or fatigue, sputum production, headache, hemoptysis, and diarrhea [173]. Bilateral diffused alveolar damage, hyaline membrane formation, desquamation of pneumocytes, and fibrin deposits are observed in the lungs of patients with severe COVID-19 via histopathology analyses [174]. Several hypotheses have been proposed for the mechanisms of COVID-19 including imbalanced innate immune responses promoting the pathogenesis of COVID-19 [175], in which aberrant IFN response is the key player driving the progression of COVID-19. Appropriate activation of IFN signaling controls SARS-CoV-2 infection [176]. However, overactivated IFN response amplifies inflammatory signals and induces inflammation in COVID-19 patients [177]. People genetically deficient in IFN response are more vulnerable to SARS-CoV-2 infection [178, 179]. Moreover, the mice model infected with SARS-CoV-2 demonstrates the activation of type I interferon signaling [180].

Thus, early interferon therapy is associated with reduced mortality and accelerated recovery [181, 182]. Of note, a truncated isoform of ACE2, the receptor for SARS-CoV-2, could be induced by interferon response activation [183]. On the other side, SARS-CoV-2 proteins, such as nonstructural protein 6 (nsp6), nsp13, and open reading frame 6 (ORF6), could antagonize cellular IFN response [184].

NF-κB signaling and COVID-19 IL-6, an inflammatory cytokine controlled by the activated NF-κB signaling, is commonly increased in COVID-19 patients [185, 186]. The maximal level of IL-6 and C-reactive protein level, lactate dehydrogenase (LDH) level, ferritin level, d-dimer level, neutrophil count, and neutrophil-to-lymphocyte ratio are highly predictive of the need for mechanical ventilation and mortality in COVID-19 patients [187, 188]. Strikingly, repurposing of anti-IL-6 therapeutics by tocilizumab reduces mortality and/or morbidity in severe COVID-19 from clinical trials [189, 190].

Inflammasome and COVID-19 Activation of the inflammasome was also found in COVID-19 lungs [191]. Fatal COVID-19 cases showed a higher number of ASC inflammasome specks [192, 193]. Thus, innate immune responses may represent a new target for COVID-19 therapy.

4.9.4 Role of Innate Immune Responses in Other Pulmonary Diseases

Dysfunctions of innate immune responses also lead to other pulmonary diseases, such as idiopathic pulmonary fibrosis (IPF) and pulmonary arterial hypertension (PAH). The SNPs in TOLLIP, an important regulator of innate immune responses mediated by the Toll-like receptor, are associated with IPF susceptibility [194]. Yin Yang 1 (YY1), a downstream gene of NF-κB signaling, regulates fibrogenesis by increasing α-SMA and collagen expression [195]. Statin, uric acid, and extracellular ATP enhance lung fibrosis through promoting NLRP3 inflammasome activation [196, 197]. In patients with PAH, serum IFN levels were elevated, and expression of TLR3 in lung tissue is reduced [198, 199]. IFNAR1-deficient mice were protected from PAH [198]. In contrast, Tlr3−/− mice showed a more severe PAH phenotype [199]. Besides, NLRP3 inflammasome activation may contribute to the pathogenesis of PAH, representing a possible target for PAH treatment [200].

4.10 Conclusion

In response to environmental stimulation signals, PRRs, including TLRs, NLRs, RLRs, and other nucleic acid sensors, trigger a variety of signaling pathways for defense to control and eventually eliminate such stimulation. However, aberrant immune responses lead to severe inflammatory diseases especially pulmonary diseases, such as COPD, asthma, COVID-19, IPF, and PAH. Thus, the optimal regulation and fine-tuning of innate immune responses are necessary. Distinct mechanisms have been revealed in immune response regulation. Various post-translational modifications control the intensity, duration, and timing of activated innate immune responses by manipulating protein stability, activity, and subcellular localization. Additional regulators control mRNA levels and stability to regulate innate immune responses. Discoveries of these and additional mechanisms modulating innate immune response will guide and illuminate current and future clinical trials for pulmonary diseases.

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5 Interstitial Lung Disease Associated with Connective Tissue Diseases

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Abstract

Pulmonary manifestations of connective tissue diseases (CTD) carry high morbidity and potential mortality, and the most serious pulmonary type is interstitial lung disease (ILD). Identifying and promptly intervening CTD-ILD with immune suppressor therapy will change the natural course of the disease resulting in survival improvement. Compared to idiopathic pulmonary fibrosis, the most common presentation of idiopathic interstitial pneumonia (IIP), CTD-ILD carries a better prognosis due to the response to immune suppressor therapy. Nonspecific interstitial pneumonia (NSIP) is the most common type of CTD-ILD that is different from the fibrotic classical presentation of IPF, known as usual interstitial pneumonia (UIP). An exception is rheumatoid arthritis that presents more frequently with UIP type. Occasionally, IPF may not have typical radiographic features of UIP, and a full assessment to differentiate IPF from CTD-ILD is necessary, including the intervention of a multidisciplinary team and the histopathology. Interstitial pneumonia with autoimmune features (IPAF) shows promising advantages to identify patients with ILD who have some features of a CTD without a defined autoimmune disease and who may benefit from immune suppressors. A composition of clinical, serological, and morphologic features in patients presenting with ILD will fulfill criteria for IPAF. In summary, the early recognition and treatment of CTD-ILD, differentiation from IPF-UIP, and identification of patients with IPAF fulfill the assessment by the clinician for an optimal care.

Keywords

Interstitial lung disease · Connective tissue disease · Interstitial pneumonia with autoimmune features

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5.1 Introduction

Connective tissue disease (CTD) is a loosely defined term which is now often replaced with "systemic rheumatic diseases," usually referring

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to disturbance in immune tissue resulting in widespread inflammatory tissue injury [1, 2]. Connective tissue diseases frequently target the respiratory system, affecting one or several of the pulmonary compartments, such as the airways, pleura, vasculature, and interstitium. When it comes to the latter, the lung involvement usually carries more morbidity and mortality [3–6]. Interstitial lung disease (ILD) refers to variable degrees of invasion and replacement of normal parenchymal space by inflammatory cell infiltrates and fibrosis or a mixture of both with different degrees. Depending on the magnitude of pulmonary inflammation, ILD may present with respiratory features ranging from asymptomatic to impending respiratory failure or even death. Early identification, classification, and intervention, subsequently, will define the treatment and outcome. Fibrosing lung disease may be associated with environmental exposure but also with other conditions, like sarcoidosis [7], chronic asbestosis and other occupational exposures [8], hobbies, drugs, and secondary to CTD (CTD-ILD) [9]. In the absence of any known possible causes of ILD, then the diagnosis of idiopathic interstitial pneumonia (IIP) is likely [10]. In addition, high-resolution chest tomography (HRCT) is required to narrow the differential diagnosis of type of ILD. Histopathology may be required to assist in confirming the diagnosis [11]. Idiopathic pulmonary fibrosis/usual interstitial pneumonia is a progressive fibrotic lung disease which carries a poor prognosis compared to other ILDs [12–17]. Idiopathic interstitial pneumonias (IIPs) in general have distinct clinical, histological, and radiographic features. Interstitial pulmonary fibrosis is the most common cause for morbidity (Table 5.1) [10].

Many clinical challenges complicate identifying a CTD to be the inflammatory component underlying the ILD process. A thorough and systematic evaluation will achieve the accurate CTD-ILD diagnosis and management [18]. Patients with CTD-ILD, classified as IIP, will have less chances to receive immune-modulating drug therapy, depriving them from all the benefits they could obtain. Conversely, classifying mistakenly a patient with CTD-ILD of a true case of IIP may cause potential harm by exposing the patient with a drug that has no impact on IIP. Moreover, some immune-modulating drugs may cause more deleterious effects on the overall outcomes in patients with IIP [19]. The systematic and comprehensive evaluation of a patient with ILD will define presence of underlying CTDs, for which an integrated approach with contribution of different specialists, pulmonologists, radiologists, pathologists, and rheumatologists is necessary [20]. We will assess the key points for this methodology.

Table 5.1 Revised American Thoracic Society/European Respiratory Society classification of idiopathic interstitial pneumonias: multidisciplinary diagnoses [10]

Major idiopathic interstitial pneumonias
Idiopathic pulmonary fibrosis
Idiopathic nonspecific interstitial pneumonia
Respiratory bronchiolitis-interstitial lung disease
Desquamative interstitial pneumonia
Cryptogenic organizing pneumonia
Acute interstitial pneumonia
Rare idiopathic interstitial pneumonias
Idiopathic lymphoid interstitial pneumonia
Idiopathic pleuroparenchymal fibroelastosis
Unclassifiable idiopathic interstitial pneumonias*

Causes of unclassifiable idiopathic interstitial pneumonia include (1) inadequate clinical, radiological, or pathologic data and (2) major discordance between clinical, radiological, and pathologic findings that may occur in the following situations: (a) previous therapy resulting in substantial alteration of radiological or histological findings (e.g., biopsy of desquamative interstitial pneumonia after steroid therapy, which shows only residual nonspecific interstitial pneumonia; (b) new entity or unusual variant of recognized entity, not adequately characterized by the current American Thoracic Society/European Respiratory Society classification (e.g., variant of organizing pneumonia with supervening fibrosis)[2]; and (c) multiple high-resolution computed tomography and/or pathologic patterns that may be encountered in patients with idiopathic interstitial pneumonia. Information obtained from Travis et al. [10]

5.2 Evaluation of ILD Associated with CTD

Connective tissue diseases encompass a series of heterogeneous autoimmune diseases, each one of them differentiating from one another, based on the specific pathogenic mechanisms and a pleth-

ora of clinical and laboratory characteristics (Table 5.2). In addition, the disease expression in the lungs and the different compartments affected varies within each specific CTD, complicating the interpretation, classification, treatment modality, and prognosis. For example, rheumatoid arthritis (RA) and Sjogren's syndrome may involve the airway compartment with or without ILD (parenchyma) [21], which complicates the pulmonary function tests' (PFTs) interpretation consisting in obstruction/restriction or both. On other situations, like in lupus, pleural effusions or shrinking lung syndrome may cause restriction, leading to the same difficulties [22, 23]. In idiopathic inflammatory muscle disease, the presence of a restrictive pattern on the spirometry might simply (or additionally to the presence of ILD) be a diaphragmatic muscular weakness [24]. Esophageal dysmotility and recurrent aspiration will contribute to the same in systemic sclerosis, idiopathic inflammatory myopathies, and Sjogren's syndrome [25]. Furthermore, frequently, patients with CTD are on corticosteroids and other immune suppressor drugs, a fact that predisposes them a higher susceptibility for infections. *Pneumocystis jiroveci* pneumonia (PCP) may present with pulmonary changes mimicking ILD as an example and needs to be ruled out with a thorough clinical history and the bronchoalveolar lavage [26].

Many caveats will complicate determining the underlying CTD in presence of ILD. Interstitial lung disease may be the initial presenting feature of a CTD in an estimate of 15% [21, 27, 28], and the absence of the classical overt manifestations expected to be seen for the specific CTD may mistakenly classify the disease as IIP. Moreover, subclinical and subtle manifestations of a CTD may be unidentified or overlooked. For instance, subset of patients with Sjogren's syndrome may run with minimal sicca symptoms and positive anti-SSA/Ro antibodies and the disease to be confirmed, once the histopathology of minor salivary glands is explored [29, 30]. The latter procedure is available in only few specialized centers, limiting the access for a complete assessment, a fact to keep in mind at the time of evaluation of patients with ILD.

5.2.1 History and Physical Exam

The history may reveal symptoms such as dyspnea, tachypnea, and cough. In addition, nonspecific symptomatology like malaise, weight loss, and a decreased functional capacity may contribute poorly as a screening method. On the physical exam, the most common finding might relate to pulmonary basilar inspiratory Velcro crackles and, rarely, clubbing nails. These findings are nonspecific but easily identified. However, not every patient will disclose the respiratory symptoms, such as dyspnea in patients with active and symptomatic rheumatoid arthritis that may run inadvertently as they avoid any physical activity. Even patients with systemic sclerosis may have no respiratory symptoms, and to avoid missing the lung involvement, a baseline screening HRCT is recommended. In fact, a demographic screening study, using the HRCT, demonstrated that 90% of consecutive patients with systemic sclerosis had variable degrees of ILD [31].

Occasionally, patients with a CTD undergo procedures for other reasons that will uncover ILD, especially if the disease is mild, subclinical, or asymptomatic (e.g., pre-surgical evaluation, radiographic imaging for coronary artery calcification scoring, routine exams, lung cancer screening, and other circumstances) [24].

Each one of the CTDs will present with specific features with a plethora of manifestations (Table 5.2), allowing the clinician to identify the specific disease. Occasionally, the CTD may be inapparent at early stages, and/or the clinical features are not always apparent. We suggest looking for specificities on the history and exam for each disease (Table 5.2). Additionally, most of the CTDs may reveal capillary changes, visible on the periungual skin in the fingers. They are more notorious in systemic sclerosis and inflammatory myopathies, but also, the changes may occur in other diseases like systemic lupus erythematosus, Sjogren's syndrome, mixed connective tissue diseases, and rheumatoid arthritis [32]. The nailfold capillaroscopy will guide the clinician toward continuing searching for a CTD. If abnormal, it may associate with Raynaud's phenomenon.

Table 5.2 Clinical, serological, and pulmonary manifestations of connective tissue diseases [21]

Autoimmune condition	Common clinical presentations	Specific clues	Common associated serological markers	Common pulmonary manifestation
Rheumatoid arthritis	Inflammatory polyarthritis Rheumatoid nodules Inflammatory eye disease Rheumatoid vasculitis Pericarditis	Early tenosynovitis Extra-articular manifestations (e.g., scleritis, pericarditis)	Rheumatoid factor Anti-CCP antibody	RA-ILD Pleural effusion Obliterative bronchiolitis Follicular bronchiolitis Bronchiectasis Rheumatoid lung nodules
SLE	Inflammatory arthritis Cutaneous lupus Raynaud's phenomenon Hematologic abnormalities Neuropsychiatric lupus Lupus nephritis	Subtle CNS manifestations Microhematuria Photosensitivity Serositis Cytopenia in the three series	ANA Anti-ds DNA antibody Anti-Smith antibody Anti- RNP antibody SSA and SSB Anti-ribosomal P antibody Low C3 and C4	Pleural effusion Acute pneumonitis Pulmonary hemorrhage SLE-ILD Thromboembolic disease Pulmonary hypertension Shrinking lung syndrome
Systemic sclerosis	Sclerodactyly Raynaud's phenomenon GI dysmotility Calcinosis Telangiectasia Scleroderma Renal crisis	Abnormal nailfold capillaries Tendon friction rubs	ANA Centromere antibody Scl-70 antibody RNA polymerase III antibody	ILD Pulmonary hypertension Pleural effusion
Sjogren's syndrome	Sicca syndrome (the eyes, mouth, dyspareunia) Inflammatory arthritis Raynaud's phenomenon Neuropathy Renal tubular acidosis	Extra-glandular manifestations Neonatal lupus Fibromyalgia-like symptoms	ANA Anti-SSA/Ro and anti-SSB/La antibodies Sjogren's syndrome-specific antibodies	ILD Cystic lung disease Bronchiolitis
Myositis	Muscle weakness Raynaud's phenomenon Morbilliform Rash Inflammatory arthritis Dysphagia	Gottron's papules in the elbows, knees, and elsewhere Abnormal nailfold capillaries	ANA Myositis-specific antibodies Anti-SSA antibodies	ILD Organizing pneumonia Diffuse alveolar damage
Undifferentiated connective tissue disease	Arthralgia Arthritis Raynaud's phenomenon Rashes Dry mouth and/or eyes Morning stiffness Proximal muscle weakness	Not full enough criteria to define a specific CTD	ANA Rheumatoid factor Anti-SSA/Ro and anti-SSB/La antibodies	ILD with more prevalence on nonspecific interstitial pneumonia

Abbreviations: *ILD* interstitial lung disease, *CTD* connective tissue disease, *anti-CCP* antibodies: anti-citrullinated cyclic peptide antibodies, *ANA* antinuclear antibodies

5.2.1.1 Raynaud's Phenomenon and the Nailfold Capillaroscopy in the Assessment of CTD-ILD

Raynaud's phenomenon (also named as Raynaud) is the cutaneous change to the cold exposure and/or to situations with high level of anxiety (Fig. 5.1a). Digits (the hands or feet) and areas distant to the core body temperature are the most frequent target (e.g. the nose, ears). Raynaud associates with small-vessel and capillary dysfunction, given the underlying abnormal vasospasm and dysregulation of vessels, causing a slowed blood flow to the distal tissues. Raynaud has three phases, starting with a pale discoloration, turning bluish-purplish, and then transitions to erythema, once the environmental insult has ceased. The latter's color associates a compensatory distal blood flow, while the prior ones associate with ischemia. Raynaud can be primary or without a relationship to a systemic disease or secondary. Belonging to the latter group, Raynaud is part of almost all CTDs, with systemic sclerosis being the most common disease. The nailfold capillaroscopy (Fig. 5.1b) will be abnormal in association with CTDs, information that will give a hint along with other clinical features (Table 5.2), and positive abnormal serology to establish a CTD-ILD diagnosis. Under normal conditions, the capillaries at the periungual skin, and seen on a magnifying capillaroscopy, are uniformly aligned revealing tight loops lined up one next to the other. Loss of capillaries; dilated, misaligned loops; and leaking hemorrhage disclose evidence of a CTD. Based on the findings, experts have established the scleroderma pattern that can determine early, active, and late scleroderma [33]. The nailfold capillaroscopy plays a major role to identify this disease when systemic sclerosis has no apparent skin thickening as is scleroderma *sine scleroderma* [34]. Other authors have proposed a predictive role of the nailfold capillary patterns to determine internal organ involvement [35, 36]. Moreover, the giant loops seem to be predictive of pulmonary involvement across CTDs [37], but other additional patterns also have been described for lung involvement (e.g., pulmonary artery hypertension) [38, 39].

5.2.2 Serology

It is worth mentioning that the initial traditional screening resource for a CTD-ILD evaluation relies solely on serology testing (Table 5.3). However, serology may be absent in several CTDs [21, 29, 30]. Again, Sjogren's syndrome

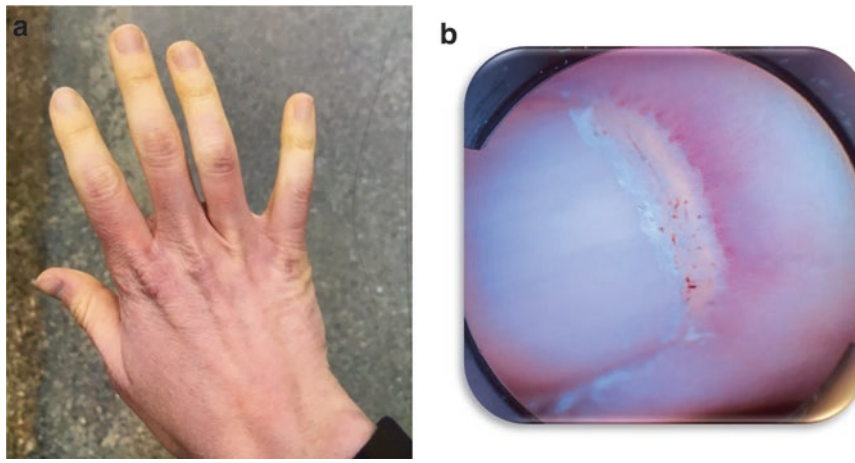

Fig. 5.1 Evaluation of Raynaud's phenomenon (RP). Evaluation of RP in a patient with clinical features of an underlying connective tissue disease: (**a**) finger blanching in a patient with cold exposure. RP in young women suggests the presence of an underlying connective tissue disease. (**b**) Abnormal nailfold capillaries support presence of RP as part of the underlying probable interstitial lung disease. Thickened capillaries (arrows) are visible

Table 5.3 Antibodies and clinical aspects associated with connective tissue diseases [77, 100–102]

Disease	Antibodies	Clinical features
Systemic sclerosis		
	Anti-topoisomerase (Scl-70)	Linked with diffuse systemic sclerosis
	Anti-Th/To	Linked with limited cutaneous systemic sclerosis
	Anti-U3 RNP	Associated with myositis and PH
	Anti-U11/U12 RNP	Selective for systemic sclerosis
Systemic sclerosis and myositis overlap		
	Anti-RuvBL1/2	Diffuse skin thickening and myositis
	Anti-EIF2B	Present with overlap syndrome
	Anti-PM-Scl	Inflammatory myositis and systemic sclerosis
	Anti-Ku	Associated with myositis and lupus overlap
	Anti-Trim21	High risk for ILD
Mixed connective tissue disease		
	Anti-U1 RNP	Features of systemic sclerosis, arthritis, and myositis
Sjogren's syndrome		
	Anti-SSA/Ro	Associated with myositis-specific antibodies and anti-synthetase syndrome
Systemic lupus erythematosus		
	ANA, speckled	Pleuritis and ILD
	Anti-RNP	Overlap; myositis; Sjogren's syndrome
Rheumatoid arthritis		
	Anti-CCP antibodies	High risk for ILD
	Rheumatoid factor	
Inflammatory myopathy		
Dermatomyositis		
	Anti-MDA-5	Associated with cancer; amyopathic dermatomyositis; rapidly progressive ILD (East Asians)
Anti-synthetase syndrome		Mechanic hands, Raynaud's phenomenon, arthritis, myositis, ILD, and fevers
	Anti-Jo1 (histidyl)	
	Anti-PL12 (alanyl)	
	Anti-PL-7 (threonyl)	
	Anti-KS (asparaginyl)	
	Anti-OJ (isoleucyl)	
	Anti-EJ (glycyl)	
	Anti-Zo (phenylalanyl)	
	Anti-Ha (tyrosyl)	

Table adapted from Cotton CV et al. [100] and Betteridge ZE et al. [103]

Abbreviations: *PH* pulmonary hypertension, *ILD* interstitial lung disease, *MDA5* melanoma differentiation-associated gene 5

frequently presents with negative serology, so do idiopathic inflammatory muscle diseases. Rheumatoid arthritis presents with positive rheumatoid factor only in 85% of patients at the onset of the disease, and anti-CCP antibodies may be negative. Moreover, there are specific antibodies not tested regularly, as is in idiopathic inflammatory myopathy, including the ones pertinent to anti-synthetase antibody syndromes and systemic sclerosis (and the anti-Th/To ribonucleoprotein) [40]. Conversely and to complicate the serology screening method, low titers of rheumatoid factor or antinuclear antibody still fall under the IIP definition, based on the American Thoracic Society/European Respiratory Society/Japanese Respiratory Society 2011 statement [32]. In other situations and as a confounder, other autoimmune diseases may present with positive serology (e.g., autoimmune thyroiditis, celiac disease), unrelated with the infiltrative fibrotic pulmonary process that may probably lead to misinterpretations. The ANA pattern contributes to the differentials, being the nucleolar and centromere of most significance in association with a CTD and pulmonary involvement [33]. This assumption, however, does not exclude cases with a speckled or even a homogeneous pattern at high titers. In

our experience, the ANA pattern and other results should be interpreted in the context of each patient and especially in association with demographic and clinical features. For instance, the age (young patients) and gender (females) suggest that the ANA test might associate with a CTD. We, again, advocate for a structured history and directed interview and specific physical exam aimed at detecting a possible underlying CTD in presence of ILD.

The thoracic radiographic images may reveal interstitial features, with reticulations and nodularity, and the pulmonary function tests may reflect various degrees of a restrictive pattern. These tests, although useful and accessible for most of the providers, may overlook subtle changes. The most sensitive test is the HRCT, which should ensure ILD confirmation and baseline data, useful as a predictor for CTD-ILD [41–47].

5.2.3 Pulmonary Function Tests

The restrictive ventilatory pattern and a reduced diffusion capacity of carbon monoxide (DLCO) are the usual findings in ILD. The reduced total lung capacity (TLC) and forced vital capacity (FVC) with normal or increased forced expiratory volume per second (FEV1) and a normal FEV1/FVC ratio are the usual features. However, the PFTs are not always sensitive enough to pinpoint an ongoing inflammatory/fibrotic parenchymal ILD [48]. The best and most sensitive additional exam is the complementary HRCT. Once adjusted to the reduced lung volumes, the DLCO may still remain reduced, suggestive of an overlap with pulmonary artery hypertension or emphysema overlap [49]. In addition, an obstructive physiology with reduced FEV1 and FEV1/FVC is common in CTDs affecting the airways (Table 5.4).

5.2.4 Radiology

The chest tomographic analysis has revolutionized the current approach on assessing patients with ILD. The technique of thin (1.5 mm or less) slices of coronal and sagittal volumetric reconstruction allows accurate description and fine interpretation of pulmonary findings (and their compartments) [50]. Based on the patterns seen on the HRCT, studies have been able to determine predictors for survival [51]. The different patterns are described according to the ATS consensus criteria used for IIPs [11, 55–57]. In CTD-ILD, as in IIP-ILD, there are similar radiographic presentations, like the nonspecific interstitial pneumonia (NSIP), usual interstitial pneumonia (UIP), lymphocytic interstitial pneumonia (LIP), organizing pneumonia (OP), acute interstitial pneumonia/diffuse alveolar damage (DAD), and a combination of them.

The radiological patterns often correlate with the histopathological findings, but this depends on the type. In IIP with a UIP variant, the concordance between the HRCP and the histopathology is excellent [52, 53]. In intermediate UIP definition or NSIP pattern obtained on the HRCT, this concordance with histopathology is not as optimal as desired, showing patterns of either NSIP or UIP in the biopsy [54]. These findings, in addition, have a predictive value. Patients with a radiological definitive or probable UIP pattern have a shorter survival than those with indeterminate UIP or definitive NSIP pattern. The biopsy of patients consistent with a UIP profile and with a non-UIP radiological pattern does better as those with histological UIP pattern and radiological of definite UIP but worse than those with a radiological NSIP pattern [53]. Even though this concept applies to IIPs, the similar findings seem to be extended to CTD-ILDs. In both, the correlations of definite UIP pattern on the HRCT predict a similar pattern on the histopathology, while in NSIP and other presentations, the HRCT is not an accurate predictor of an expected equivalent histopathology pattern [55].

Some patterns prevail over the others, and classical combinations are almost the signature for defined CTDs (Table 5.4). Organizing pneumonia is more frequently seen in combination of NSIP in inflammatory myositis (dermatomyositis, polymyositis) and RA; LIP is found in RA but

Table 5.4 Computed tomography imaging patterns of different connective tissue diseases

Disease	UIP	NSIP	OP	LIP	DAD	Airway[a]	Serositis[b]	Vascular	DAH
RA	+++	+++	++	+	+	+++	+++	+	–
SSc	+	+++	+	–	+	–	–	+++	+
PM/DM	+	+++	+++	–	++	–	–	+	–
SjS	+	++	–	++	+	+	+	++	–
SLE	+	++	+	++	++	+	+++	++	+++
MCTD	+	++	+	–	–	+	+	+	–

Table adapted from Mira-Avendano et al. [61], Bryson et al. [101], and Fischer et al. [25]
Legend: absence of findings: –; lowest: +; highest: +++
CTD connective tissue disease, *DAD* diffuse alveolar damage pattern, *LIP* lymphocytic interstitial pneumonia pattern, *MCTD* mixed connective tissue disease, *NSIP* nonspecific interstitial pneumonia pattern, *OP* organizing pneumonia pattern, *PM/DM* polymyositis/dermatomyositis, *RA* rheumatoid arthritis, *SjS* Sjogren's syndrome, *SLE* systemic lupus erythematosus, *SSc* systemic sclerosis, *UIP* usual interstitial pneumonia pattern
[a]Airway disease includes bronchiectasis, bronchial wall thickening, small centrilobular nodules (representing follicular bronchiolitis), and constrictive bronchiolitis
[b]Pleural or pericardial fluid or thickening

mainly in Sjogren's syndrome; DAD is seen in RA, systemic lupus erythematosus (SLE), inflammatory myositis, and undifferentiated connective tissue disease (UCTD). The overall prevalence of NSIP runs across all the CTDs, except for RA, which presents more frequently with a UIP form [15, 56, 57]. Presence of other compartment involvement is highly likely associated with an underlying CTD: pleural–pericardial effusions, pulmonary arterial hypertension (PAH) (either alone or associated with ILD), and the diaphragm pathology (as seen in inflammatory myopathies) or the skin (as seen in systemic sclerosis of diffuse type) and causing a restrictive pattern on the pulmonary function tests [24, 58] (Table 5.4). Even though about 25% of cases with ILD cannot classify into a defined CTD, they fall under the category of UCTD [28]. The differential of IIP with ILD-UCTD is crucial given that the prognosis is much better in the later [28, 59, 60].

We describe the most common types of HRCT.

5.2.4.1 Usual Interstitial Pneumonia (UIP)

This pattern is characterized by fibrosis and mostly localized in the periphery, basal, and subpleural areas, adjacent to the pleura. The hallmark is honeycombing, with reticulation and peripheral traction bronchiectasis or bronchiolectasis. The latter (traction bronchiectasis) represents the presence of architectural distortion, varicosity, coexisting with honeycombing and the absence of features suggesting an alternative diagnosis [11] (Fig. 5.2). The latter includes profuse ground-glass attenuation, peribronchovascular predominance, perilymphatic distribution, discrete cysts, micronodules, centrilobular nodules, significant mosaic perfusion, and air trapping and consolidation [11, 61]. Probable UIP pattern presents on the HRCT in the absence of honeycombing but presence of reticular abnormalities with basal and subpleural distribution, traction bronchiectasis, or bronchiolectasis [11, 62]. Indeterminate form of UIP pattern refers to the atypical features of UIP but a histopathological pattern of UIP. In this category, the HRCT features show very limited subpleural ground-glass opacities or reticulation without clear features for fibrosis. The prone position will help in excluding subpleural atelectasis (Table 5.5). Additionally, other diagnoses should be investigated in images of pleural plaques, dilated esophagus, distal clavicular erosions, extensive lymph node enlargement, or pleural effusion or thickening (Table 5.5) [11].

5.2.4.2 Non-interstitial Pneumonia (NSIP)

This other pattern, the most frequent type present in CTD-ILD, displays bilateral basal-predominant ground-glass opacities with or without reticulation. The subpleural space is usually spared, opposed to the UIP pattern, being a hallmark for NSIP [63]. The spectrum ranging from inflammatory NSIP with cellular predominance

Fig. 5.2 Usual interstitial pneumonia in a patient with rheumatoid arthritis. Peripheral reticulation, traction bronchiectasis, and honeycombing in made lower lung predominant distribution. Subpleural nodularity without subpleural sparing or focal consolidation

(Fig. 5.3) to the fibrotic pattern (Fig. 5.4) depends on the variable fibrotic tissue causing traction bronchiectasis and deformity in the latter. Moreover, the differences between the fibrotic NSIP and UIP patterns rely on the temporal uniformity of the pathologic features seen in NSIP as compared to the key findings described in UIP (honeycombing pattern, lack of subpleural sparing). In NSIP, the appearance is homogeneous of dense or loose interstitial fibrosis. Lower lobe volume loss and other signs of pulmonary fibrosis are another feature of NSIP [64].

5.2.4.3 Organizing Pneumonia (OP)

Infiltrates in a patchy, peripheral distribution may suggest OP. It prefers the subpleural spaces, but also, it is peribronchiolar. Other features are the perilobular distribution, nodules, and the reversed ground-glass halo sign (Fig. 5.5) [61].

5.2.4.4 Lymphocytic Interstitial Pneumonia (LIP)

Many presentations are considered, including the variable cystic lesions within the parenchyma. Lymphocytic interstitial pneumonia along with NSIP patterns is highly suspicious for an underlying CTD [65]. In addition, as in Sjogren's syndrome, the presence of mild thickening of interlobular septa, bronchovascular bundles and cystic lesions may represent the associated follicular bronchiolitis [66]. Additional frequent localizations are in the perilymphatic interstitium and the pleura. Areas of ground-glass attenuation and poorly defined centrilobular and subpleural nodules of varying sizes might be also present. Lymph node enlargement is also seen. Cysts are usually less than 3 cm and have variable wall thickness and shape. Occasional cysts may show a multiseptated appearance [67].

5.2.4.5 Airway Disease and Respiratory Bronchiolitis-Associated Interstitial Lung Disease

Various patterns may represent bronchial airway disease, like bronchiectasis, mosaic attenuation, bronchial wall thickening, air trapping, and centrilobular or branching nodules [66]. The airways may accompany with interstitial disease, like in respiratory bronchiolitis-associated interstitial lung disease. Representing features are bronchial wall thickening with ground-glass opacity (patchy) with a diffuse distribution and additionally centrilobular nodules.

Table 5.5 High-resolution computed tomography scanning patterns

UIP	Probable UIP	Indeterminate for UIP	Alternative diagnosis
Subpleural and basal predominant; distribution is often heterogeneous[a]	Subpleural and basal predominant; distribution is often heterogeneous	Subpleural and basal predominant	Findings suggestive of another diagnosis, including:
Honeycombing with or without peripheral traction bronchiectasis or bronchiolectasis[b]	Reticular pattern with peripheral traction bronchiectasis or bronchiolectasis	Subtle reticulation; may have mild GGO or distortion ("early UIP pattern")	CT features: Cysts Marked mosaic attenuation Predominant GGO Profuse micronodules Centrilobular nodules Nodules Consolidation
	May have mild GGO	CT features and/or distribution of lung fibrosis that does not suggest any specific etiology ("truly indeterminate for UIP")	Predominant distribution: Peribronchovascular Perilymphatic Upper or mid-lung
			Others: Pleural plaques (consider asbestosis) Dilated esophagus (consider CTD) Distal clavicular erosions (consider RA) Extensive lymph node enlargement (consider other etiologies) Pleural effusions and pleural thickening (consider CTD/drugs)

Definition of abbreviations: *CT* computed tomography, *CTD* connective tissue disease, *GGO* Ground-glass opacities, *RA* rheumatoid arthritis, *UIP* usual interstitial pneumonia
Information obtained from Raghu et al. [11]
[a]Variants of distribution: occasionally diffuse; may be asymmetrical
[b]Superimposed CT features: mild GGO, reticular pattern, and pulmonary ossification

5.2.4.6 Diffuse Alveolar Damage (DAD)

Overall, the pattern is of a diffuse ground-glass opacity pattern, with lower and peripheral zone and posterior preference. Details show ground-glass attenuation and reticular lines.

5.3 Pathogenesis

While the several mechanisms are implicated in the pathogenesis for each CTD, several hypotheses try to explain the inflammatory etiology in the lung parenchyma.

5.3.1 Sjogren's Syndrome Model

In Sjogren's syndrome, the concept of autoimmune epithelitis, or the invasion of inflammatory cells surrounding the epithelial cells of a specific organ, is present in different tissues as part of a systemic inflammation [68, 69]. The histopathological pattern is seen in interstitial nephritis, cholangitis, and lymphocytic clusters surrounding salivary ducts as part of the pathognomonic histopathology features of Sjogren's syndrome [70]. Epithelial cells seem to be the antigenic source to elicit the cellular

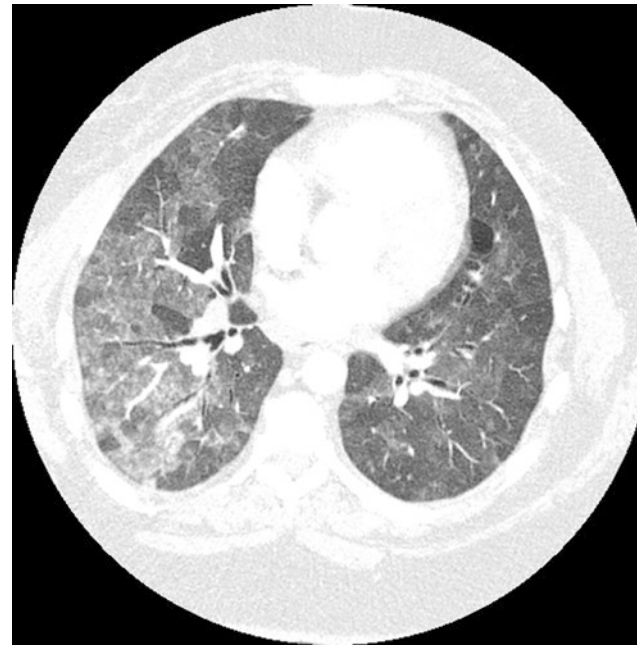

Fig. 5.3 Cellular nonspecific interstitial pneumonia in a patient with systemic lupus erythematosus de novo. Extensive bilateral ground-glass infiltrates

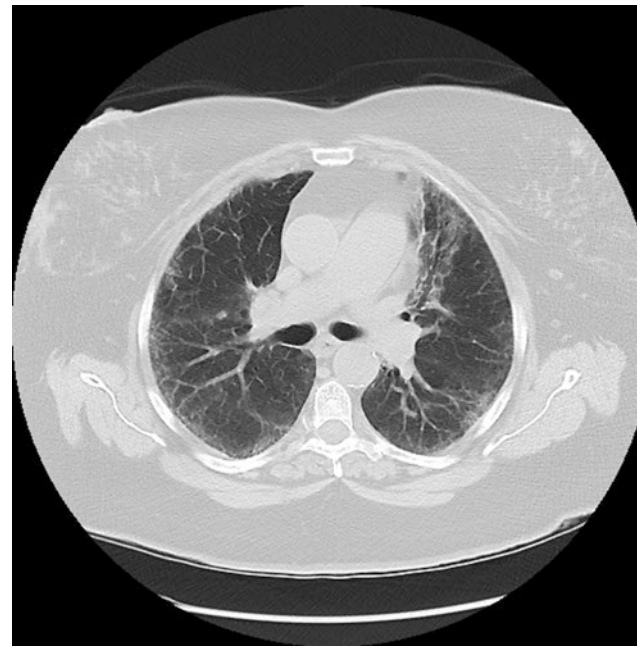

Fig. 5.4 Fibrotic non-interstitial pneumonia. Prominent diffuse bilateral subpleural interstitial thickening and subpleural preservation. Scattered traction bronchiectasis. Scattered ill-defined ground-glass infiltrates

immune attack. In the terminal bronchioles, this phenomenon replicates the same pattern of clusters of inflammation surrounding the epithelial cells in bronchioles, termed as follicular bronchiolitis [71]. The latter is seen in the HRCT as enhancement of the bronchovascular bundles and air trapping [72]. The proposed inflammatory cell invasion into the lung parenchyma and as a continuum of the adjacent follicular bronchiolitis is described as nonspecific inflammatory pneumonitis (NSIP), a subtype of ILD.

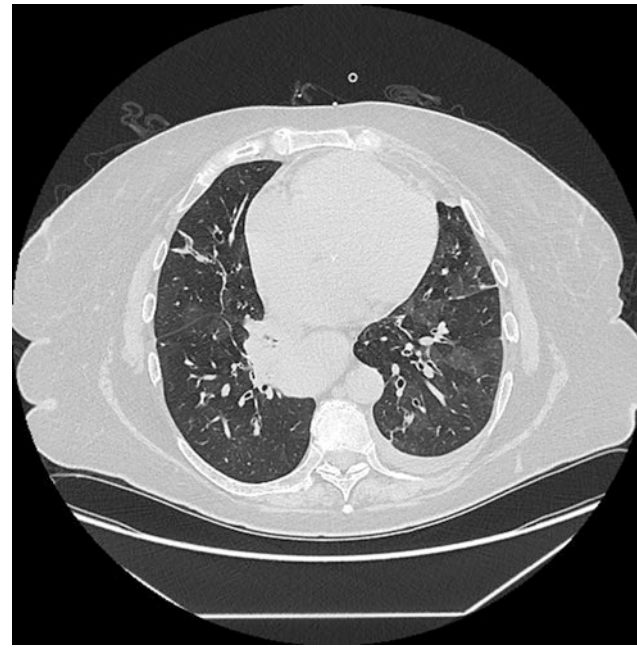

Fig. 5.5 Organizing pneumonia. Patient with rheumatoid arthritis. Mild to diffuse bronchial wall thickening, with mild bronchiectasis. A diffuse mosaicism pattern throughout the lungs bilaterally is seen, with linear opacities in the right middle lobe and right lower lobe possibly associated with atelectasis vs. scaring

5.3.2 Rheumatoid Arthritis Model

In another hypothesis, the lungs may account for the initial tissue for the immune tolerance loss and possibly secondary to a local insult. In a recent epidemiological prospective study among patients with established asthma and chronic obstructive pulmonary disease (COPD) vs. controls and the incident rheumatoid arthritis, asthma was associated with the latter, so was COPD and more pronounced in ever-smokers older than 55 years [73]. Moreover, RA-related autoantibodies are detectable in sputum in preclinical RA and in early RA [74]. Not only this but also the generation of anti-citrullinated protein antibodies (ACPA) is present in bronchial tissue and bronchoalveolar lavage in patients with early untreated RA without clinical signs of lung involvement, strengthening the role of the lung compartment as an important player in ACPA-positive RA [75]. Moreover, this is seen in cases of ILD with positive serology and no findings of RA [76–78]. In time, it appears that the antibodies may play an active role in the pathogenesis of lung disease [79].

5.3.3 Pathology

Histopathology analysis is required under uncertain cases to define the type of ILD and the etiology. In other situations, the biopsy will help in identifying a different disorder (e.g., carcinoma, sarcoidosis). This is especially important in patients with an indeterminate UIP pattern on the HRCT, needed to differentiate between IIP from other causes with potential immune suppressor treatment efficacy, like hypersensitive pneumonitis or CTD-ILD. Finally, proceeding to the biopsy is ideal in younger patients with features of vasculitis or patients with clinical features of ILD without clear-cut findings on the HRCT. Different techniques will yield an optimal tissue sample, depending on the preferred localization and patient's clinical status. Available procedures are the video-assisted thoracoscopic surgery as the standard and most important technique. Other options are the transbronchial lung biopsy and thoracotomy. The transbronchial cryobiopsy technique is currently evolving.

5.3.3.1 Usual Interstitial Pneumonia (UIP)

The nature of ILD will help in defining management and will predict response to therapy. Therefore, it is key to differentiate the UIP from other non-UIP patterns, as the latter have more options for treatment. Currently, the concept of unresponsive therapy to fibrotic lung disease is challenged given the available contribution of new anti-fibrotic therapies (nintedanib, pirfenidone) that show promising favorable outcomes.

The hallmark for a UIP pattern shows dense fibrosis with distortion of lung architecture, subpleural and/or paraseptal fibrosis, patchy involvement with fibrotic lung alternating with areas of normal parenchyma, and honeycombing [11, 80]. In indeterminate UIP, the findings are consistent with fibrosis with or without architectural distortion or features of either UIP (fibrosis) or other pathologies. In the latter, there might be granulomas, hyaline membranes, prominent airway-centered changes, interstitial inflammation without fibrosis, chronic fibrous pleuritis, or organizing pneumonia [11].

5.3.3.2 Nonspecific Interstitial Pneumonia (NSIP)

Nonspecific interstitial pneumonia is an ILD type of different etiologies (e.g., HIV and hypersensitivity pneumonitis) and is the most frequent presentation of CTD-associated lung disease. It is important to differentiate NSIP from UIP as the former has shown to have better outcomes with a lower mortality rate of 18% among patients with idiopathic NSIP [81]. During the evaluation of new-onset idiopathic NSIP, 17% of them may associate with a CTD. This frequency increases at different time points of follow-up [82], while new features of a CTD ensue. A fraction of patients will classify as having interstitial lung disease with autoimmune features, a feature that is still under development (see ahead) [83]. The histopathological features in NSIP reveal varying degrees of interstitial inflammation and fibrosis, with uniform appearance. The lung architecture is usually preserved, unless traction bronchiectasis was present, a notable feature of the fibrotic NSIP type [84]. Some authors hypothesize a transition between NSIP and UIP, and this is represented by the excessive accumulation of collagen synthetized by an abnormal fibroblast-myofibroblasts and supported by the presence of both histopathological patterns in individual patients from biopsies of different pulmonary sites [52]. Furthermore, it is clearly difficult to differentiate NSIP from UIP in situations when these two changes coexist in an individual with biopsies from different locations [52, 85, 86].

5.3.3.3 Organizing Pneumonia (OP)

This type considered as ILD is characterized by the intra-alveolar accumulation of fibroblasts and loose connective matrix, potentially reversible with corticosteroid (CS) therapy. Depending on the alveolar infiltrate material, different variants may suggest the stages of OP. In the early stages, fibrin fills the alveoli, along with inflammatory cells, known as the fibrinous variant. It associates with extensive necrosis of alveolar epithelial type I cells. During the second stage, the formation of fibroinflammatory buds is gradually intermixed with newly invading fibroblasts and myofibroblasts that in turn will ensue abundant collagen deposits. In the third stage, mature fibrotic buds are composed of myofibroblasts, organized in concentric rings alternating with collagen bundles. This process clears out gradually if the basal laminae had remained intact during the inflammation. The granulation tissue may extend to the adjacent bronchiole, and the lumen might get obstructed. Inflammation in alveolar interstitium is present, and foamy alveolar macrophages may be localize in alveoli without granulation tissue [87].

5.3.3.4 Lymphocytic Interstitial Pneumonia (LIP)

It is characterized by the dense interstitial lymphocytic infiltrates, consisting of polymorphic lymphocytes, admixed with variable number of plasma cells, immunoblasts, macrophages, and rarely histiocytes. The extent of infiltrative cellular proliferation may expand the interlobular and alveolar septa [67]. A feature of CTD-

associated LIP is the presence of B lymphocytes expressing CD20, usually from germinal centers localized in nodular lymphocytic aggregates. In contrast the CD3(+) T lymphocytes are predominant in the interstitial compartment. The infiltrates are present in areas surrounding the lymphatic channels, alveoli septa, peribronchovascular regions, and subpleural lung zones [67].

5.3.3.5 Diffuse Alveolar Damage (DAD)

This acute lung injury shows different phases, with the initial exudative (acute) phase with associated edema, hyaline membranes, and interstitial acute inflammation and then followed by a subacute phase. The latter consists of loosely organizing fibrosis localized in the alveolar septa with type II pneumocyte hyperplasia. These findings associate with thrombi in small- and medium-sized pulmonary arterioles [88]. The hallmark in this presentation is the presence of hyaline membranes. They consist of dense eosinophilic amorphous material of cellular debris, plasma proteins, and surfactant components and lined up along the alveolar septa [89]. Even DAD is considered the pathologic correlate of acute respiratory distress syndrome (ARDS); pathologic findings for DAD may be present in half of ARDS cases [90].

5.4 Differences Between CTD and IIP

The official ATS/ERS/JRS/ALAT Clinical Practice Guideline defines interstitial pulmonary fibrosis (IPF, a common form of IIP) as UIP pattern in the HRCT and the exclusion of other known causes of ILD (e.g., domestic, occupational, and environmental exposures; infections; CTDs; or drug toxicity). In addition, there should be either presence of the HRCT pattern of UIP or specific combinations of HRCT patterns and histopathology findings of UIP in patients who had the lung biopsy [11]. Usual interstitial pneumonia is an atypical feature linked with CTD-ILD, except for rheumatoid arthritis that has a predilection for the latter type. Subsequently, the analog features between UIP in IPF and RA-UIP make the latter to be the most susceptible group for misclassification. In cases of uncertainty, the histopathology gives many clues favoring a CTD-ILD (e.g., RA-UIP): 1) in CTD-UIP, presence of fibroblast foci is scarce [17, 91] and shows smaller honeycomb spaces as compared to IPF-UIP [92]; 2) in RA-UIP presentations, there are more lymphoplasmacytic aggregates as in IPF-UIP; 3) germinal centers are a feature of CTD-ILD [92]; and 4) IPF, contrary to CTD-ILD, presents with heterogeneous ILD patterns in an individual patient from different pulmonary biopsy sites (lobes) (e.g., NISP in one sample and UIP in another sample), which can be considered as a hallmark for IPF [85, 91]. Furthermore, survival in RA- UIP is better compared to IPF (specifically IIP-UIP) [17]. This probably relates to the potentially treatable inflammatory niches in the histopathology (e.g., as described, lymphoplasmacytic aggregates, germinal centers), but not the honeycombing that implies the fibrotic tissue.

Given the better survival in CTDs-ILD, it is crucial to determine if the lung disease associates with any of them. Some authors suggested that all ILD patients with a NSIP pattern on the HRCT might have a potential underlying CTD [93]; however, these criteria are too loose, and if applied, many patients may falsely be classified as having some form of CTD. Refinements on this concept, however, showed that cumulative incident diagnosis of CTD-ILDs from previously labeled idiopathic NSIP patterns may increase in time, at one (3.6%), two (15.2%), and three years (20.0%). In this study, however, no predictor to determine CTD-ILD (serology, extrapulmonary findings) was found, but results imply re-evaluating patients prospectively [82]. An alternative to differentiate idiopathic vs. CTD-related ILD, as said, is the histopathology review in the context of clinical findings suspicious for a CTD. In a study assessing demographic, clinical, and laboratory associations with histopathological NSIP vs. IPF, patients who had a diagnosis of undifferentiated connective tissue disease (UCTD) were more frequently associated with NSIP (31% vs. 13%, respectively) [94]. In this

same study, predictors identified for NSIP in the histopathology were the absence of HRCT typical for idiopathic pulmonary fibrosis (IPF), demographic features (women younger than 50 years), and features of UCTD, like Raynaud's phenomenon and positive serology for autoimmunity [94]. Compared to IPF, NSIP has the potential to respond to the immune suppressor therapy, which is the main reason to explore for the latter. The definition of UCTD is the clinical findings of a systemic CTD, without meeting the criteria for a particular disease [95]. Most of the patients may have a positive ANA and clinical features such as Raynaud's phenomenon, nonspecific rash, sicca symptoms, arthralgias, or arthritis. Over time, 34%–50% will develop a specific CTD [96–98], but others will remain as having UCTD. Definition for UCTD has changed several times, adding more difficulties to accurately define who would fall into the UCTD criteria. Despite these difficulties and in order to favor patients to have a justifiable immunosuppressor treatment (rather than anti-fibrotic therapy), many authors, in an attempt to classify patients within IPF (on HRCT) with some features of a CTD without fulfillment of a unique entity, have grouped clinical, radiological, histological, and laboratory findings to come up with a syndromic definition. They have generated several of such syndromic entities, named as "undifferentiated CTD," "autoimmune-featured ILD," and "lung-dominant CTD" (Table 5.6) [25]. Each one of them varies in sensitivity and specificity and has different criteria that for the medical community cause more confusion. To unify criteria, the one proposed by the ERS/ATS research statement known as interstitial pneumonia with autoimmune features appears to have great value.

5.4.1 Interstitial Pneumonia with Autoimmune Features (IPAF) [20]

This term is the one that is currently under universal approval. As seen, to use different criteria, trial designs and retrospective reviews for comparison become cumbersome. The current definition for IPAF includes presence of an interstitial pneumonia by HRCT or surgical lung biopsy (SLB) and a full scrutiny to exclude alternative etiologies, and the patient should not meet criteria for a defined CTD. In addition, patient should have presence of at least one feature from at least two of the following domains (Table 5.6):

5.4.1.1 Clinical Domain

It includes all possible extra-thoracic presentations of a CTD without a full definition for a specific disease. They include distal digital fissuring (i.e., "mechanic hands"), distal digital tip ulceration, inflammatory arthritis or polyarticular morning joint stiffness ≥60 min, palmar telangiectasia, Raynaud's phenomenon, unexplained digital edema, and unexplained fixed rash on the digital extensor surfaces (Gottron's sign). In this domain, other nonspecific features were left aside as in previous definitions (e.g., arthralgia, myalgia, photosensitivity, and sicca symptoms).

5.4.1.2 Serological Domain

Conditions to include the ANA and rheumatoid factors are to have high titers to avoid false positives. In addition, regardless of the ANA titers, if they have a centromere or nucleolar patterns, they are incorporated as positive, as they are specific for possible lung involvement. They include (1) ANA ≥1:320 titer, diffuse, speckled, and homogeneous patterns; (2) rheumatoid factor ≥2x upper limit of normal; (3) anti-CCP; (4) anti-ds-DNA; (5) anti-SSA/Ro; (6) anti-SSB/La; (7) anti-ribonucleoprotein; (8) anti-Smith; (9) anti-topoisomerase (Scl-70); (10) anti-tRNA synthetase (e.g., Jo-1, PL-7, PL-12, EJ, OJ, KS, Zo, tRS); (11) anti-PM/Scl; and (12) anti-MDA-5.

5.4.1.3 Morphologic Domain

It consists of three subdomains, radiographic, histopathological, and multicompartment (thoracic compartments supporting presence of CTD features). If any of these subdomains is present, then this domain has fulfilled the criteria: (1) suggestive radiology patterns by HRCT:

Table 5.6 Clinical, radiographic, histopathological, and serological features of syndromic autoimmune disorders linked with interstitial lung disease

Lung-dominant connective tissue disease [65]	Autoimmune-featured interstitial lung disease (ILD) [54]	Interstitial pneumonia with autoimmune features [20, 83]
(1) All of the following three clinical features:	This term includes as follows: (1) One or more of the following symptoms: dry eyes or dry mouth; gastro-esophageal reflux disease; weight loss; foot or leg swelling; joint pain or swelling; rash; photosensitivity; dysphagia; hand ulcers; mouth ulcers; Raynaud's phenomenon; morning stiffness; proximal muscle weakness	The current definition includes the following: (1) Presence of an interstitial pneumonia by HRCT or SLB (2) Exclusion of alternative etiologies (3) The patient does not meet criteria for a defined CTD (4) Presence of at least one feature from at least two of the following domains
(a) NSIP, UIP, LIP, OP, or DAD (or desquamative interstitial pneumonia if no smoking history, defined by the lung biopsy or suggested by the HRCT)		
(b) Insufficient extra-thoracic features of a definite CTD		
(c) No identifiable alternative cause for interstitial pneumonia		
(2) (a) One or more ANA ≥1:320; nucleolar or centromere patterns; rheumatoid factor >60 IU/mL; anti-SSA/Ro; anti-SSB/La; anti-Smith; anti-RNP; anti-ds-DNA; anti-topoisomerase I (Scl-70); anti-CCP; anti-tRNA synthetase; anti-PM/Scl	(2) One or more of the following positive or high laboratories: ANA ≥1:160; rheumatoid factor; anti-SSA/Ro, anti-SSB/La; anti-Smith; anti-ribonucleoprotein; anti-ds-DNA; anti-topoisomerase (Scl-70); anti-Jo-1; aldolase; creatinine phosphokinase	A. Clinical domain: (1) Distal digital fissuring (i.e., "mechanic hands") (2) Distal digital tip ulceration (3) Inflammatory arthritis or polyarticular morning joint stiffness ≥60 minutes (4) Palmar telangiectasia (5) Raynaud's phenomenon (6) Unexplained digital edema (7) Unexplained fixed rash on the digital extensor surfaces (Gottron's sign)
(b) Two or more of lymphoid aggregates with germinal centers; extensive pleuritis; prominent plasmacytic infiltration; dense perivascular collagen		B. Serological domain: (1) ANA ≥1:320 titer, diffuse, speckled, homogeneous patterns or a) ANA nucleolar pattern (any titer) or b) ANA centromere pattern (any titer) (2) Rheumatoid factor ≥2x upper limit of normal (3) Anti-CCP (4) Anti-ds-DNA (5) Anti-SSA/Ro (6) Anti-SSB/La (7) Anti-ribonucleoprotein (8) Anti-Smith (9) Anti-topoisomerase (Scl-70) (10) Anti-tRNA synthetase (e.g., Jo-1, PL-7, PL-12, EJ, OJ, KS, Zo, tRS) (11) Anti-PM/Scl (12) Anti-MDA-5

(continued)

Table 5.6 (continued)

Lung-dominant connective tissue disease [65]	Autoimmune-featured interstitial lung disease (ILD) [54]	Interstitial pneumonia with autoimmune features [20, 83]
		C. Morphologic domain: (1) Suggestive radiology patterns by HRCT: (a) NSIP; (b) OP; (c) NSIP with OP overlap; d) LIP (2) Histopathology patterns or features by surgical lung biopsy: (a) NSIP; (b) OP; (c) NSIP with OP overlap; (d) LIP; (e) interstitial lymphoid aggregates with germinal centers; (f) diffuse lymphoplasmacytic infiltration (with or without lymphoid follicles) (3) Multicompartment involvement (in addition to interstitial pneumonia): (a) unexplained pleural effusion or thickening, (b) unexplained pericardial effusion or thickening, (c) unexplained intrinsic airways disease (by PFT, imaging, or pathology, including airflow obstruction, bronchiolitis, or bronchiectasis), and (d) unexplained pulmonary vasculopathy

Source and adaptation: Fisher A et al. [65], Vij R et al. [54], and Graney BA et al. [20]
Abbreviations: *NSIP* nonspecific interstitial lung disease, *UIP* usual interstitial pneumonia, *LIP* lymphocytic interstitial pneumonia, *OP* organizing pneumonia, *DAD* diffuse alveolar damage, *HRCT* high-resolution chest computed tomography, *CTD* connective tissue disease, *ANA* antinuclear antibody, *anti-CCP* anti-citrullinated cyclic peptide, *SLB* surgical lung biopsy, *PFT* pulmonary function test

(a) NSIP, (b) OP, (c) NSIP with OP overlap, and (d) LIP; (2) histopathology patterns or features by surgical lung biopsy: (a) NSIP, (b) OP, (c) NSIP with OP overlap, (d) LIP, (e) interstitial lymphoid aggregates with germinal centers, and f) diffuse lymphoplasmacytic infiltration (with or without lymphoid follicles); (3) multicompartment involvement (in addition to interstitial pneumonia): (a) unexplained pleural effusion or thickening, (b) unexplained pericardial effusion or thickening, (c) unexplained intrinsic airways disease (by PFT, imaging, or pathology, including airflow obstruction, bronchiolitis, or bronchiectasis), and (d) unexplained pulmonary vasculopathy [83].

According to the domain definitions, UIP was not included as it has less likelihood to associate with features of CTD-ILD. A bias to this definition criteria is that patients with RA-UIP or any other CTD-UIP presentation would not be considered to have the same weight as other patterns in the HRCT. Despite this presentation, patients may classify as IPAF with a UIP pattern, if the other two domains (at least one item of each domain) fulfill criteria.

The utility of IPAF application has allowed authors to analyze predictive features for survival. Patients with IPAF criteria had slightly better outcomes in survival, when separated between those with the UIP and non-UIP patterns. Those with IPAF-UIP did worse and was comparable to IPF as compared to those patients with IPAF and non-UIP whose survival was similar to CTD-ILD [99]. Overall, however, the heterogeneity of patients fulfilling IPAF criteria within several cohorts makes difficult to identify unique features of all the studies performed that may predict better a survival other than when they present with UIP pattern [20]. Future diagnostic criteria will help unify IPAF with more precision, allowing researchers to avoid heterogeneity of inclusion criteria (especially in the morphologic domain) to achieve possible predictors of survival.

5.5 Conclusions

The current review is an approach focused on the integrated evaluation of patients with ILD. The main purpose is to establish a CTD in the initial assessment. A stepwise and thorough review is necessary to follow, including the history, physical exam, exam of key components for a connective tissue disease, laboratory review, and evaluation of the HRCT and histopathology. This methodology will avoid missing key components, including the evaluation of the nailfold capillaries and, if necessary, a biopsy of minor salivary glands from the lower lip. The knowledge of the new serology is important for the evaluation of specific syndromes among inflammatory myopathies, including the anti-synthetase syndrome.

A subset of patients will not fulfill a diagnosis of a specific CTD but may have several components favoring autoimmunity. In such situations, the three domains that are part of IPAF need to be reviewed to establish the diagnosis. This modality will help the clinician make appropriate and accurate management decisions. Except for RA-UIP, most of the CTD-ILD may respond to the immune suppressor therapy that ultimately will improve survival. Future therapies (anti-fibrotic) will improve survival in patients with a fibrotic pattern of ILD.

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6 Molecular Mechanisms of Vascular Damage During Lung Injury

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Abstract

A variety of pulmonary and systemic insults promote an inflammatory response causing increased vascular permeability, leading to the development of acute lung injury (ALI), a condition necessitating hospitalization and intensive care, or the more severe acute respiratory distress syndrome (ARDS), a disease with a high mortality rate. Further, COVID-19 pandemic-associated ARDS is now a major cause of mortality worldwide. The pathogenesis of ALI is explained by injury to both the vascular endothelium and the alveolar epithelium. The disruption of the lung endothelial and epithelial barriers occurs in response to both systemic and local production of pro-inflammatory cytokines. Studies that evaluate the association of genetic polymorphisms with disease risk did not yield many potential therapeutic targets to treat and revert lung injury. This failure is probably due in part to the phenotypic complexity of ALI/ARDS, and genetic predisposition may be obscured by the multiple environmental and behavioral risk factors. In the last decade, new research has uncovered novel epigenetic mechanisms that control ALI/ARDS pathogenesis, including histone modifications and DNA methylation. Enzyme inhibitors such as DNMTi and HDACi may offer new alternative strategies to prevent or reverse the vascular damage that occurs during lung injury. This review will focus on the latest findings on the molecular mechanisms of vascular damage in ALI/ARDS, the genetic factors that might contribute to the susceptibility for developing this disease, and the epigenetic changes observed in humans, as well as in experimental models of ALI/ADRS.

Keywords

Lung injury; Vascular damage; Epithelial barrier; Endothelial activation; Epigenetics; Histone acetylation, DNA methylation; Inflammation

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Abbreviations

ALI	Acute lung injury
ANGPT2	Angiopoietin 2
APC	Activated protein C
ARDS	Acute respiratory distress syndrome
BMDM	Bone marrow-derived macrophage
COPD	Chronic obstructive pulmonary disease
COVID	Coronavirus disease
DNAm	DNA methylation
DNMT	DNA methyltransferase
DNMTi	DNA methyltransferase inhibitor
ECs	Endothelial cells
EPCR	Endothelial protein C receptor
EWAS	Epigenome-wide association study
GWAS	Genome-wide association studies
HAT	Histone acetyltransferase
HDAC	Histone deacetylases
HLMVEC	Human lung microvascular endothelial cells
HPAEC	Human pulmonary artery endothelial cells
IL	Interleukin
LPS	Lipopolysaccharides
MLE-12	Murine lung epithelial cell line
MODS	Multiorgan dysfunction syndrome
MYLK	Myosin light chain kinase
ncRNAs	Noncoding RNAs
PA	Plasminogen activators
PAI	Plasminogen activator inhibitor
PAN	Panobinostat
ROS	Reactive oxygen species
S1P	Sphingosine-1-phosphate
S1PRs	S1P receptors
SARS-CoV-2	Severe acute respiratory syndrome coronavirus 2
SB	Sodium butyrate
SELPLG	Selectin P ligand
SFTPB	Surfactant protein B
SNPs	Single-nucleotide polymorphisms
TF	Tissue factor
TM	Thrombomodulin
TNF-α	Tumor necrosis factor α
TSA	Trichostatin A
Tub A	Tubastatin A
VAP	Ventilator-associated pneumonia
VEGFR1	Vascular endothelial growth factor receptor 1
VILI	Ventilator-induced lung injury
VPA	Valproic acid
VWF	Von Willebrand factor

6.1 Introduction

Acute lung injury (ALI) and the more severe form, acute respiratory distress syndrome (ARDS), are described as clinical syndromes of acute respiratory failure with substantial morbidity and mortality [1]. ALI and ARDS develop most commonly in the setting of pneumonia, non-pulmonary sepsis (with sources that include the peritoneum, urinary tract, soft tissue, and skin), aspiration of gastric and/or oral and esophageal contents, and major trauma (such as blunt or penetrating injuries or burns) and may be part of a systemic failure consisting in multiorgan dysfunction syndrome (MODS) [2, 3]. Mortality rates, while improving, remain persistently high at near 30% [4]. ARDS is a major public health burden that causes substantial morbidity, mortality, and healthcare cost [5]. ALI/ARDS mortality is associated with the development of pulmonary edema, a major factor for hypoxemia [6], as well as fibrin microthrombi in the alveoli and pulmonary vasculature [7]. The clinical features of the patient with ALI/ARDS consist of acute hypoxemic respiratory failure with bilateral pulmonary infiltrates [8, 9]. The disease is characterized by an acute exudative phase involving pulmonary edema and inflammation, accompanying abnormal gas exchange and variable late-phase responses [10]. All these features can lead to severe hypoxemia often necessitating mechanical ventilation. Patients with multiple comorbidities,

chronic alcohol abuse, or chronic lung disease have increased risk for lung injury [9]. Moreover, recent clinical data indicate that novel coronavirus disease (COVID)-19 most commonly manifests as viral pneumonia-induced ARDS mediated by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [11]. COVID-19 pandemic-associated ARDS is now a major cause of mortality worldwide. This virus directly impacts the lung endothelium to promote leakage and microthrombi [11, 12]. However, the mechanisms that govern how the comorbidities affect these pathophysiological processes driving lung damage and our understanding of the mechanisms and heterogeneity of sepsis- and COVID-19-associated ARDS, and in particular the effects of SARS-CoV-2 in the endothelium, are still in an early stage [13]. It is becoming increasingly clear that endothelial dysfunction is a common denominator in all these processes. Critically, the mechanical ventilation that is required to restore blood oxygenation during ARDS can in itself promote local tissue damage through a mechanism called ventilator-induced lung injury (VILI). Many of these changes may be driven by intracellular signals in the endothelium, as reviewed recently [2]. For example, ROS generation through the multiple cell types within the lungs, including epithelial cells (EC) and immune cells, may mediate ARDS/VILI-induced damage, and previous studies showed that antioxidants can reduce the severity of ARDS/VILI [14, 15]. Other mechanical stress signals are mediated through changes in the cytoskeleton network, as well as transmembrane proteins mediating cell-cell adhesion [16, 17].

6.2 Molecular Mechanisms of Vascular Damage in ALI/ARDS

6.2.1 Endothelial Activation

The lung vascular endothelium forms a continuous uninterrupted layer of endothelial cells (ECs) that is located at the interface between the bloodstream and lung tissue and provides a semi-selective barrier. This endothelial layer is held together by two complex junctional structures: the adherens junctions and the tight junctions. These junctions are gatekeepers for the movement of fluid, proteins, and cells from the bloodstream to the lung interstitium (reviewed elsewhere [18–20]). Due to their localization, ECs play key roles not only in optimizing gas exchange but also in controlling barrier integrity and function [21].

A lack of understanding of the pathologic mechanisms and how the ECs are involved in ALI remains an obstacle to new and effective therapies that reduce vascular leakage [22, 23]. It is well accepted that the inflammatory process during ALI causes disruption of the lung endothelial and epithelial barriers, leading to respiratory epithelial dysfunction and surfactant depletion [1, 24, 25]. This disruption of the lung endothelial barriers is modulated by multiple signaling pathways, such as those involving reactive oxygen species (ROS), actomyosin contractility through action of Rho GTPases, and tyrosine phosphorylation of junctional proteins [20, 26–29]. The breakdown of endothelial and epithelial barriers in ALI occurs in response to intense inflammation and local production of pro-inflammatory cytokines (e.g., tumor necrosis factor α (TNF-α), interleukin (IL)-1β, IL-6), chemokines such as IL-8, and other edemagenic factors such as thrombin- or platelet-activating factor. Inflammatory cytokine signaling leads to a compromised EC barrier, elevated vascular permeability, and edema [30]. The activated endothelium then shows increased activation of pro-inflammatory transcription factors and release of inflammatory mediators, which in turn lead to increased oxidative stress, a prothrombotic phenotype, and miscommunication with adjacent vascular cell walls [31]. Loss of the endothelial barrier during ALI causes pulmonary edema by increasing alveolar-capillary permeability to fluid, proteins, neutrophils, and red blood cells [24]. Direct exposure to bacterial endotoxins, including lipopolysaccharides (LPS) and intercellular interactions with activated inflammatory cells, may also play an important role [32, 33]. Alveolar macrophages, neutrophils, and

other immune effector cells, including monocytes and platelets, are critical components of a successful lung defense against external challenges and have key activities in acute lung injury (reviewed by Matthai et al. [2]). The endothelium is not only a major target of cytokine signaling but also a major source of danger signals. At least during an influenza virus-induced lung injury, the pulmonary endothelium is a key regulator of the cytokine storm, demonstrating its central role as a mediator of innate immunity cellular and cytokine responses [34].

Lung infiltration is intrinsically dependent on endothelial regulation. In response to cytokine stimuli, the EC promotes a large increase in the expression levels of multiple leukocyte adhesion molecules on the EC surface, including E-selectin, P-selectin, ICAM-1, and VCAM-1 [35]. These changes are accompanied by alterations in oxygen and nitrogen free radicals as the superoxide radical and NO, prostaglandins, leukotrienes, and growth factors, which mediate leukocyte adhesion and migration, as well as platelet accumulation [36].

A hypercoagulatory state is another hallmark of ARDS/ALI pathophysiology [5, 37]. The endothelium is a key regulator of the coagulation cascade through modulation of the thrombogenicity of its surface. During basal conditions, the endothelial surface is non-thrombogenic through the expression of inhibitors of the coagulation cascade and platelet activation and aggregation, including tissue factor (TF) inhibitor and thrombin inhibitors [38]. Vascular injury during ALI/ARDS initiates coagulation by promoting both activation of procoagulant factors and platelets and a reduction of anticoagulant components and fibrinolysis. Chiefly, the endothelial surface may express high levels of TF in response to TNF-α and IL-1β [39]. Further, the endothelium can control platelet adhesion and activation through the release of Von Willebrand factor (VWF), which promotes binding of platelets; plasminogen activators (t-PA and u-PA) that promote fibrinolysis; and electrical repulsion by negatively charged heparan sulfates, among others [38]. Conversely, the regulation of TF and the coagulation cascade is not only a critical effector of inflammation but also a modulator of the inflammatory response [40]. In human studies, the intravenous administration of LPS leads to an increase in microparticles containing TF into the circulation, resulting in thrombin production [37, 41], thereby increasing the formation of fibrin, and resulting in the consumption of clotting factors. Similarly, a study with 45 patients with ALI/ARDS from septic and non-septic causes reported that the low activated protein C (APC) and high plasminogen activator inhibitor (PAI)-1 levels were associated with increased mortality [42]. Protein C is an endogenous anticoagulant that is activated by a complex consisting of thrombin, thrombomodulin (TM), and the endothelial protein C receptor (EPCR) within the endothelial lumen [43, 44]. APC inhibits coagulation via the suppression of fVa and fVIIIa and exerts anti-inflammatory effects as well, by suppressing cytokine production [45]. In addition, APC activates the fibrinolytic process, as it inhibits PAI-1 [37]. In a murine model, EPCR is a critical participant in APC-mediated protection of pulmonary vascular permeability [46]. Despite the important roles of APC in the regulation of coagulation and inflammation, recombinant activated protein C, the only approved pharmacological agent targeting the endothelial response, was withdrawn because of its lack of improvement of patient survival [47], emphasizing our lack of a full understanding of this complex response.

6.2.2 Genetic Factors

Studies designed to identify genetic factors that might contribute to the susceptibility for developing ALI/ARDS have been reported in the past decade. However, no specific loci with genome-wide significance for associations with the diseases have been identified, probably in part because of the phenotypic complexity of ALI/ARDS engendered by the different risk factors [48]. The challenges for finding a specific molecular marker can be explained by the heterogeneity of the disease, in which multiple different pathogenic processes contribute in varying ways in different patients, depending on the specific

combination of clinical factors and genetics [49]. Moreover, the requirement for such a large environmental insult prevents the use of genetic linkage studies of family pedigrees to identify genetic influences [50]. One example of genetic background that affects the ALI is the identification of Nrf2 as a susceptibility gene in the murine model of ALI [51, 52]. Genomic approaches have also led to success in identifying VILI-associated genes, novel biomarkers (NAMPT/PBEF), and pro-inflammatory cytokines such as IL-6. IL-6 is produced by the endothelium, monocytes, and macrophages stimulated by the TLRs and is directly associated with the inflammatory response in ALI (reviewed in [53]). A previous study described two single-nucleotide polymorphisms (SNPs) consisting of T-1001G and C-1535 T transversions in the promoter region of the NAMPT gene (also known as pre-B-cell colony-enhancing factor, PBEF) that confer susceptibility to sepsis-induced ARDS (the GC haplotype conferred a 7.7-fold increased risk). Consistent with a lower risk, the -1543T variant showed an 1.8-fold reduced gene expression [54, 55]. In vitro, NAMPT gene downregulation led to lower IL-8 expression and reduced monolayer permeability of human pulmonary artery endothelial cells after IL-1β or thrombin challenges [56, 57]. Consistently, NAMPT overexpression led to increased IL-8 in these cells [55, 57].

Few reports exist regarding genome-wide association studies (GWAS) on ARDS. Data obtained from 600 trauma-induced ARDS patients and 2266 health controls of European descent found around 2.5 million SNP candidates across the genome [58]. Follow-up of the top 1% most significant SNPs with 212 trauma-induced ARDS patients and 283 at-risk controls showed an association between ARDS and variants from PPFIA1, a protein-associated focal adhesions, and the actin cytoskeleton [59], as well as other genes including IL-10, myosin light chain kinase (MYLK), angiopoietin 2 (ANGPT2), and Fas cell surface death receptor (FAS) [58]. A second and more recent GWAS study compared 232 African American patients with ARDS with 162 control subjects with an ARDS risk factor who never developed ARDS. The authors identified one SNP rs2228315 in intron 3 of the selectin P ligand (SELPLG) gene. The selectin pathway is critically involved in the transmigration of leukocytes from the vascular lumen to sites of inflammation [60]. Confirming a role in lung injury, SELPLG gene expression was significantly increased in VILI- and LPS-induced mouse models of lung injury. Moreover, antibody-mediated neutralization of PSGL-1, the SELPLG-encoded protein, attenuated experimental VILI- and LPS-induced lung, and SELPLG knockout mice are protected against LPS-induced lung injury [60]. Together, these findings suggest that variants in genes regulating leukocyte adhesion and migration may affect the risk of developing ARDS.

Importantly, other variants of genes regulating the vasculature may also be involved. By performing a prioritization of candidate genes integrating genomic data from a transcriptomic study in an animal model of ARDS and the data from the first published genome-wide association study described above, Hernandez-Pacheco et al. identified a variant in FLT1 (rs9513106) associated with ARDS, with on odds ratio of 0.75 (CI = 0.58–0.98) [61]. FLT1 encodes for the vascular endothelial growth factor receptor 1 (VEGFR1), a molecule critically involved in angiogenesis and endothelial barrier regulation [62].

6.2.3 Epigenetic Changes in Experimental Models of ALI/ADRS

Because it is generally considered that genetic variants contribute only a small proportion of ARDS/ALI risk [48], it is imperative to understand other mechanisms that can explain this disease. The increasing understanding about the many epigenetic mechanisms that strongly influence multifactorial diseases led to a growing interest in exploring how nongenetic variations, including epigenetic factors, influence the etiology of ALI and ARDS [63, 64].

Epigenetic processes play a critical role in transcriptional regulation by influencing genomic

regulatory sequences in a cell-type-specific manner, in response to the extracellular environment [65]. The cell epigenome is extremely dynamic, being coordinated by complex mechanisms that interface genetics and environmental factors [66]. Different epigenetic mechanisms regulate gene expression in different ways in the different cell types and during development to orchestrate cellular responses to external stimuli [67]. Epigenetic information in mammals can be transmitted in a variety of ways, including DNA methylation (DNAm), posttranslational modifications of histones, and noncoding RNAs (ncRNAs) [68]. DNA methylation plays an important role in DNA repair, recombination, and replication, as well as regulation of gene activity, while the histones are highly conserved proteins that can become posttranslationally modified and play an important role in the organization of chromatin structure, particularly in the homeostasis between euchromatin, transcriptionally active, and heterochromatin, transcriptionally inactive (reviewed elsewhere [69, 70]). Multiple epigenetic modifications have been evaluated as markers of ALI. However, their role in driving the disease is yet not well understood.

Zhang et al. [71] analyzed microarray data of human blood samples from ARDS patients and healthy volunteers and found significant changes in 44,439 DNA methylation sites. The regions that showed differences in the DNA methylation comprised genes involved in the regulation of inflammation or immunity, endothelial function, epithelial function, and coagulation function, including the chemokine receptor CX3CR1 and the tyrosine kinase Fyn in both ARDS animal models and in vitro experiments [71]. Another study conducted an epigenome-wide association study (EWAS) between DNA methylation and 28-day survival time in 185 moderate-to-severe ARDS patients from intensive care units, and the results showed four CpG sites that were significantly associated with ARDS survival, with two sites related to inflammation and infection, on the genes encoding prostaglandin D2 receptor, and an integral membrane P4 ATPase [72], which has been suggested to act as a lipid flippase essential to inhibit the response to LPS [73]. Reduced endothelial histone acetylation during ALI can lead to an increased expression of adhesion molecules and regulate endothelial permeability [74].

Most of the human studies with epigenetic changes and lung disease are concentrated at chronic obstructive pulmonary disease (COPD). Recently, one study observed that a genetic variant in 19q13.2 region identified in genome-wide association studies of COPD is associated with differential DNA methylation in blood as well as gene expression in blood and the lungs [75]. Another study that evaluated the COPD in two family-based cohorts found 330 genes associated with 349 differentially methylated CpGs. Further analysis of these genes identified an enrichment in genes modulating the immune response, inflammatory pathways, and coagulation cascade [76]. However, another study aimed at identifying cell-free DNA methylation biomarkers to discriminate between overlapping and multifactorial lung diseases, such as cancer, ILD, and COPD, showed a moderate sensibility and specificity, suggesting a need for improved molecular techniques [77].

Specific therapies do not currently exist for the treatment of ALI or for the alleviation of the unremitting vascular leak, which serves as a defining feature of these illnesses. Given the possible links between DNA methylation and disease severity, a better understanding of the effect of DNA methyltransferase inhibitor (DNMTi) such as 5-Aza-2 deoxycytidine (Aza) or HDAC inhibitors such as trichostatin A (TSA) and sodium butyrate (SB) may be useful for studies in humans in the near future. Understanding these new mechanistic insights can lead to novel strategies, biomarkers, and therapies to reduce the morbidity and mortality of these acute and subacute inflammatory injuries [78]. Aza incorporates into DNA CpG sites opposite to a methylated CpG site, thereby inhibiting the DNA methyltransferase enzyme action in the DNA. This inhibition causes loss of DNA methylation in one daughter DNA strand because DNA methyltransferase is not available to remethylate the hemimethylated sites generated during the first round of DNA replication [79]. Also, the Aza and TSA have well-established biological activities and

known safety and side-effect profiles [80, 81]. Evidence suggests that members of the HDAC family play a critical role in the development of ALI, and thus, manipulation of HDAC signaling pathways is a strategy that would provide novel therapeutic strategies for the protection of endothelial barrier function and for the intervention of the inflammatory profile in ALI [23].

Zhang et al. investigated the anti-inflammatory effects of HDAC inhibitors TSA and SB by assessing the degree of lung injury and the expression of inflammation-related genes after cecal ligation and puncture, a common animal model of sepsis. The results of the study showed that TSA and SB significantly alleviated septic lung injury, as evidenced by reduced lung wet to dry weight ratio, and attenuated pathohistological lesions. Moreover, treatment with TSA or SB significantly prolonged the survival time of CLP mice, providing evidence of the anti-inflammatory effect of HDAC inhibitors in sepsis [82]. It is important to highlight that TSA is a chemotherapeutic agent that induces differentiation and promotes apoptosis in transformed cells at higher concentrations [83] and also suppresses the production of inflammatory cytokines in animal models of autoimmune and inflammatory disease [84]. TSA also showed a reduction of the inflammatory cytokines MMP-9 and PAI-1, collagen gene expression, and total collagen production in mice exposed to bleomycin treatment, a process that required at least in part suppression of HDAC4 and Akt pathways [85]. Further support for these inhibitors was provided by studies evaluating the response of bone marrow-derived macrophage (BMDM) from endotoxin-treated mice treated with the same HDAC inhibitor, TSA in combination with Aza. This combination was more effective than either inhibitor alone to reduce pyroptosis and apoptosis [86]. Moreover, they observed significant changes in the mitochondrial membrane structure, lower levels of DNA fragmentation, and reduced expression of apoptotic and pyroptotic genes in LPS-induced BMDMs treated by a combination of Aza and TSA than in LPS-induced BMDMs treated with either drug alone. Consistently, inhibition of HDAC using panobinostat (Pan) and TSA showed a protection against LPS-mediated endothelial barrier dysfunction in HLMVEC [87].

Thangavel et al. showed that a single dose of Aza+TSA in a mouse model of ALI prevented lung vascular hyperpermeability and inflammatory lung injury and promoted survival rate that compared with treatment with either Aza or TSA alone [88]. LPS-induced infiltration of neutrophils and generation of inflammatory cytokines in lung tissues were also significantly reduced in Aza+TSA-treated mice. The same treatment significantly reduced LPS-induced apoptosis of lung endothelial cells. Mechanistically, Aza+TSA treatment suppressed phosphorylation of MLC2 and eNOS and activated Cav1. The above effects are attributed to Aza+TSA-mediated epigenetic modulation of acetylated and methylated histone 3 protein of the VE-cadherin promoter [88]. Similarly, Aza+TSA treatment of endotoxemic mice induced a putative anti-inflammatory process, including lower levels of pro-inflammatory cytokines IL1β, TNFα, and IL-6 and higher levels of IL-10 that correlated with an increased M2/M1 macrophage ratio [89]. Mechanistic studies demonstrated that BMDM exposed to LPS showed a significant increase in phosphorylated p38MAPK and reduction in phosphorylated STAT3, which was ameliorated following treatment with Aza+TSA [89]. Multiple cell types may be mediating this response: Aza treatment promoted inflammation resolution in mouse models of lung injury, through a mechanism that involved an increase activity of regulatory T cells via an upregulation of FoxP3 [90].

Valproic acid (VPA) is another HDAC inhibitor [91] that may be effective in reducing lung injury. VPA treatment reduced the damage to the lungs in a rat hemorrhagic shock model [92]. Similarly, the lungs injured following an ischemia/reperfusion model displayed reduced histone H3 acetylation, and treatment with VPA significantly attenuated all the parameters of lung injury, oxidative stress, apoptosis, and inflammation [93].

Studies using intratracheal LPS instillation in mice as well as human lung microvascular ECs suggested a role for sphingosine-1-phosphate (S1P) and SphK1 signaling in histone acetylation

and chromatin modification, since inhibition of S1P lyase attenuated LPS-induced histone acetylation and secretion of pro-inflammatory cytokines [78]. S1P, S1P receptors (S1PRs), and enzymes of S1P metabolism have been identified as key modulators of several human pathologies including pulmonary diseases [94]. A protective role of S1P in LPS-induced lung injury has been proposed [95, 96]. Intravenously administered S1P or S1P analogs reduced vascular leak and pulmonary edema in murine and canine models of sepsis-induced lung injury [97]. In vitro studies showed that LPS enhanced global acetylation of histones in human lung microvascular endothelial cells (HLMVEC). Moreover, treatment of HLMECs with a histone acetyltransferase (HAT) inhibitor reduced the LPS-induced release of IL-6 [78]. Consistently, histone modifications may mediate the inhibition of an angiogenic transcriptional profile observed in a murine model of ventilator-associated pneumonia (VAP) [98]. Interestingly, the changes on gene expression for genes encoding components of the Tie2/angiopoietin and VEGF/VEGFR systems were observed not only in the affected lungs but also in the kidneys and livers, suggesting that VAP leads to a systemic change in the epigenetic landscape of these genes [98].

Lung injury promotes important epigenetic changes in lung epithelium, but their effects are still not well understood. Using a murine lung epithelial cell line (MLE-12), Chen et al. demonstrated that changes in histone acetylation leads to altered cell proliferation [99]. Specifically, they found deacetylation of MORF4L1 at Lys-148, mediated by histone deacetylase (HDAC)-2. MORF4 produces massive cell death and senescence, but the biological function of MORF4L1 homodimers is not clear. One possibility is that MORF4L1 homodimers probably exist as an intermediate product for further assembly into larger functional complexes, such as a corepressor complex. MORF4L1 homodimerization augments MORF4L1 corepressor complex formation to repress cell proliferation [99]. These findings highlight a potential mechanism by which inflammatory factors can influence epigenetic regulation and drive maladaptive changes in the endothelium.

Little effort has been devoted to inhibiting specific acetylases and deacetylases that can contribute to a reduction in pulmonary edema in the LPS-induced ALI. In vitro, pharmacological inhibition of HDAC6 by tubacin in HPAEC blocked the thrombin-induced endothelial barrier dysfunction through increased acetylation of α-tubulin and microtubule stabilization [100]. Consistently, the selective inhibition of HDAC6 by tubastatin A (Tub A) inhibited TNF-a-induced lung endothelial permeability and prevents endotoxin-induced pulmonary edema in HPAECs and HLMVECs [101]. However, HDAC6 is thought to regulate predominantly cytoplasmic proteins, not histones [102]. How this enzyme can modulate cytokine production is still unknown.

Research to unravel the interactions between genetic and epigenetic factors is critical to better understand lung disease. A well-designed study began to define the contribution of specific transcription factors, ARDS-associated SNPs, and promoter demethylation to NAMPT transcriptional regulation in response to mechanical stress. As described above, NAMPT has been found to be a novel biomarker of lung injury [54], and single-nucleotide polymorphisms in a GC sequence of NAMPT were associated with increased risk of ALI in a Caucasian population [54]. Further, pulmonary epithelial-cell-specific knockdown of NAMPT gene expression significantly attenuated LPS-induced mouse lung inflammation. Inhibition of NAMPT upregulated surfactant protein B (SFTPB) expression by enhancing histone acetylation to increase its transcription, whereas overexpression of NAMPT inhibited SFTPB expression in both H441 and A549 cells [103]. Follow-up research, using a mouse model of VILI, found NAMPT promoter demethylation on putative PAX5 binding sites. CHIP data from human pulmonary artery endothelial cells (HPAEC) demonstrated increased STAT5 binding to this promoter region in response to demethylation [104].

In summary, the studies using DNMTi and HDAC inhibitors strongly support the notion that

modulation of epigenetic mechanisms is a promising therapeutic strategy to reduce the inflammatory response during ARDS and ALI. However, the mechanisms that mediate this response are not well understood, and more studies are necessary to understand how these drugs affect the inflammatory process and whether their actions directly impact the sustained vascular barrier breakdown as seen in lung injury.

6.3 Conclusion

Key aspects of the pathophysiology of ALI/ARDS involve endothelial dysfunction driven by a strong inflammatory milieu. These endothelial changes lead to increased edema, leukocyte infiltration, and thrombosis, inducing lung damage and further aggravating the local and systemic inflammatory response. Mechanical ventilation, usually required to sustain blood oxygenation levels, can induce further damage, leading to a self-feeding process that may lead to multiorgan dysfunction syndrome and death. Following acute inflammation, excessive reactive oxygen species (ROS) can induce damaged pulmonary epithelia to secrete pro-inflammatory and profibrotic cytokines that lead to imbalances between histone acetylation and deacetylation [85, 105].

Despite an ever-increasing understanding of the inflammatory mechanisms orchestrating this response, there are very few therapeutical advances to improve the survival odds. Here, we summarized the evidence accumulated over the last 15–20 years that strongly point to key roles for epigenetic mechanisms mediating vasculopathy. Use of enzyme inhibitors such as DNMTi and HDACi may offer new alternative strategies to prevent or reverse the vascular damage that occurs during lung injury. The use of HDAC inhibitors is associated with anti-inflammatory processes and activates an array of key anti-inflammatory signaling pathways not only in ALI but also in other inflammatory lung diseases including COPD and asthma [23, 106]. HDAC inhibition already showed a decrease in the severity of disease in several animal models of inflammation [107] as well as in in vitro models [87, 100]. Changes in histone acetylation modify chromatin structure and the activity of transcription factors that serve as an important mechanism for the regulation of gene expression [108], and with the advance of the knowledge of the molecular basis of the inflammation and pathways, new opportunities linked with the HDAC inhibitors surge as new treatment possibilities. HDAC inhibitors can act as effective anti-inflammatory or antifibrotic drugs by changing histone acetylation or suppressing the activity of multiple transcription factors [109–111]. Future work is required to fully understand how epigenetic mechanisms affect the vascular dysfunction in lung injury, and early-phase clinical trials will provide data to analyze the safety and efficacy of this strategy for the treatment of ALI and ARDS.

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7 Neurotrophin Regulation and Signaling in Airway Smooth Muscle

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Abstract

Structural and functional aspects of bronchial airways are key throughout life and play critical roles in diseases such as asthma. Asthma involves functional changes such as airway irritability and hyperreactivity, as well as structural changes such as enhanced cellular proliferation of airway smooth muscle (ASM), epithelium, and fibroblasts, and altered extracellular matrix (ECM) and fibrosis, all modulated by factors such as inflammation. There is now increasing recognition that disease maintenance following initial triggers involves a prominent role for resident nonimmune airway cells that secrete growth factors with pleiotropic autocrine and paracrine effects. The family of neurotrophins may be particularly relevant in this regard. Long recognized in the nervous system, classical neurotrophins such as brain-derived neurotrophic factor (BDNF) and nonclassical ligands such as glial-derived neurotrophic factor (GDNF) are now known to be expressed and functional in non-neuronal systems including lung. However, the sources, targets, regulation, and downstream effects are still under investigation. In this chapter, we discuss current state of knowledge and future directions regarding BDNF and GDNF in airway physiology and on pathophysiological contributions in asthma.

Keywords

Brain-derived neurotrophic factor · Glial-derived neurotrophic factor · Calcium · Contractility · Remodeling · Asthma · Lung disease

7.1 Introduction

Throughout life, including fetal growth, bronchial airways are key structural and functional elements of the respiratory system. Diseases of the bronchial airway such as asthma or chronic obstructive pulmonary disease (COPD) result from both intrinsic factors such as developmental

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abnormalities and environmental exposures including allergens, microbes, pollutants, and tobacco smoke products. These detrimental effects lead to functional changes such as airway irritability and hyperreactivity, as well as to structural changes including enhanced cellular proliferation of airway smooth muscle (ASM), epithelium, and fibroblasts, and altered extracellular matrix (ECM) and airway fibrosis. While environmental and other exposures trigger the initial inflammatory response within the airway leading to initiation of disease, there is now increasing recognition that disease maintenance after initial triggers or inflammatory cells disappear involves resident nonimmune airway cells taking a prominent role. Here, beyond their expected roles in barrier maintenance and airway tone, cells such as epithelium, ASM, and fibroblasts can modulate the local inflammatory milieu, produce pro-fibrotic factors, and enhance cell-cell interactions, overall resulting in maintenance of cellular dysfunction that can then be exacerbated by intermittent stimuli such as additional allergens, infection, or inflammation. Thus, understanding the mechanisms that initiate vs. maintain airway disease becomes important for developing targeted therapeutics for asthma and COPD, particularly in the chronic state. Here, it is imperative to determine whether mechanisms common to different cell types or airway diseases can be identified, allowing for development of a wide range of novel therapeutic approaches.

An emerging aspect of resident airway cell function is expression and function of growth factors that can have autocrine or paracrine effects in airway structure and function in both health and disease. In this regard, the family of neurotrophins may be particularly relevant. Long recognized in the brain in the context of neuromodulation, neuronal plasticity, growth, and particularly regeneration, and in the pathophysiology of diseases such as depression and Alzheimer's [1–3], there has been increasing interest and recognition regarding neurotrophins in non-neuronal systems including lung [4–14]. In this regard, from both neuronal and non-neuronal work, it is clear that while neurotrophins are a broad concept, there is substantial heterogeneity in their expression and function which is key towards understanding their roles in health and disease. While information is less, this is also true in the lung (or airways). Most of the work, including our own, has focused on specific neurotrophin family members such as nerve growth factor (NGF) and brain-derived neurotrophic factor (BDNF) [5, 6, 11, 15–18], and even here, the cell sources vs. targets, and importantly physiological or pathophysiological relevance, are still under exploration. There is now even more limited but emerging information regarding another aspect, the glial-derived neurotrophic factor (GDNF) family of neurotrophins [19–28]. In this chapter, we discuss neurotrophins in airway physiology and focus on pathophysiological contributions in asthma, expanding on BDNF and the emerging GDNF family.

7.2 Mechanisms of Neurotrophin Expression

Understandably, much of our knowledge regarding neurotrophin expression or signaling derives from exploration in the nervous system, starting with studies in the 1950s (e.g., Levi-Montalcini, Hamburger, Hempstead, etc.) on neural regeneration in the embryonic limb [29–31]. Here, it is important to delineate what qualifies as neurotrophin. While several factors can act as growth factors in influencing neuronal structure and function, there are classical and nonclassical neurotrophins. The classical neurotrophins are considered to consist of four polypeptides of comparable structure and function: NGF, the original, best-characterized member, BDNF, neurotrophin-3 (NT3), and neurotrophin-4 (NT4) [31–33]. Separately, the nonclassical GDNF family consists of GDNF, neurturin, artemin, and persephin [34–37]. While their signaling pathways differ substantially (described below), neurotrophins do not function in a vacuum, and it is now increasingly clear that their expression and signaling are intricately tied to several regulatory pathways including other neurotrophins, sex steroids, glucocorticoids, and particularly inflammation [38–40]. Of course, in the context of

asthma, these pathways are quite relevant [14, 41–43]. Accordingly, understanding how neurotrophin expression and signaling occur is insightful towards recognizing their role in airway diseases.

7.2.1 BDNF Production

The BDNF gene has at least nine promoters allowing for multiple mRNA transcripts each with the full ORF for BDNF protein [44–46]. Via alternative promoters, splicing, and poly(A) sites, at least 22 transcripts can be generated. Such transcriptional complexity can result in complex regulation of BDNF generation and its intracellular localization, transport, and extracellular release. For example, cellular stimulation leading to intracellular calcium ($[Ca^{2+}]_i$) enhancement can induce BDNF in the context of activity-dependent regulation [46] involving Ca^{2+}-responsive elements in regulatory regions of several BDNF exons via cAMP response element binding protein (CREB) and protein kinase A (PKA), NFκB, and NFAT. In addition to transcriptional regulation, at least in neuronal cells, epigenetic mechanisms such as histone acetylation/methylation and DNA methylation also regulate BDNF [44, 46] in a complex, context-dependent fashion, affecting the different BDNF exons differentially.

The elements of BDNF regulation (Fig. 7.1) happen to be important in the airway as well, particularly in the context of inflammation. However, unlike in neurons, there is currently limited data on the mechanisms by which BDNF transcription occurs in the airway, with no data on epigenetic regulation. We previously explored BDNF production in human ASM in the context of inflammation (TNFα) effects, focusing on specific $[Ca^{2+}]_i$ regulation- and inflammation-related signaling cascades [16]. We found that TNFα enhances BDNF via the Ca^{2+} regulatory channels transient receptor potential channels TRPC3 and TRPC6 (but not TRPC1) and signaling intermediates such as ERK 1/2, PI3K, PLC, and PKC, Rho kinase, CREB, and NFAT. These elements, albeit to different extents, are increased in asthmatic ASM and with TNFα exposure and contribute to greater BDNF expression in diseased tissues [16]. Such local regulation and upregulation of neurotrophins can thus allow for potential downstream influences on parameters such as contractility and remodeling in the context of asthma.

BDNF protein synthesis has again been largely examined in neurons (Fig. 7.1) and to a limited extent in ASM. Classically endoplasmic reticulum synthesis of BDNF occurs as a precursor protein (pre-pro-BDNF; ~27 kDa) [47–49] which is then cleaved of its signal peptide to produce pro-BDNF that is transported to the Golgi to be sorted into constitutive or regulated secretory vesicles. It is vesicular pro-BDNF that is detected intracellularly, but it can be converted into mature BDNF by endoproteases (e.g., furin) or intragranule by convertases [50], again providing another level of regulation for BDNF expression. Vesicles can thus contain both pro-BDNF and mature BDNF, which are then released into the extracellular space. Regulated release involves SNARE protein complexes as in neurotransmission [51] and requires Ca^{2+} and cAMP. Upon extracellular release, pro-BDNF is cleaved by plasmin or importantly matrix metalloproteinases (MMPs) into mature BDNF.

7.2.2 GDNF Production

GDNF, neurturin, persephin, and artemin all have low amino acid sequence homology, and they all function as via the Ret receptor along with ligand-specific GDNF family receptor (GFR) isoforms (see below). Although only slightly similar in sequence, GDNF is related to TGF-β2 and is a distant member of the TGFβ superfamily [52]. Originally isolated from cultured rat glial cells, GDNF was recognized to enhance survival and differentiation of dopaminergic neurons [52]. Since then, GDNF has been detected in multiple mammalian cell types [53] and is widely distributed in both central and peripheral nervous systems. Several neuronal cells such as glia, astrocytes, oligodendrocytes, and motor neurons can synthesize and secrete GDNF.

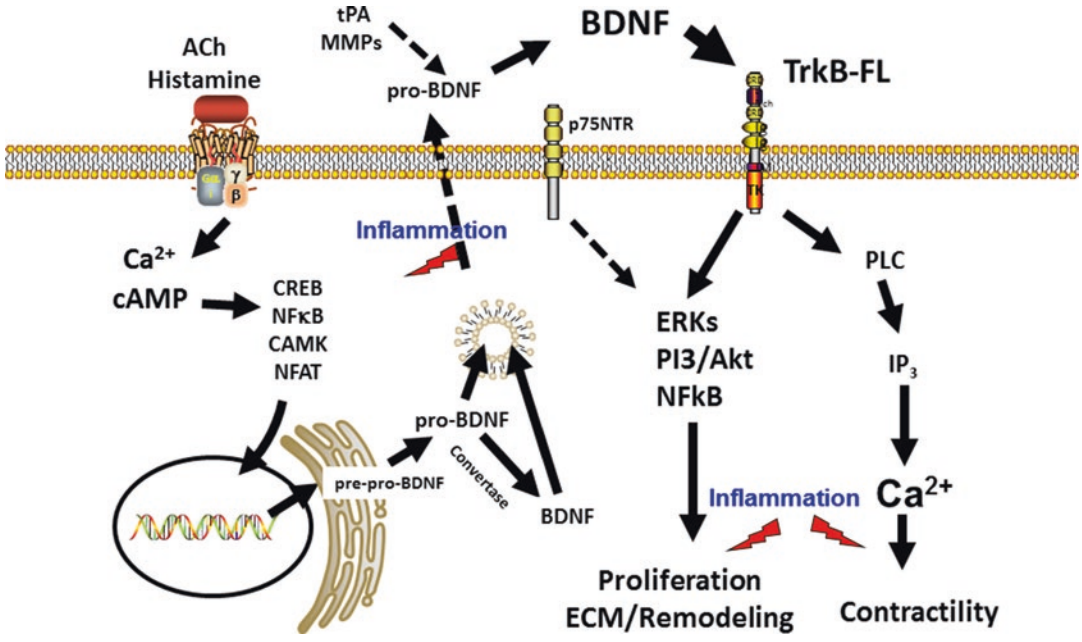

Fig. 7.1 Production and downstream effects of brain-derived neurotrophic factor (BDNF) in airway smooth muscle. Factors such as Ca^{2+} and signaling intermediates (relevant to asthma) stimulate production of pre-pro-BDNF that is cleaved into pro-BDNF that is packaged into vesicles and secreted. Pro-BDNF can also be intracellularly cleaved via convertases (e.g., furin) into mature BDNF that is also packaged into vesicles, and thus both pro- and mature BDNF are released into the extracellular space. Extracellular pro-BDNF can be cleaved to mature BDNF via proteases such as tissue plasminogen activator or matrix metalloproteinases. BDNF acts on plasma membrane high-affinity full-length tropomyosin-related kinase TrkB-FL receptors or low-affinity p75NTR receptors. In ASM, TrkB-FL is of functional importance. Downstream, TrkB increases $[Ca^{2+}]_i$ via the PLC/IP_3 pathway and increases ASM proliferation and extracellular matrix (ECM) production via different signaling intermediates also relevant to inflammation. Thus, ASM-derived BDNF can interact with inflammatory signaling in the context of asthma

As a secretory protein (Fig. 7.2), GDNF is first formed as a 211-amino acid precursor that is trafficked to the endoplasmic reticulum for secretion when the protein folds with disulfide bonds and dimerizes, later being modified by N-linked glycosylation and finally proteolytic processing into a mature form of 134 amino acids [52, 54]. Thus, GDNF differs from BDNF in being first created as pro-form rather than a pre-pro form. However, as with BDNF, proteases such as furin and protein convertases are involved in cleavage of pro-GDNF to mature GDNF [55]. Additionally, GDNF can be secreted with or without proteases [56]. Nonetheless, glycosylation appears to be a key step for proper folding and processing of GDNF protein [54]. Studies have also found a shorter GDNF mRNA transcript in humans and rodents [57, 58], although it is unclear if the resultant protein is functional. With alternative splicing, two mRNAs, a full-length pre-(α)pro-GDNF and a shorter pre-(β)pro-GDNF, are created which can both be cleaved to mature GDNF [59, 60]. Interestingly, the two pro-forms of GDNF are secreted into the extracellular space using different regulatory pathways [55] where cellular depolarization promotes (β)pro-GDNF and mature GDNF secretion, while (α)pro-GDNF and its corresponding mature GDNF are mostly localized in the Golgi where they colocalize with secretory granules. In contrast, (β)pro-GDNF and its mature form are localized in other types of vesicles and are released much more rapidly via the secretory pathway [55, 58].

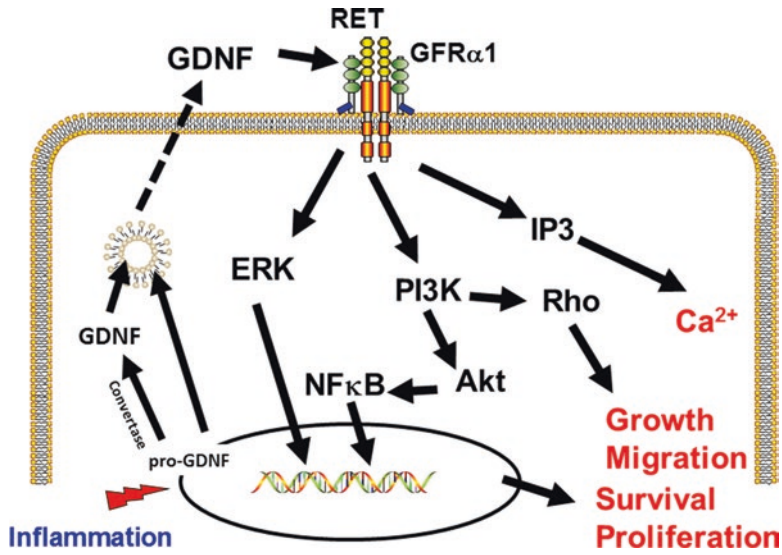

Fig. 7.2 Glial-derived neurotrophic factor (GDNF). While there is minimal data on GDNF in airways or ASM, information from other organ systems including brain and gut show that GDNF is first generated in a pro-form that is intracellularly cleaved into mature GDNF that can be packaged into vesicles and secreted. Extracellularly, pro-GDNF can be cleaved. GDNF acts via a heterodimer of the RET receptor and the GDNF family receptor alpha isoform 1 (GFRα1). Similar to BDNF, GDNF induces pathways that promote $[Ca^{2+}]_i$ as well as cell proliferation and fibrosis: elements that might be important in asthma

7.3 Mechanisms of Neurotrophin Signaling

There is substantial heterogeneity in neurotrophin signaling within the classical family as well as in the nonclassical GDNF family with the potential for interactions between neurotrophins, and cross-reactivity of ligands across different receptors, overall making for extremely complex systems that are likely cell type and context dependent. Nonetheless, again via work in neurons, the basics of neurotrophin signaling are now recognized.

7.3.1 BDNF Signaling

Interestingly, both pro- and mature BDNF are active ligands. They signal through two distinct, major receptor types: high-affinity tropomyosin-related kinase (Trk) receptors (~140 kDa), specifically TrkB which binds to BDNF and also to NT4 [61–63], and the low-affinity "pan-neurotrophin" receptor p75NTR that is a member of the TNF receptor superfamily. Other neurotrophins bind other Trks: NGF to TrkA and NT3 to TrkC [30, 31, 64].

The TrkB gene on chromosome 9q22 contains 24 exons [65, 66] which are responsible for four major isoforms, but 36 alternatively spliced isoforms. Among these, the full-length transmembrane TrkB receptor (TrkB-FL) is particularly important. Cellular responses to BDNF (Fig. 7.1) require expression of TrkB-FL which also contains an intracellular tyrosine kinase domain essential for downstream functionality [65–67]. Following ligand binding, TrkB-FL is autophosphorylated, engaging Shc, GRB2, ATP, and importantly PLCγ. Downstream, three tyrosine kinase pathways are activated [66–70]: PLCγ1/PKC important for the IP_3 pathway and thus $[Ca^{2+}]_i$ release, the ERK pathway, and PI3K/Akt, the later promoting cell survival and proliferation. There is also a truncated TrkB-T1 isoform, but since it lacks the tyrosine kinase domain, its role in downstream activation is not clear and thus may be more of a dominant negative receptor or serve to sequester BDNF limiting its

signaling [71–74]. In terms of the low-affinity p75NTR receptor, upon binding either pro-BDNF or mature BDNF, a variety of intracellular pathways can be modulated including PI3KAkt, NFκB, MAPK, RhoA, and even PKA and HIF, all potentially relevant to airways in the context of asthma and inflammation [14, 41, 75–81]. Thus, in any cell type, the relative levels of pro- vs. mature BDNF and TrkB-FL vs. TrkB-T1 vs. p75NTR influence the overall effects of BDNF. These effects generally tend to be genomic in nature. However, there is also data that BDNF has rapid, "non-genomic" effects that occur in the timeframe of seconds to minutes via TrkB [82–85] which is important in the context of Ca^{2+} regulation and neurotransmission or neuromodulation [82–85].

7.3.2 GDNF Signaling

The Ret receptor is critical to signaling of all GDNF family member ligands. GDNF and other ligands use Ret for signaling, but these ligands cannot activate Ret alone. Ret activation requires a co-receptor glycosylphosphatidylinositol-linked GDNF (GFRα). Similar to the classical neurotrophins such as BDNF, ligand-binding specificity for the GDNF family of ligands is dependent on four GFRα receptor proteins: GFRα1, GFRα2, GFRα3, and GFRα4. GDNF preferentially binds GFRα1 but can act via GFRα2 with lower affinity [37, 86, 87]. GDNF functionality involves a disulfide-stabilized homodimer that first binds to a glycosylphosphatidylinositol (GPI)–anchored GFRα1 (usually within lipid rafts) and forms a high-affinity complex. This complex recruits two Rets resulting in transphosphorylation of tyrosine residues and subsequent intracellular signaling [37, 87]. Downstream pathways (Fig. 7.2) involve MAPK, PI3K, ERK, and Akt that promote cell survival [37, 87, 88]. Further potentiation of GDNF effects can occur through membrane microdomains enriched with Src family kinases, making Src a major signaling molecule for GDNF [89]. GDNF signaling can also occur without Ret, i.e., via GFRα alone [90], but involves transmembrane proteins such as NCAM [91] that activate Src-like kinase Fyn and focal adhesion kinase FAK, a non-receptor tyrosine kinase.

7.4 "Local" Neurotrophins in the Airway

7.4.1 Neurotrophins in Airway Nerves

Given that neurotrophins promote neuronal structure and function, it is reasonable to assume that innervated organs such as skin, skeletal muscles, epithelia, and smooth muscles express neurotrophins including BDNF [36, 92]. Indeed, neurotrophins have been found to contribute to neuronal plasticity in airways (recently reviewed in [93]). For example, in the context of asthma, there is a role for NGF, mediated through inflammatory cells, where NGF can inhibit eosinophil apoptosis and conversely NGF release from eosinophils increases [93]. In mouse models of asthma, anti-NGF antibody can reduce airway irritability while NGF overexpression is exacerbating [93, 94]. Overexpression of NGF results in increased density of tachykinin-expressing sensory fibers in the airway [95] resulting in increased irritability [96]. NGF can increase substance P in airway nodose neurons [97, 98], induce remodeling of airway parasympathetic ganglia, and enhance dendritic sprouting in parasympathetic neurons.

In spite of these data regarding NGF in airway neuronal plasticity, in terms of asthma pathogenesis, it may be BDNF that is of more interest [12, 99] given its expression in the airways (see below) [12]. BDNF treatment induces increased airway contractility in response to electrical field stimulation of airway nerves, whereas BDNF inhibition blunts ovalbumin effects [100]. There are some data that BDNF effects may be primarily via neuronal changes [100, 101], but several other groups (including ours) have reported BDNF effects on inflammation and ASM per se

[12, 13, 16–18, 102–104]. BDNF itself can induce a phenotypic shift of nodose ganglia neurons such that they express TRPV1 channels [23] and promote airway sensitivity.

Compared to BDNF, there is far less information on GDNF in the airways. GDNF is known to be important in development of airway innervation [105]. In the guinea pig, nodose tracheal Aδ fiber neurons express GFRα1 and are thus likely responsive to GDNF [23, 106]. Indeed, GDNF promotes allergen-induced TRPV1 in these neurons [23] and thus could contribute to AHR.

Locally production of BDNF or GDNF can result in autocrine/paracrine effects on non-neuronal cell types as long as the relevant receptors and signaling pathways are present. There is now data that Trks are widely distributed in non-neuronal tissues [5, 7, 11, 107]. BDNF, TrkB, and p75NTR are localized to different lung compartments including resident immune cells, bronchial and alveolar epithelium, smooth muscle, fibroblasts, and endothelium [11, 108, 109]. The relevance of BDNF to airways then lies in the finding that circulating BDNF and local (airway) receptor expression are both increased in asthma, while BDNF is increased in sputum and bronchoalveolar lavages in patients with asthma or those exposed to cigarette smoke [4, 110–113]. These studies highlight the concept of "local" BDNF as a source as well as target.

While one could expect a similar role for local GDNF in the airways, there is currently little to no data in this regard. GDNF is important for early lung innervation [105] with Ret signaling required for neurogenesis in trachea and primary bronchi [114]. Guinea pigs exposed to ovalbumin show elevated epithelial GDNF, while tracheal neurons show increased TRPV1 in response to GDNF, enhancing airway irritability [23]. However, these studies largely underline a neuronal aspect of GDNF, but there may be other airway cell types that are GDNF sources or targets, particularly in the context of AHR and remodeling. GDNF in bronchial biopsies of COPD patients is associated with mucus hypersecretion [21], and Ret fusion genes and Ret function are thought important in non-small cell lung cancer [115–117].

7.4.2 BDNF in ASM

The ASM layer occupies a major area and mass of the bronchial airways, and thus if any, BDNF produced by ASM has the potential to reach physiological levels. Such ASM-derived BDNF (or that from other resident cells of the airway) can act on ASM itself (i.e., autocrine effects) and have physiological effects. There is now evidence that ASM is a significant source of BDNF. Both the ASM within human lungs [109] and isolated human ASM cells [16] have constitutive ASM BDNF expression. BDNF is localized to ASM of larger airways as well as small airways that are involved in bronchial tone. Importantly, human ASM expresses TrkB [18, 103, 118–121] as well as p75NTR [118] and is thus responsive to BDNF, irrespective of the source of the ligand.

We and others have now demonstrated both mRNA and protein for BDNF in human ASM [18, 103, 120], further showing that asthmatic ASM expresses higher BDNF at baseline [16, 18] while pro-inflammatory cytokines such as TNFα and IL-13 can increase BDNF in non-asthmatic ASM [16], overall consistent with the idea of BDNF linking to asthma. In human ASM, elevation of $[Ca^{2+}]_i$ stimulates BDNF secretion [103]. The mechanisms that regulate $[Ca^{2+}]_i$ in ASM can also modulate BDNF secretion with particular roles for Ca^{2+} influx pathways such as TRPC and Orai1 channels [103, 122–124], which are also involved in exocytosis of other proteins [125]. Pathways that regulate BDNF expression such as PLCγ, TRPC6, Rho kinase, PI3K, ERK, and PKC can also modulate BDNF secretion in human ASM [16]. Thus, it is likely that agonist stimulation and resultant $[Ca^{2+}]_i$ increases in the context of bronchoconstriction enhance BDNF secretion in the airway, while factors such as inflammation increase BDNF. Indeed, smooth muscle-specific BDNF knockout mice that undergo a mixed allergen model of asthma show reduced AHR [17].

In ASM, BDNF can have both rapid, non-genomic as well as longer-term genomic effects. Application of BDNF can rapidly enhance $[Ca^{2+}]_i$ in human ASM cells and potentiate responses to agonists such as acetylcholine or histamine [118].

Such effects of BDNF on $[Ca^{2+}]_i$ mediated exclusively through TrkB (not involving p75) are enhanced by cytokines [119] and in asthmatics [16, 18]. As with neurons, rapid BDNF effects in ASM involve effects on Ca^{2+} influx [118], particularly via store-operated Ca^{2+} entry via TRPC3 and Orai1 [120]. Via PLCγ, BDNF also enhances Ca^{2+} release via IP_3 receptor channels of the sarcoplasmic reticulum. Prolonged BDNF exposure also increases expression of $[Ca^{2+}]_i$ regulatory proteins [120] that allow for increased $[Ca^{2+}]_i$ responses. Furthermore, with activation of pathways such as MAPK, PI3K/Akt, and NFκB, BDNF also increases ASM proliferation [15].

In addition to $[Ca^{2+}]_i$ increase and proliferation, BDNF has been shown to also affect airway fibrosis relevant to asthma [78, 126–129] by enhancing extracellular matrix (ECM) production [130]. In this regard, ECM and BDNF are linked in that matrix metalloproteinases (MMPs), particularly MMP-2 and MMP-9, are involved in extracellularly cleaving pro-BDNF [131–133], while MMPs also process ECM proteins (collagens and fibronectin) produced by ASM and are now shown to be modulated by BDNF. In human ASM, BDNF increases MMP-9 secretion [130, 134].

7.4.3 GDNF in ASM

There are currently no data on GDNF in the ASM beyond the understanding that GDNF is necessary for fetal airway development [105]. GDNF is known to be present in gut smooth muscle [135]. In intestinal smooth muscle, cytokines such as TNFα can upregulate GDNF [136] with downstream effects on enteric neurons that are exacerbated by MMP-9 [137]. The urinary bladder and intestine both express GFRα1 [138]. In ongoing studies (Roos, Teske, Bhallamudi, Sathish, Prakash, unpublished observations), we find that human ASM cells and tissues do express both GDNF and GFRα1 with some, albeit variable, expression of Ret. GDNF is released by human ASM indicating the presence of the machinery required for functional GDNF, especially given that the factors necessary for extracellular cleavage of pro-GDNF such as MMP-9 are known to be expressed also by ASM. Inflammatory factors such as TNFα and TGFβ increase ASM GDNF, GFRα1, and Ret mRNA (albeit to different extents). Importantly, we also find that GDNF is increased in asthmatic ASM and TNFα or TGFβ enhance GDNF in asthmatic ASM, thus linking inflammation, GDNF, and asthma. From a functional perspective, ongoing studies suggest that similar to BDNF, GDNF can also increase $[Ca^{2+}]_i$ in human ASM and promote production of some ECM components such as fibronectin (unpublished observations). Thus, at least preliminarily, it appears GDNF may be important in the asthmatic airway.

7.5 Summary and Conclusions

While signaling via BDNF and to a lesser extent GDNF in the airway has been recognized, a more integrated model for neurotrophin expression and function in the airway, particularly in the context of disease, is relatively underdeveloped. A number of questions regarding neurotrophins in asthma become relevant for future research: (A) Other than ASM, what are the major sources of BDNF or GDNF in the airways, and do their contributions change with disease? (B) What are the primary targets for BDNF vs. GDNF, and by what mechanisms do these neurotrophins exert their effects? Here, given the complexity of signaling by either neurotrophin, understanding cell and context heterogeneity in terms of receptor expression becomes important. Furthermore, a related question becomes what functions BDNF or GDNF are intended to have in specific cell types, e.g., contractility of ASM, neural function, epithelial barrier function, etc. (C) Are there interactions between classical neurotrophins such as BDNF and nonclassical neurotrophins such as GDNF, i.e., can the two mutually enhance (or inhibit) their expression and function. (D) Do BDNF and GDNF play a role across the age spectrum, e.g., how do they contribute to lung development vs. changes in the airway (or in asthma) of the elderly? Ongoing research using in vitro and in vivo approaches ideally with human samples should help address these issues.

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8

Novel Thoracic MRI Approaches for the Assessment of Pulmonary Physiology and Inflammation

Jonathan P. Brooke and Ian P. Hall

Abstract

Excessive pulmonary inflammation can lead to damage of lung tissue, airway remodelling and established structural lung disease. Novel therapeutics that specifically target inflammatory pathways are becoming increasingly common in clinical practice, but there is yet to be a similar stepwise change in pulmonary diagnostic tools. A variety of thoracic magnetic resonance imaging (MRI) tools are currently in development, which may soon fulfil this emerging clinical need for highly sensitive assessments of lung structure and function. Given conventional MRI techniques are poorly suited to lung imaging, alternate strategies have been developed, including the use of inhaled contrast agents, intravenous contrast and specialized lung MR sequences. In this chapter, we discuss technical challenges of performing MRI of the lungs and how they may be overcome. Key thoracic MRI modalities are reviewed, namely, hyperpolarized noble gas MRI, oxygen-enhanced MRI (OE-MRI), ultrashort echo time (UTE) MRI and dynamic contrast-enhanced (DCE) MRI. Finally, we consider potential clinical applications of these techniques including phenotyping of lung disease, evaluation of novel pulmonary therapeutic efficacy and longitudinal assessment of specific patient groups.

Keywords

Thoracic MRI · Hyperpolarized gas · Helium-3 · Xenon-129 · Oxygen-enhanced MRI · Ultrashort echo time · Dynamic contrast-enhanced MRI

Abbreviations

^{129}Xe	Xenon-129
^{3}He	Helium-3
ADC	Apparent diffusion coefficient
ASL	Arterial spin labelling
BOS	Bronchiolitis obliterans syndrome
CF	Cystic fibrosis
CFTR	Cystic fibrosis transmembrane receptor
COPD	Chronic obstructive pulmonary disease
CT	Computed tomography
CTPA	CT pulmonary angiography
DCE	Dynamic contrast enhancement
D_{LCO}	Diffusion capacity of the lung for carbon dioxide
DPD	Dynamic proton density

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DWI	Diffusion-weighted imaging
FEV_1	Forced expiratory volume in 1 second
GRE	Gradient recall echo
ILD	Interstitial lung disease
IPF	Idiopathic pulmonary fibrosis
LAM	Lymphangioleiomyomatosis
LCI	Lung clearance index
LVR	Lung volume reduction
MRA	Magnetic resonance angiography
MRI	Magnetic resonance imaging
OE-MRI	Oxygen-enhanced MRI
OTF	Oxygen transfer function
PE	Pulmonary embolism
PET	Positron emission tomography
PFT	Pulmonary function test
RBC	Red blood cell
RER	Relative enhancement ratio
RF	Radiofrequency
SS	Systemic sclerosis
SUV_{max}	Maximum standardized uptake value
T	Tesla
UTE	Ultrashort echo time
V/Q	Ventilation-perfusion
VDP	Ventilation defect percentage
VDV	Ventilation defect volume
ZTE	Zero echo time

8.1 Introduction

Inflammation dictates much of the discrete repertoire of responses the lungs employ against injury. Sophisticated filtration, removal and immune-mediated pulmonary defences work in parallel to limit entry of pathogens and environmental particulates. When initial defences are overwhelmed, a vigorous acute inflammatory response confines and destroys noxious agents and promotes recovery [1]. An extreme manifestation of this response is the acute respiratory distress syndrome, in which an exaggerated inflammatory cascade disrupts the alveolar-capillary membrane, leading to severe respiratory failure [2]. Persistence of acute inflammation may be followed by a chronic inflammatory response designed to clear necrotic tissue, isolate remaining infective organisms and repair damaged lung. Abnormal chronic inflammation is implicated in many lung diseases, including asthma, chronic obstructive pulmonary disease (COPD), cystic fibrosis (CF) and interstitial lung disease (ILD). In these conditions, chronic inflammation can lead to progressive tissue damage, airway remodelling or established structural lung disease [3–5]. The location and mechanism (including immune cell and cytokine expression) of this inflammation vary, which gives rise to distinct patterns of lung disease.

Novel pulmonary therapeutics such as biologics and cystic fibrosis transmembrane receptor (CFTR) modulators can modify abnormal and excessive inflammation, either by targeting an element of the inflammatory pathway or indirectly downregulating its activity. These therapies mark a paradigm shift in lung disease management towards precision medicine and personalized care, but there is yet to be a similar stepwise change in diagnostic tools.

Conventional respiratory diagnostics include blood tests, pulmonary function tests (PFTs) and a range of thoracic imaging. While the plain radiograph remains a key screening and diagnostic investigation, it is frequently complemented by several other modalities including ultrasound, computed tomography (CT), positron emission tomography (PET) and ventilation-perfusion (V/Q) imaging. CT remains the gold standard for assessment of lung structure and is tremendously versatile as a diagnostic tool for parenchymal lung disease, pulmonary vascular disorders, malignancy and pulmonary infection. The demand for CT imaging in healthcare is continually growing, and developments such as low-dose CT screening for lung cancer will likely see this increase further [6]. However, CT has limited scope for functional assessment, and while PFTs offer a global assessment of airflow, lung volumes and gas transfer, they are insensitive to regionally heterogeneous lung disease.

Although unlikely to replace CT, the novel thoracic magnetic resonance imaging (MRI) approaches discussed in this chapter may offer highly sensitive assessments of regionally heterogeneous lung disease that complement existing

diagnostics. The absence of ionizing radiation also provides a new avenue for longitudinal imaging, which could be useful for the detection of early lung disease progression and evaluation of therapeutic interventions.

8.2 Basic Principles of MRI

MRI is widely used in clinical medicine, most notably for neuro-, cardiac, vascular, soft tissue and abdominal imaging. Standard images are acquired by exploiting the magnetic 'spin' property of protons in hydrogen atoms, applying a complex series of magnetic fields and then using radiofrequency (RF) pulses to localize and characterize those protons in a target tissue [7].

The MRI Scanner

The MR signals used to create an image are generated by a series of magnetic coils contained within the housing of the MRI scanner (Fig. 8.1). The main magnetic coil is a superconducting magnet cooled to approximately −269 °C using cryogenic liquid helium. At this temperature, resistance to the flow of electric current is minimal. Thus, a high electric current flowing through the coil's loops of wire creates a high-strength magnetic field orientated in the z-axis. This strong magnetic field is referred to as B_0 and its field strength is measured in Tesla (T) units [8]. Clinical MRI scanners generally employ 1.5 or 3 T fields, but ultra-high-field scanners up to 11.7 T are currently in development for future research in human subjects [9].

Gradient coils create a secondary magnetic field that distorts B_0 in orthogonal directions. Most MR systems employ three sets of gradient coils, one for each orthogonal plane – x, y and z. The primary function of these coils is spatial encoding of MR signals. Shim coils also adjust B_0, but their purpose is to increase magnetic field homogeneity. This action minimizes local susceptibility effects (e.g. due to a person lying in the scanner) that would otherwise disrupt B_0 field homogeneity and degrade image quality.

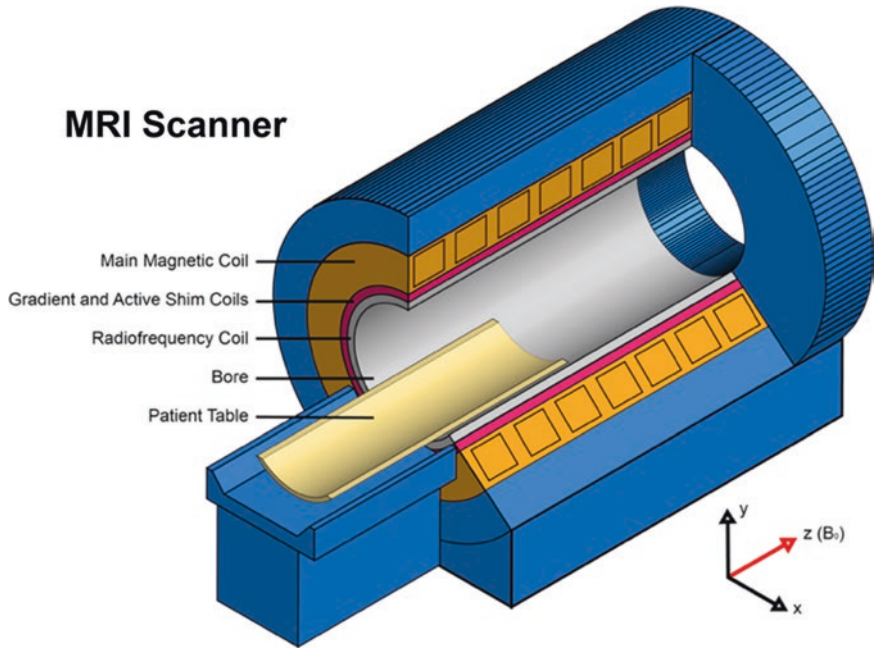

Fig. 8.1 Cross section of an MRI scanner. A closed bore MRI scanner is shown. A concentric series of magnet coils surrounds the bore of the scanner. The main magnetic field (B_0) is orientated in the z-axis, parallel to the scanner's bore. A sliding table allows a subject to be moved into and out of the scanner. (Adapted from Introduction to neuroimaging analysis [10])

RF coils transmit RF energy and detect proton RF signals. Some RF coils only transmit or receive, whereas others can do both. The transmit coil generates an RF pulse of electromagnetic energy that alters the spin of protons in B_0. When the RF pulse is switched off, protons create their own RF signal, which the receive coil can detect. The RF coil magnetic field is called B_1.

The sum of B_1, B_0 and gradient coil magnetic fields is a spatially localized output signal which is detected by the receive RF coil. Complex computer algorithms encode these output signals as volume elements (voxels) which are combined to create an MRI [8].

Basic MRI Physics

The following is an abbreviated explanation of MRI physics, which can be expanded upon with the literature referenced in this section.

The magnetic susceptibility of hydrogen and its abundance within the body are fundamental to conventional MRI. The atomic nucleus of hydrogen consists of a single positively charged proton that spins on its axis. This spinning proton generates a small magnetic field perpendicular to the direction of spin called a 'magnetic moment' [8]. When placed in the strong magnetic field of an MRI scanner, these magnetic moments become aligned to B_0. Most protons stay in a low energy state lining up parallel to B_0, but the remainder occupy a high energy state and instead line up anti-parallel to B_0. This results in protons having a net longitudinal magnetization parallel to B_0 [11, 12]. When in B_0, the spin axis of a proton is altered in a similar fashion to gravity acting upon a spinning top. The rotational motion of this spin axis is called precession. The resonance element of MRI occurs when an RF pulse is applied at the same frequency as the precession rate of these protons in a given magnetic field [13].

When an RF pulse is applied, some protons are flipped from a low to a high energy state, which reduces longitudinal magnetization. Proton spins are also pushed together so they precess in phase. The result is a net transverse magnetization vector relative to B_0 called a flip angle [7].

After the RF pulse is turned off, two types of proton relaxation effect can be measured. T1 relaxation occurs when high energy protons relax into the low energy state, release heat and restore longitudinal magnetization parallel to B_0. T2 relaxation occurs when the positively charged protons repel one another and no longer precess in phase [7]. Tissues in the human body exhibit characteristic differences in T1 and T2 relaxation dependent upon the quantity of hydrogen they contain and the molecular structure of hydrogen containing compounds. This allows for contrast between different tissues and anatomical structures to be detected on an MRI scan.

Greater contrast can be achieved by altering RF pulses or delivering multiple RF pulses in a so-called pulse sequence. Underpinning these concepts are two key MRI parameters: echo time and repetition time. Echo time is the time between delivery of an RF pulse and sampling of the resultant proton MR signal. Repetition time is the duration of one pulse sequence. Adjustment of these parameters can emphasize T1 and T2 relaxation effects resulting in T1- or T2-weighted images [14].

The eventual MRI is comprised of voxels, which represent the location and relative magnetic signal of protons in the scanned tissue. Voxels are conventionally displayed in grayscale, and their brightness varies based on MR signal strength: the stronger the signal, the brighter the voxel. MR signals are localized by gradient coils that apply a magnetic gradient to a slice of tissue and then encode the orthogonal position of protons by adjusting precession frequency (frequency encoding) and precession phase (phase encoding). A composite MR signal is then generated, which is initially stored as K-space data. After MRI acquisition, Fourier transformation is performed by computer software to convert the raw K-space data into an image [12, 15].

8.3 Technical Challenges of Thoracic MRI

MRI has advanced significantly since 1977 when the first in vivo human imaging of a finger and the thorax were performed [16, 17]. Despite this historical starting point, the lungs have been

somewhat of an orphan organ amongst the otherwise extensive use of MRI in contemporary medical care. Instead, CT has been dominant in thoracic imaging given its affordability, speed and ease of interpretation [18]. Modern CT imaging rapidly delivers localized structural data and protocol improvements have significantly reduced ionizing radiation doses without compromising image quality [19]. As such, MRI is perhaps best thought of as a complement to, rather than a replacement for, current thoracic imaging methods. However, the difficulties of applying conventional MRI techniques to the lungs have been a hindrance to its mass adoption. The fundamental issues with performing MRI of the lungs are:

- Low tissue density
- Numerous air-tissue interfaces
- Physiological motion of the heart and thoracic cavity

MRI typically relies on protons in the target tissue to generate an MR signal. Lungs have a relatively low density, with a combined mass of approximately 1 kg in a thoracic volume of 4–5 L for a typical adult [20]. As such, lung proton density is significantly lower than that of other solid organs, which leads to reduced MR signal. Signal is further attenuated by magnetic susceptibility artefact due to the millions of air-tissue interfaces in the lower respiratory tract. These interfaces cause substantial local magnetic field inhomogeneity with rapid loss of proton MR signal during imaging [21]. The result is lung that appears uniformly black and featureless on standard MRI. Third, the physiological motion of the heart and thoracic cavity can produce ghost images and further artefact during MR acquisition, which also degrade image quality [22]. The key strategies used to tackle these issues are:

- Use of intravenous or inhaled contrast agents
- Implementation of specialized lung MR sequences
- Respiratory and cardiac gating

Intravenous gadolinium contrast is widely used for clinical MRI scans, notably in vascular and neuroimaging. Its ability to shorten T1 relaxation creates greater contrast between tissues, and thus pathology can be more easily identified [23]. While this is helpful for pulmonary vascular imaging, the approach does not appreciably improve lung parenchymal images. Instead, lung MRI has seen a predominant focus on inhaled contrast agents such as hyperpolarized noble gases, oxygen and more recently fluorinated hydrocarbons. These substances generate an inherently higher MR signal than the lung itself and facilitate visualization of the airways alongside functional information concerning flow, ventilation and gas exchange [24].

For structural imaging, specialized sequences have been designed to overcome the rapid signal decay that inhibits the use of conventional MRI in the lungs. These sequences minimize so-called echo time, which allows lung MR signal to be acquired before decay occurs. Ultrashort and zero echo time (UTE and ZTE) sequences employ this principle and can produce images of lung parenchyma comparable to CT [25].

Finally, thoracic motion can be addressed in a few ways. For short sequences, a single breath hold may suffice, but longer sequences typically require gating. Respiratory gating allows the subject to free breathe and can be achieved during imaging with an external sensor or belt worn by the subject set to trigger acquisition at the same point in each respiratory cycle [26]. Alternatively, respiratory navigated sequences that identify the diaphragm and automatically trigger acquisition when the diaphragm is in a specified imaging window can be used [27]. ECG gating may also be used to control for cardiac motion, but this significantly prolongs examination time and is probably a lesser priority than control of respiratory motion [28]. All of these methods also assume control of extra-thoracic motion, and as such, subjects must remain as still as possible during an imaging sequence.

8.4 Thoracic MRI Modalities

8.4.1 Overview of Hyperpolarized Gas MRI

As discussed, the lungs are an inherently challenging organ to image with conventional MRI

techniques. An inhaled noble gas was one of the first solutions as demonstrated by Albert et al. in 1994, using hyperpolarized xenon-129 (^{129}Xe) to image ex vivo mouse lungs [29]. Compared with lung, the inherently greater signal of the hyperpolarized gas allowed the airways to be visualized, and this work was soon translated in vivo to human subjects in 1997 by Mugler et al. [30].

A close competitor for ^{129}Xe was another noble gas: helium-3 (^{3}He). The first hyperpolarized ^{3}He images were acquired in guinea pig lungs by Middleton et al., with an improved MR signal when compared to the ^{129}Xe images from 1 year before [31]. ^{3}He then became the favoured hyperpolarized gas in thoracic MRI for many years, as polarization methods and imaging quality were superior. However, scarcity and expense when compared to ^{129}Xe has seen ^{3}He use decline more recently.

A number of adjustments to conventional MRI are required for hyperpolarized gas imaging. First, a polarizer is needed to manufacture hyperpolarized gas by means of spin exchange optical pumping. The scanner itself must also be calibrated for resonance of the noble gases, given the gyromagnetic ratios, and hence Larmor frequencies of ^{129}Xe and ^{3}He differ from that of a proton. Finally, a dedicated radiofrequency (RF) coil, again attuned to the appropriate frequency, is necessary for an image to be generated [32]. While some of this equipment is commercially available, many research teams have developed their own bespoke polarizers and coils instead.

8.4.2 Hyperpolarized ^{3}He MRI

^{3}He is an inert gas, and unlike the more abundant ^{4}He isotope, the odd number of nucleons (two protons and one neutron) facilitates the magnetic spin required for MRI. Early adoption in thoracic MRI was facilitated by sophisticated hyperpolarization techniques, allowing levels of polarization of around 30%, compared with 1–2% for ^{129}Xe [33]. This equated to superior MR signal and image quality, which placed ^{3}He as the frontrunner in hyperpolarized gas MRI research for many years. However, ^{3}He used in medical research is derived from the radioactive decay of tritium (hydrogen-3), a substance historically used in the manufacture of nuclear weapons. In recent years, the supply of tritium has dwindled, which has made use of ^{3}He prohibitive and prompted a move back towards ^{129}Xe [34].

^{3}He imaging is typically performed during a breath hold, where hyperpolarized ^{3}He rapidly diffuses through the airways and remains confined in the lungs. Given its insolubility in lung tissue, side effects are uncommon (~6–7% of subjects) and often mild, for example a self-limiting cough or dry mouth [35]. The inhaled ^{3}He mixture is typically anoxic, and so modest oxygen desaturation (~4%) may be observed, but recovery is usually rapid upon free breathing of room air [36]. An anoxic mixture delays loss of polarity by limiting ^{3}He interaction with paramagnetic oxygen. However, once inhaled, ^{3}He undergoes rapid depolarization, both due to its interaction with oxygen in the airways and the application of RF pulses during imaging [37]. This rapid loss of polarity, alongside the constraint of a single breath hold, means images need to be obtained within approximately 20 seconds. Given the MRI scanner and RF coil are specifically attuned to ^{3}He, the resulting image isolates structures that contain the hyperpolarized gas – in this case, the airways – and excludes the surrounding tissues [38].

Static Ventilation ^{3}He Imaging

In static ventilation imaging, ventilation heterogeneity is localized and quantified during a ^{3}He breath hold. Areas of decreased ^{3}He signal imply a reduction in ventilation, referred to as ventilation defects. These are typically described as the ventilation defect volume (VDV) or ventilation defect percentage (VDP), which are regionally mapped and quantitative measures of pulmonary ventilation [39].

One of the earliest uses of hyperpolarized ^{3}He in human subjects by Kauczor et al. demonstrated ventilation defects in a spectrum of lung diseases. Defects were visible in patients with COPD, bronchiectasis, lung cancer and pleural effusion and correlated well with pathology visible on conventional imaging [40]. Mathew et al. showed defects

in COPD patients varied little for same-day imaging, but changed more after a 1-week interval, despite stable spirometry [41]. As perhaps would be expected, similar studies in asthma have shown ventilation defects can be induced by exercise and methacholine challenge [42] and improve with inhaled beta-agonist administration [43]. More interestingly, longitudinal studies in asthma have shown defects may persist or recur in the same locations, which is thought to reflect areas of chronic inflammation and airway remodelling [44]. Small ventilation defects can also be seen in healthy patients with normal lung function, and these should not be mistaken as pathological during image analysis [45].

In CF, ventilation defects correlate with forced expiratory volume in 1 second (FEV_1) but are also seen in patients with normal range spirometry (Fig. 8.2) [46]. While studies with chest physiotherapy and nebulized DNase have shown little change in global measures of ^{3}He ventilation, regional differences before and after treatment can be detected, which may represent shifting airway secretions [46, 47]. Altes et al. demonstrated ventilation defects decrease in patients with G551D mutation taking ivacaftor, but return to baseline after washout of the drug. Improvements were even seen in patients with normal range spirometry and those with small changes in FEV_1, which supports the potential role of hyperpolarized gas MRI as a sensitive biomarker [48].

Diffusion-Weighted ^{3}He Imaging

Diffusion-weighted imaging (DWI) in conventional MRI assesses the net diffusion of water molecules in tissues [49]. This technique is commonly used in neuroimaging to identify restricted diffusion as seen in acute ischaemic stroke, malignancy and white matter disease [50]. DWI lung MRI instead measures the diffusion of hyperpolarized gas through the airways. ^{3}He DWI is performed during a breath hold, and diffusion is quantified as the apparent diffusion coefficient (ADC). ADC is a relative measure of diffusion restriction and can be represented visually as an ADC map to compare regions of interest [51].

ADC characteristically reduces as airway calibre decreases. This is well demonstrated in healthy lungs where ADC in the major airways is higher, and lower but homogeneous in peripheral airways [52]. In contrast, small airway destruction causes foci of increased ADC as seen in emphysematous lung (Fig. 8.3) [53]. Subclinical lung disease can also be detected, with even very mild emphysematous change demonstrating increased ADC values [54]. In COPD, mean ADC is well correlated with diffusion capacity of the lung for carbon monoxide (D_{LCO}), reinforcing the role of ADC as a surrogate marker of alveolar damage [55]. ADC also shows greater sensitivity than spirometry to detect deterioration in lung function of COPD patients over periods of up to 2 years [56].

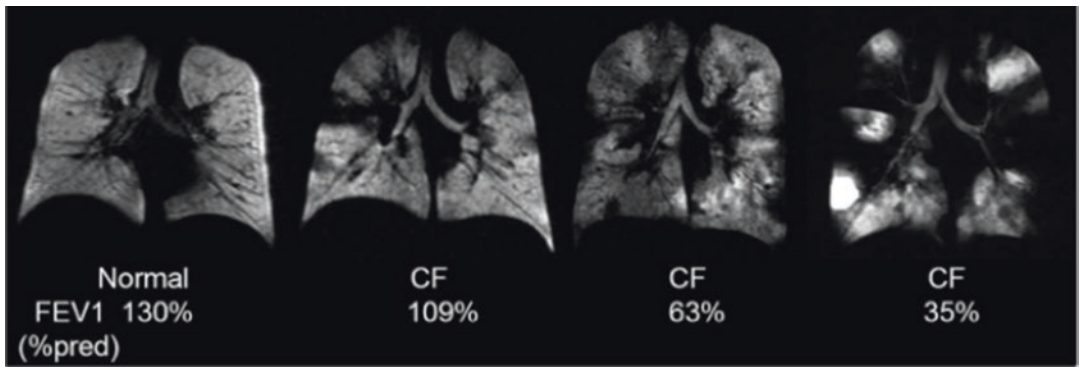

Fig. 8.2 ^{3}He MRI of static ventilation in CF. Comparison of a healthy subject and three adults with CF. An increasing burden of ventilation defects is demonstrated with deteriorating lung function [46]. (Image reproduced with permission of the rights holder. Elsevier – License number: 4858760327184)

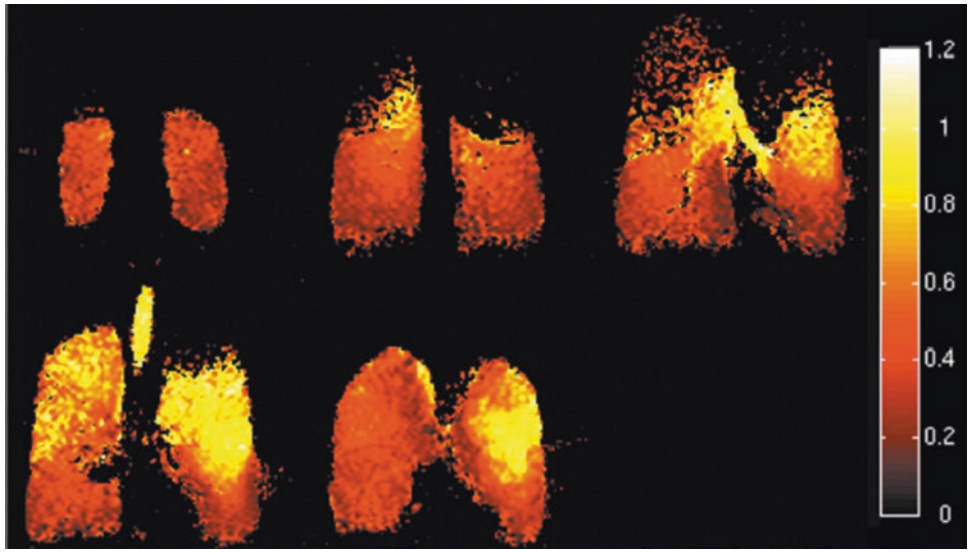

Fig. 8.3 ^{3}He MRI ADC map in severe COPD. Coronal views of a patient with severe COPD show increased ADC values (yellow pixels) in both upper lobes in keeping with emphysematous lung. Similar ADC values are also seen in large calibre airways (trachea and main bronchi). Coloured bar units are cm^2/second [53]. (Image reproduced with permission of the rights holder. John Wiley and Sons – License number: 4858820929850)

In idiopathic pulmonary fibrosis (IPF), mean ADC is also increased as damaged alveoli lose surface area and ^{3}He diffusion becomes less restricted [57]. Chan et al. showed mean ADC correlates with D_{LCO} and CT fibrosis scores and used an alternate DWI metric – the derived mean diffusive length scale – which estimates the mean alveolar dimension in a voxel [58] to demonstrate DWI is sensitive to small changes in IPF lung morphometry over a 1-year period [57].

8.4.3 Hyperpolarized ^{129}Xe MRI

In contrast to ^{3}He, xenon is lipophilic, making it readily soluble in pulmonary tissues as well as the bloodstream. This property is key to its anaesthetic effect but also the basis of dissolved phase MR imaging [30]. Approximately 2% of inhaled xenon dissolves, leaving ample gas for airspace MR signal [34]. The ^{129}Xe isotope used in hyperpolarized MRI is conveniently abundant, comprising roughly a quarter of naturally occurring xenon derived from the atmosphere [32]. ^{129}Xe imaging has demonstrated an excellent safety profile in both healthy volunteers and patients with various lung diseases [59]. Common side effects include tingling, dizziness and euphoria, which are invariably mild and short-lived [60].

Many of the techniques developed for ^{3}He MRI have been applied to ^{129}Xe including ventilation and DWI. ^{129}Xe's solubility in pulmonary tissues has also led to great interest in dissolved phase imaging. As such, the use of ^{129}Xe MRI has grown considerably over the past decade as a virtue of favourable economics, better polarization technology and its scope for unique and sensitive functional lung imaging [34].

Static Ventilation ^{129}Xe Imaging

When the transition of hyperpolarized gas MRI from ^{3}He to ^{129}Xe began, various research groups sought to compare the two modalities. In 2010, Altes et al. showed the imaging quality of both was comparable, and similar ventilation defects could be detected in healthy volunteers and patients with COPD, asthma and CF [61]. However, subsequent work by other groups has highlighted important differences between ^{3}He and ^{129}Xe static ventilation imaging.

An intriguing finding was that some ventilation defects are seemingly missed or 'masked'

with ^{3}He when compared side by side to ^{129}Xe imaging [62]. This was reflected by greater ^{129}Xe VDP in COPD [62] and asthma [63] compared to ^{3}He. Svenningsen et al. investigated asthmatic patients who had previously undergone ^{3}He imaging after methacholine challenge [64] with repeat ^{3}He and ^{129}Xe imaging 1 year later. They found that follow-up ^{129}Xe imaging without provocation testing revealed defects that had previously only been detectable with ^{3}He once methacholine had been given (Fig. 8.4) [63].

The rationale behind this may be the lower diffusion coefficient and higher density of ^{129}Xe, which results in its slower airway transit and delayed filling of poorly ventilated lung [62, 63]. Gas mixtures using ^{129}Xe are typically closer in density to air; hence, their diffusion coefficients are similar. This similarity allows clinically relevant ventilation defects to be visualized with ^{129}Xe, which may otherwise be undetectable with ^{3}He [62].

Static ventilation studies with ^{129}Xe have otherwise explored similar lung diseases to ^{3}He. In COPD, ^{129}Xe ventilation correlates with functional measures including spirometry [62] and V/Q imaging [65]. Ventilation defects improve after beta-agonist use in asthma [63] and may be a more sensitive measure than spirometry to detect lung function decline with advancing age [66]. Elevated VDP and ventilation heterogeneity have been shown in CF subjects with even mild lung disease ($FEV_1 \geq 100\%$) [67], and ^{129}Xe defects correlate with lung clearance index (LCI) in this group [68]. In lymphangioleiomyomatosis (LAM), co-registered ^{129}Xe and CT images have also shown significant ventilation heterogeneity between similarly sized cystic lung volumes, which highlights the merit of combining functional images alongside conventional structural assessments [69].

Diffusion-Weighted ^{129}Xe Imaging

The majority of ^{129}Xe DWI research has been conducted in COPD, where ^{3}He and ^{129}Xe ADC measurements have shown good correlation with one another [62]. When compared to ^{3}He, absolute ^{129}Xe ADC values are smaller [70], which likely reflects xenon's lower diffusion coefficient as described previously.

^{129}Xe ADC correlates with emphysematous burden and alveolar destruction on both CT [71] and ex vivo histological samples [72]. Various groups have also shown strong correlations with spirometry and D_{LCO} measurements. Research in other lung diseases has been more limited, but ^{129}Xe ADC measurements have been successfully performed in CF [73], LAM [69] and ex vivo IPF lungs [72].

Dissolved Phase ^{129}Xe Imaging

Dissolved phase ^{129}Xe MR takes advantage of xenon's solubility in pulmonary tissue to generate quantifiable and spatially localized gas exchange imaging. Xenon follows the same transfer pathway as oxygen, diffusing through the alveolar-capillary unit and then transiently

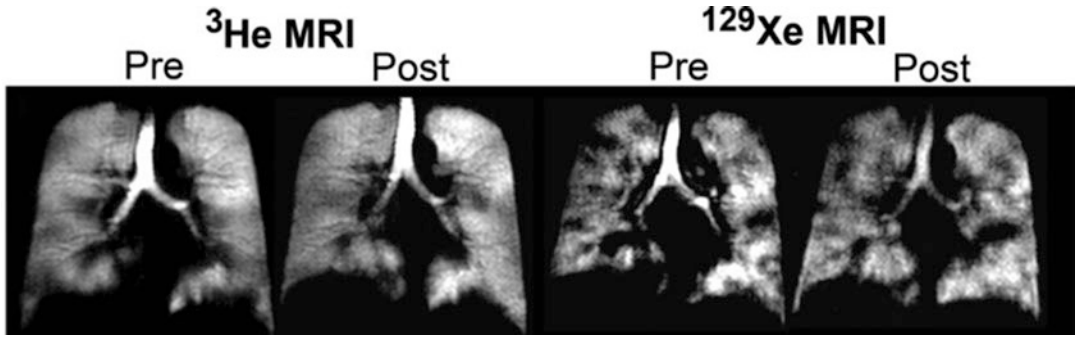

Fig. 8.4 Comparison of ^{3}He and ^{129}Xe static ventilation MRI in a subject with asthma. Coronal views of a patient with asthma taken pre- and post-bronchodilator. ^{129}Xe MRI reveals ventilation defects that are not detected with ^{3}He [63]. (Image reproduced with permission of the rights holder. John Wiley and Sons – License number: 4858821365032)

binding with haemoglobin once in the bloodstream [74]. A chemical shift relative to the gaseous phase occurs when ^{129}Xe diffuses into the pulmonary interstitium (referred to as 'barrier tissues' in dissolved phase imaging) and again upon diffusion into red blood cells (RBCs). Due to chemical shift, each compartment has a distinct ^{129}Xe MR signal – gas, barrier and RBC – that can be detected by selective excitation of the appropriate ^{129}Xe resonant frequency [75].

Early attempts to acquire a dissolved phase image were hampered by low ^{129}Xe polarization levels and poor MR signal [30]. In contrast to the gas phase, relatively little ^{129}Xe dissolves into barrier tissues (roughly 2%), and once there MR signal degrades rapidly [75]. These problems were overcome with frequency-selective RF pulses to isolate a combined barrier/RBC dissolved phase signal sufficient to create an image. These initial studies in healthy volunteers showed a dissolved phase gradient, where MR signal increases in the dependent lung. This is thought to represent increased perfusion and alveolar compression of those areas during imaging [75].

Later studies refined the technique further to generate separate barrier and RBC dissolved phase images [74]. This has allowed better discrimination of the gas exchange mechanics in lung pathology, with a particular focus on ILD. In IPF, Kaushik et al. showed mean RBC signal was decreased and barrier signal increased when compared with healthy controls. This results in a low RBC : barrier ratio which strongly correlates with D_{LCO} [74]. Low RBC/barrier ratio is also seen in COPD, again correlating with D_{LCO} as well as CT emphysema score [76] (Fig. 8.5).

Regional mapping has helped identify three patterns of impaired gas exchange in the dissolved phase imaging of IPF. These are thought to represent different levels of disease activity, which are [78]:

1. Diffusion block – high barrier and low RBC signal
2. End stage fibrosis – low/normal barrier and low RBC signal
3. Early/active disease – high barrier and normal RBC signal

While the 'end stage fibrosis' pattern overlaps with areas of severe fibrosis on CT, the 'early/active disease' pattern lacks such change on conventional imaging. Given a single MRI voxel contains upwards of 40,000 alveoli, these areas may represent early disease that could be used as a functional MR biomarker of inflammation [78]. Finally, recent work with higher field strength MRI has shown the sensitivity of dissolved phase ^{129}Xe can be augmented further to provide greater imaging resolution in IPF as well as other lung diseases [79].

8.4.4 Oxygen-Enhanced MRI (OE-MRI)

Oxygen can also be used as an MR contrast agent in oxygen-enhanced MRI (OE-MRI). However, unlike hyperpolarized gases, oxygen itself is not directly visualized. Instead, the weakly paramagnetic molecular oxygen (O_2) shortens T1 relaxation in lung tissue and the pulmonary circulation during MRI. When 100% oxygen is inhaled, T1 relaxation is shortened by approximately 9% [80], leading to a rise in T1-weighted signal.

Oxygen transport in the lungs is dependent upon ventilation, diffusion and perfusion, such that the T1-weighted signal in OE-MRI is representative of all three processes. It follows that disruption to any of these elements in lung pathology can then affect the oxygen-enhanced signal [81]. Maximal T1 signal is obtained when alveolar capillary blood is saturated with molecular oxygen, and Mai et al. demonstrated this could be achieved with an oxygen flow rate of 15 L/min [82]. Flow rates above this do not increase T1 signal further; hence, OE-MRI sequences typically employ sequential room air and 15 L/min acquisitions.

OE-MRI is typically performed during free breathing with acquisitions taking several minutes to complete. To improve image quality and reduce movement artefact, respiratory gating with navigator echoes that identify the diaphragm during imaging can be used [83]. High-flow oxygen and face masks are inexpensive and widely available, which means there are few barriers to performing

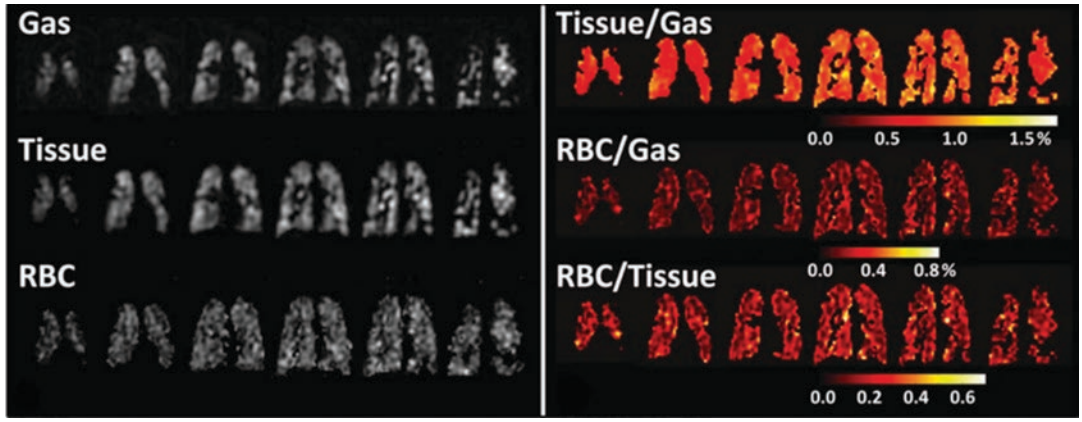

Fig. 8.5 ^{129}Xe dissolved phase MRI in severe COPD. Coronal views of the three ^{129}Xe phases and ratio maps in one subject. A large number of ventilation defects are seen in the gas phase. There is also marked heterogeneity of the dissolved phase and ratio maps [77]. (Image reproduced with permission of the rights holder. John Wiley and Sons – License number: 4858830024322)

OE-MRI with standard clinical MRI scanners. However, MR signal is relatively small when compared to hyperpolarized gases and oxygen itself can alter pulmonary physiology [80]. Data from OE-MRI can be displayed and quantified in several ways, including T1 mapping and calculation of relative enhancement or oxygen transfer. In addition, OE-MRI may also be combined with intravenous gadolinium for V/Q imaging.

T1 Mapping in OE-MRI

T1 maps are one method of visualizing OE-MRI data and are typically colour-coded to represent different T1 relaxations (Fig. 8.6). Images performed with different fractions of inspired oxygen (FiO_2) can then be compared for qualitative evaluation of lung function. In healthy subjects, 100% oxygen causes widespread reduction of T1 relaxation with some heterogeneity [81]. The T1 maps in lung disease are generally even more heterogeneous and exhibit lower T1 relaxation values due to impaired oxygen transport [84].

Renne et al. demonstrated heterogeneity of T1 maps in lung transplant recipients with bronchiolitis obliterans syndrome (BOS), but median T1 relaxation values could not discriminate between stages of disease [86]. However, other studies have verified the regional sensitivity of lung T1 measurement. Jakob et al. identified focal lung disease in CF that exhibited both blunted T1 relaxation and matched perfusion abnormality [87]. Similar findings have also been shown in patients with CF receiving nebulized hypertonic saline [88].

Relative Enhancement and Oxygen Transfer Function

To help describe and visualize regional lung function in OE-MRI quantitatively, the terms relative enhancement ratio (RER) and oxygen transfer function (OTF) have been developed. First, RER describes the change in T1 signal intensity of spatially matched voxels between room air and 100% oxygen images [89]. It can be represented visually as a relative enhancement map or alternatively several regions of interest can be identified and the RER for each one calculated. Ohno et al. used these methods to show markedly lower RER in patients with lung cancer and emphysema compared with healthy volunteers. This study also showed that mean RER strongly correlated with FEV_1 and D_{LCO} [89]. The same research group has since corroborated these findings in a larger cohort of COPD patients [90] and found similar but weaker correlations in patients with asthma [91] and ILD [92].

OE-MRI VDP can also be derived from RER and has shown strong correlation of ^{3}He VDP

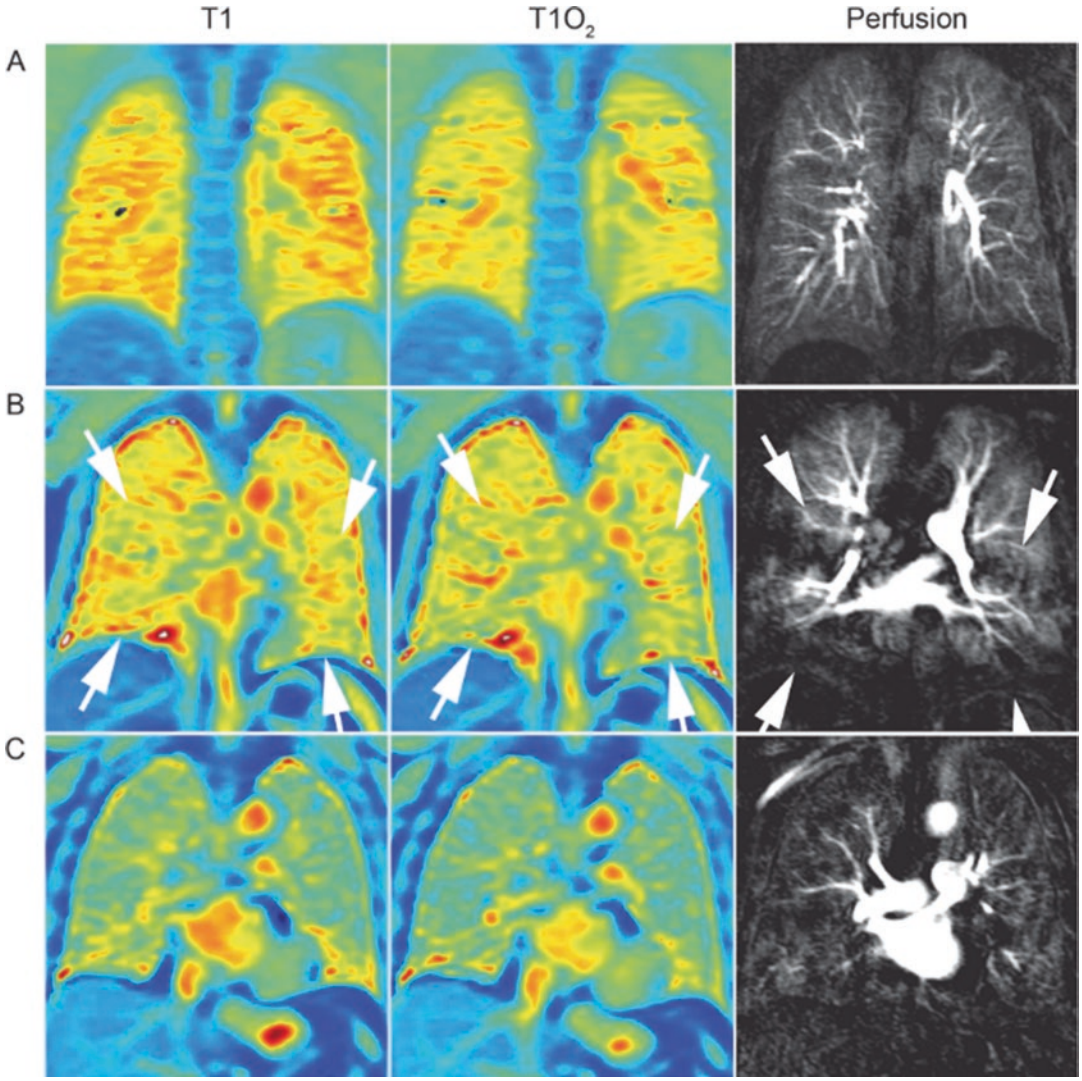

Fig. 8.6 OE-MRI T1 maps and DCE perfusion MRI. Coronal views of three subjects: (**a**) healthy subject, (**b**) and (**c**) COPD. Reduction in oxygen-enhanced signal with 100% oxygen ($T1O_2$). Signal is significantly diminished in COPD subjects. Minor ventilation and perfusion abnormalities are demonstrated in subject **b** (white arrows). More marked abnormalities are seen in subject **c** [85]. (Image reproduced under Creative Commons Attribution License)

measurements in adults with CF. However, OE-MRI VDP measures were approximately 5% lower than ^{3}He VDP [93]. This likely reflects key differences in the performance of these techniques as OE-MRI has a longer wash-in time and lower spatial resolution and measures a combination of ventilation, diffusion and perfusion as previously discussed.

OTF describes the change in lung T1 relaxation rate (R1) for a given oxygen concentration and represents a combination of airflow, oxygen diffusion and lung perfusion [86, 87]. In the original paper, adults with CF showed significant OTF heterogeneity and areas of poor oxygen transfer also demonstrated MR perfusion abnormalities [87]. Renne et al. later examined the effect of endoscopic allergen testing on OTF and

airway eosinophil count in asthma. Their study showed OTF decreased in airway segments exposed to allergen, with a corresponding airway eosinophilia. Follow-up MRI after 24 hours showed OTF then returned to baseline [94]. The same research group has also measured OTF in lung allograft recipients finding it is significantly lower in patients with evidence of BOS [86].

Ventilation/Perfusion OE-MRI

V/Q imaging was part of the inception of OE-MRI in 1996. Edelman et al. compared gadolinium-based perfusion imaging alongside oxygen-enhanced ventilation images to demonstrate V/Q mismatch [95]. In patients with COPD, oxygen enhancement is also markedly abnormal and strongly correlated with perfusion abnormalities [85].

Arterial spin labelling (ASL) has been used as alternative measure of perfusion for V/Q imaging in combination with OE-MRI. ASL precludes the need for an injected contrast agent and instead uses magnetically labelled arterial blood as a tracer [96]. In healthy volunteers, V/Q imaging has been successfully performed using this method, including the demonstration of a matched V/Q defect in a subject following left upper lobectomy [97].

8.4.5 Ultrashort Echo Time (UTE) MRI

Ultrashort echo time (UTE) is a proton-based MRI modality and was first described by Bergin et al. as a means of obtaining structural lung images [98]. This is achieved by minimizing the delay between application of an RF pulse and detection of the resulting MR signal. The resulting UTE images were comparable to CT of the time.

Given the rapid decay of lung MR signal during MRI, the echo time for UTE is by necessity ≤200 μs [21]. So-called zero echo time (ZTE) sequences reduce this further to as little as 5 μs, but the exact echo time achievable is limited by the software and hardware constraints of the MR platform used [99].

Typically, UTE sequences also employ specialized radial sampling approaches to acquire imaging data, which contrast with the Cartesian sampling methods used for conventional MRI [100]. This method helps to minimize motion artefact and facilitate free-breathing scans through respiratory gating [101]. Recent UTE techniques with self-gating discard any motion-corrupted data and use the remaining data to create the final images [102]. The result is a signal-averaged MRI scan with improved resolution by virtue of the pooled imaging data [103].

UTE MRI for Assessment of Structural Lung Disease

Neonatal intensive care patients are particularly prone to pulmonary morbidity due to prolonged periods of oxygen therapy and mechanical ventilation. Self-gated UTE can produce CT-like images in these patients by controlling for bulk movement and respiratory motion without the need for sedation [104]. In this way, end-inspiratory and -expiratory images can estimate tidal volume and identify structural lung change in bronchopulmonary dysplasia (BPD) [102, 105]. In BPD, preliminary studies have suggested UTE can be used to quantify hyperinflation to predict clinical outcomes, and could be used for longitudinal follow-up [104, 105].

In infants with CF, UTE has demonstrated good correlation with CT for bronchiectasis and bronchial wall thickening [106]. Similar structural imaging has also been demonstrated in adults with CF using free-breathing UTE acquisitions lasting 8–15 minutes (Fig. 8.7) [107].

In COPD, UTE shows short-term reproducibility over a 3-week period [108] and can produce structural information comparable to CT [109]. Chassagnon et al. compared a cohort of systemic sclerosis (SS) patients with and without evidence of ILD on CT. In this study, elastic registration of inspiratory and expiratory UTE showed increased lung stiffness in patients with SS-related ILD, corresponding with areas of fibrosis on HRCT [110].

UTE has also shown promising results in the detection and morphological characterization of lung nodules. Studies have shown UTE can detect

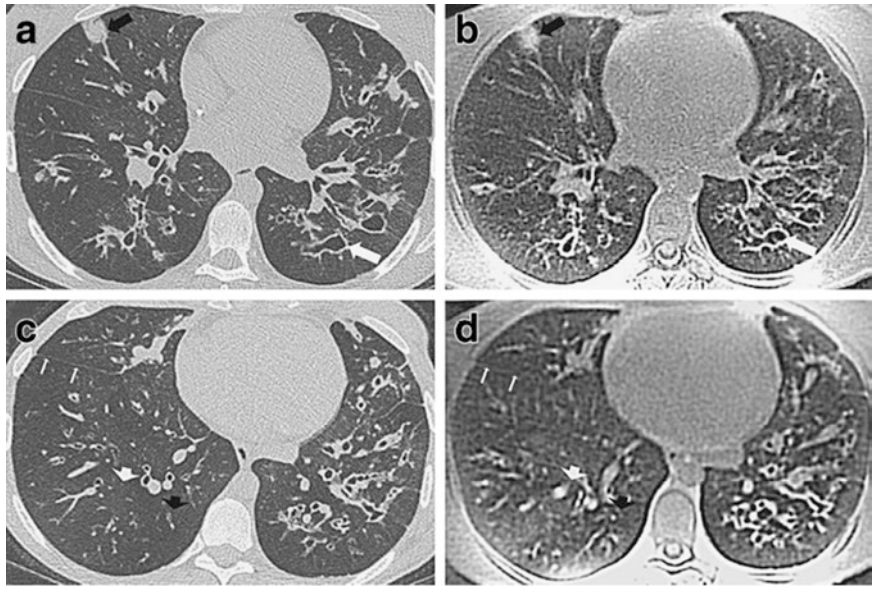

Fig. 8.7 Axial CT and UTE MRI in an adolescent with CF. CT (**a**, **c**) and UTE MRI (**b**, **d**) slices show evidence of nodular consolidation (black arrow in **a** and **b**) and widespread bronchiectatic change [107]. (Image reproduced with permission of the rights holder. Springer Nature – License number: 4858830473723)

between 73% and 86% of nodules when compared to CT, but is markedly less sensitive for identification of very small modules (i.e. those <4 mm) [111, 112]. It also tends to underestimate long- and short-axis nodule measurements by up to 1–2 mm [113].

UTE MRI for Assessment of Lung Function

UTE is an appealing foundation for co-registered structural and functional lung MRI as it is capable of reducing acquisition times and capturing motion-insensitive images during free breathing.

Sheikh et al. demonstrated a variation of UTE imaging – dynamic proton density (DPD) – in healthy volunteers and patients with asthma, comparing them to hyperpolarized ^{3}He MRI. Breath hold UTE images were acquired and used to generate DPD maps that reflect the difference in UTE signal intensity between full inspiration and expiration. This technique demonstrated ventilation heterogeneity and produced functional data comparable to ^{3}He imaging in patients given methacholine and salbutamol [114].

UTE can also be combined with inhaled contrast agents such as ^{129}Xe and oxygen to augment pulmonary assessment. For ^{129}Xe MRI, UTE sequences can improve image resolution and decrease breath hold times when compared to the conventionally used gradient recall echo (GRE) sequences [115]. Shortened T1 relaxation time in the presence of 100% oxygen also makes UTE desirable for OE-MRI and allows whole lung acquisitions with isotropic resolution in as little as 5 minutes alongside simultaneous structural imaging [116].

8.4.6 Dynamic Contrast-Enhanced MRI

Dynamic contrast-enhanced (DCE) MRI uses gadolinium-based intravenous contrast agents for pulmonary imaging. As discussed previously, gadolinium shortens T1 relaxation, which creates contrast between imaged tissues [23]. While this is less helpful for imaging lung parenchyma (given T1 relaxation values are already very short), gadolinium is well suited to pulmonary vascular imaging and can be used to evaluate abnormal lesions through measurement of changes in perfusion and vascular permeability.

Pulmonary Vascular Imaging with Gadolinium

MR angiography (MRA) with gadolinium can be used to evaluate acute and chronic pulmonary vascular disease. For the diagnosis of chronic thromboembolic pulmonary hypertension, the performance of MRA is comparable to CT angiography, but the extent of disease is still better characterized with CT [117]. The use of MRA in pulmonary embolism (PE) has historically been less successful; the multicentre PIOPED III study found a quarter of MR images were inadequate and overall 43% of PEs were missed [118]. A later study by Schiebler et al. significantly improved on this, with 97.4% of scans of diagnostic quality and a 1-year negative predictive value of 97% for PE [119]. In clinical practice, MRA may yet become a suitable alternative to CT pulmonary angiography (CTPA) when radiation exposure and iodinated contrast agents need to be avoided.

Assessment of Parenchymal Lung Disease with DCE MRI

DCE MRI may be used to evaluate inflammatory activity and characterize severity of ILD. Chin et al. measured time to peak contrast enhancement after gadolinium injection in ILD patients and correlated these findings with imaging-targeted lung biopsies [120]. Areas found to be inflammatory predominant on biopsy were characterized by early contrast enhancement, whereas fibrotic-predominant areas displayed late enhancement. More recently, Buzan et al. compared peak contrast enhancement with disease severity (assessed instead by CT) in a mixed group of ILD patients [121]. They found non-IPF patients had earlier peak enhancement than the IPF cohort, but only in the non-IPF group could severity of lung disease be discriminated by time to peak enhancement. These findings may represent different vascularity at the histological level, whereby less severe or actively inflamed lesions in ILD demonstrate greater vascularization and permeability to contrast. Conversely, severely fibrotic areas in IPF have low vascularity and hence delayed contrast enhancement. These inferences are similar to those encountered with dissolved phase ^{129}Xe MRI [78], and so DCE MRI may present an alternate avenue for assessment of lung disease activity and response to pulmonary therapeutics in ILD.

In children with CF, early detection of lung disease may also be possible with DCE MRI. Amaxopoulou et al. demonstrated a spectrum of perfusion deficits despite normal appearances of lung parenchyma on structural imaging [122]. This is likely a reflection of small airways disease that would otherwise not be detectable with standard imaging. Kellenberger et al. also measured perfusion abnormalities in a mixed cohort of paediatric patients with congenital thoracic malformations [123]. At peak enhancement, perfusion deficits were evident in areas of hyperinflation, cystic malformation, bronchopulmonary sequestration and bronchogenic cysts. Both studies show DCE MRI can add highly sensitive functional data to proton-density imaging, which together provide a comprehensive assessment of complex thoracic abnormalities in the paediatric population.

Assessment of Pulmonary Nodules and Malignancy with DCE MRI

Complex pharmacokinetic parameters of gadolinium enhancement in pulmonary nodules and lung cancers have been explored by several groups as a means of differentiating benign and malignant aetiologies. Ohno et al. found DCE MRI measures of perfusion were comparable to the PET-CT maximum standardized uptake value (SUV_{max}) in the differentiation of solitary pulmonary nodules [124]. Other groups have also suggested a role for DCE MRI in the risk stratification of malignancy, notably for evaluation of radiologically indeterminate lesions [125, 126].

DCE MRI biomarkers have also been evaluated as potential predictors of anti-cancer therapy. Huang et al. found DCE MRI-derived markers of tumour perfusion and vascular permeability (K_{trans} and K_{ep}) were correlated with both SUV_{max} and decreased tumour size in lung cancer patients 6 weeks after radiotherapy [127]. Xu et al. similarly found that after 1 week of chemotherapy, tumour K_{trans} and K_{ep} decreased significantly in lung cancer patients defined later as treatment

responders according to conventional CT criteria [128]. As such, these MR imaging-based biomarkers could offer sensitive early measures of treatment response to complement existing imaging techniques.

8.5 The Potential Role of Thoracic MRI in Respiratory Medicine

At present, the thoracic MRI modalities discussed in this chapter are predominantly used as research tools. Clinical translation of these techniques is a complex matter and requires technical hurdles to be addressed alongside consideration of application and health economics. For certain modalities, such as hyperpolarized gas MRI, their cost and technical requirements will likely be prohibitive for some institutions. Instead, delivery by specialist tertiary centres may be more feasible. It is then important to consider how these imaging techniques can answer key research questions and complement existing clinical methods of assessing lung structure and function.

One of the most often cited advantages of thoracic MRI is the absence of ionizing radiation. X-ray-based investigations can deliver substantial radiation doses, and so their use should be carefully rationalized by clinicians. The stewardship of ionizing radiation is particularly relevant in the following situations:

- For patients with long-term/lifelong conditions who may require serial imaging
- The investigation of thromboembolic disease in pregnancy, where radiation exposure to the breast tissue may increase future cancer risk [129]
- When minimizing radiation exposure is essential, such as in ataxia-telangiectasia where faulty DNA repair mechanisms greatly increase lifetime cancer risk [130]

However, potential limitations of thoracic MRI must also be considered as some techniques may be particularly challenging for certain patients:

- Modalities requiring prolonged scanning time may be uncomfortable for younger patients or patients who struggle to lie flat for extended periods due to breathlessness.
- Patients with significant breathlessness or cough may also find breath hold manoeuvres difficult during techniques like hyperpolarized gas MRI.
- Inhalation of anoxic contrast agents (viz. ^{3}He and ^{129}Xe) may be unsuitable in patients with severe lung disease due to risk of hypoxia.
- Some inhaled contrast agents can also cause sedation: ^{129}Xe is known to have anaesthetic effects [131], and high-flow oxygen can precipitate hypercapnic respiratory failure in susceptible patients [132].

Therefore, wider use of thoracic MRI requires evaluation of both its merits and its clinical practicality. As highlighted previously, there are some discrete situations where techniques such as UTE MRI or MRA could be the preferred imaging method for specific patient groups. However, the complete replacement of conventional studies that use ionizing radiation remains impractical given the current demands and financial models of healthcare [133].

Phenotyping Lung Disease with Thoracic MRI

Some thoracic MRI research has focused on the phenotyping of airways disease, namely in asthma and COPD. Increasingly, different asthma phenotypes are recognized, which has allowed treatments such as biologics to be tailored to the individual patient [134]. Phenotyping of asthma with MRI shows promise and highlights some of the difficulties encountered in the assessment of asthma severity. Hyperpolarized gas MRI can demonstrate regional ventilation defects, and while correlation with disease severity and spirometry is observed, some patients have marked ventilation defects in the presence of preserved spirometry [135]. When compared to other measurements such as CT and provocation testing, ventilation defects can also be indicative of regional airway remodelling [136]. Therefore, MRI may be particularly interesting when its findings are discordant with standard diagnostic tools like spirometry.

Historically, COPD has been divided into emphysematous and chronic bronchitis pheno-

types, but broader classification based on anatomical, physiological or pathophysiological criteria has been suggested [137]. Some of these patterns of disease can be demonstrated using MRI, which could then be used to guide therapy. One example is lung volume reduction (LVR), given the increasing use of endobronchial valves. Patient selection for LVR is key, with favourable outcomes often linked to upper lobe predominant emphysema [138]. However, valve insertion in lower lobe predominant emphysema has also proven useful when collateral ventilation is minimal [139]. Hyperpolarized ^{3}He MRI has been used retrospectively to identify alternate targets for endobronchial valve insertion undetected on CT. In theory, this may increase the number of patients to whom LVR could be offered, but further research is required [140]. ^{3}He MRI has also been used to detect bronchodilator response [141] and identify patients with the 'frequent exacerbator' phenotype [142], but these applications would likely be harder to justify in clinical practice.

Assessing Response to Novel Therapeutics

It has been established that evidence of lung disease can be detected in patients with CF who have normal spirometry using MRI and lung clearance index (LCI) [143, 144]. As such, traditional measures like FEV_1 may lack the sensitivity required for future clinical practice and research trials. Instead, thoracic MRI using hyperpolarized gases or non-contrast functional measures could serve as imaging-based biomarkers to evaluate therapies like CFTR modulators and aid longitudinal monitoring of lung disease [48, 145].

As discussed previously, hyperpolarized ^{129}Xe and DCE MRI methods may become useful in assessing different levels of disease activity in ILD [78, 121]. In particular, functional imaging with hyperpolarized ^{129}Xe demonstrates longitudinal deterioration of gas exchange in IPF with a greater sensitivity than transfer factor (D_{LCO}) [146]. In this way, early detection of lung disease progression could be feasible and become an invaluable tool for the evaluation of novel therapeutics.

8.6 Conclusion

There have been tremendous advances in thoracic MRI since the pioneering hyperpolarized gas and structural imaging studies of the mid-1990s. However, widespread adoption is yet to be realized with CT remaining the workhorse of cross-sectional lung imaging in clinical practice.

Structural imaging without ionizing radiation already has clear clinical applications, but further refinements to improve spatial resolution are needed to bridge the gap between thoracic MRI and CT. Functional imaging shows tremendous promise, and we can expect this to become increasingly relevant in the delivery of cutting-edge medical therapies that require highly sensitive measures of lung function.

Substantial work is still required for clinical translation, but the potential of co-registered structural and functional imaging without ionizing radiation is an exciting prospect for the future of respiratory care.

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9 Overview on Interactive Role of Inflammation, Reactive Oxygen Species, and Calcium Signaling in Asthma, COPD, and Pulmonary Hypertension

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Abstract

Inflammatory signaling is a major component in the development and progression of many lung diseases, including asthma, chronic obstructive pulmonary disorder (COPD), and pulmonary hypertension (PH). This chapter will provide a brief overview of asthma, COPD, and PH and how inflammation plays a vital role in these diseases. Specifically, we will discuss the role of reactive oxygen species (ROS) and Ca^{2+} signaling in inflammatory cellular responses and how these interactive signaling pathways mediate the development of asthma, COPD, and PH. We will also deliberate the key cellular responses of pulmonary arterial (PA) smooth muscle cells (SMCs) and airway SMCs (ASMCs) in these devastating lung diseases. The analysis of the importance of inflammation will shed light on the key questions remaining in this field and highlight molecular targets that are worth exploring. The crucial findings will not only demonstrate the novel roles of essential signaling molecules such as Rieske iron-sulfur protein and ryanodine receptor in the development and progress of asthma, COPD, and PH but also offer advanced insight for creating more effective and new therapeutic targets for these devastating inflammatory lung diseases.

Keywords

Inflammation · Ca^{2+} signaling · Reactive oxygen species · Rieske iron-sulfur protein · Nicotine · Contraction · Remodeling · Asthma · Chronic obstructive pulmonary disorder · Pulmonary hypertension

Abbreviations

ASK1	Apoptosis signal-regulating kinase 1
ASMC	Airway smooth muscle cell
ATM	Ataxia-telangiectasia mutated
BALF	Bronchoalveolar lavage fluid
CaM	Calmodulin
CDK	Cyclin-dependent kinase
CICR	Calcium-induced calcium release
CIRG	Calcium-induced ROS generation
COPD	Chronic obstructive pulmonary disease
CS	Cigarette smoke
DAG	Diacylglycerol

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DAMP	Damage-associated molecular pattern
ECM	Extracellular matrix
ETC	Electron transport chain
GPCR	G protein-coupled receptor
Gpx	Glutathione peroxidase
GSH	Glutathione
HIF-1α	Hypoxia-inducible factor-1α
HPV	Hypoxic pulmonary vasoconstriction
IKK	IκB kinase
IP_3	Inositol triphosphate
IP_3R	Inositol-1,4,5-triphosphate receptor
Kv	Voltage-gated potassium
LTCC	L-type voltage-gated calcium channel
MAPK	Mitogen-activated protein kinase
MLCK	Myosin light chain kinase
MMP	Matrix metalloproteinases
nAChR	Nicotinic acetylcholine receptor
NADPH	Nicotinamide dinucleotide phosphate
NEMO	NF-κB essential modulator
NF-κB	Nuclear factor-κB
NIK	NF-κB-inducing kinase
NLR	NOD-like receptor
NOS	Nitric oxide synthase
PA	Pulmonary artery
PAMP	Pathogen-associated molecular pattern
PH	Pulmonary hypertension
PKC	Protein kinase C
PPA	Pulmonary arterial pressure
PRR	Pattern recognition receptor
PVR	Pulmonary vascular resistance
RHD	Rel homology domain
RICR	ROS-induced calcium release
RISP	Rieske iron-sulfur protein
ROS	Reactive oxygen species
RyR	Ryanodine receptor
SMC	Smooth muscle cells
SR	Sarcoplasmic reticulum
TAK1	TGF-β-activated kinase 1
TLR	Toll-like receptor
TNF-α	Tumor necrosis factor-α
TRP	Transient receptor potential
TRPC	Canonical TRP

9.1 Introduction

Asthma, COPD, and PH are considered common chronic lung inflammatory diseases [1–5]. These three diseases persist in the presence of specific triggers such as environmental irritants (e.g., airborne dust particles) or inhaled irritants such as cigarette smoke (CS) [1, 3, 5]. Exposure to these triggers leads to the activation of the inflammatory cells (i.e., macrophages, neutrophils, and T cells). Although these diseases are characterized as chronic inflammatory disorders, the underlying signaling mechanisms are shared and distinct to each disease.

9.1.1 Asthma

Asthma is a chronic respiratory condition characterized by narrowing airways due to inflammation and overproduction of mucus [3, 5]. While usually minor, asthma can be a significant problem that interferes with daily activities, worsened by strenuous physical activity, and may lead to a life-threatening asthma attack [5].

Asthmatic symptoms will vary from person to person, varying in frequency in asthma attacks and severity in attacks and other symptoms. Asthma symptoms often include shortness of breath, chest tightness, wheezing when exhaling, and trouble sleeping caused by shortness of breath, coughing, or wheezing [3]. Specific environments or situations can cause asthmatic flare-ups, which include exercise-induced asthma, occupational asthma (triggered by workplace irritants like fumes, gases, or dust), and allergy-induced asthma (triggered by an airborne substance like pollen, spores, or pet dander) [3, 5].

Complications that arise from asthma can include interference with sleep, work, other activities, permanent narrowing of the airways, hospitalizations for severe attacks, and side effects from long-term use of medications to stabilize severe asthma.

9.1.2 COPD

COPD is a chronic inflammatory disease characterized by the obstruction of airflow due to the narrowing of the airways [6, 7]. It is the third leading cause of death and affects approximately 16 million people in the United States [6]. According to a report from the Centers for Disease Control and Prevention, COPD is more likely to occur in people aged 65 and older, women, current and former smokers, and people with a history of asthma [4, 6, 8, 9].

COPD presents with pulmonary and extrapulmonary manifestations. As the disease progresses, respiratory symptoms include frequent coughing and/or wheezing, excess mucous production, shortness of breath, and tight chest. Approximately 10–30% of patients with moderate to severe COPD will develop pulmonary hypertension (PH), as defined by a PA pressure greater than 20 mmHg at rest [1, 10]. This physiological state of the pulmonary vasculature is correlated with increased mortality and morbidity.

Patients with COPD often show cardiac manifestations. Patients with COPD carry an increased risk of death due to cardiac arrhythmias, myocardial infarctions, coronary artery disease, or congestive heart failure, caused by increased sympathetic tone [11–13]. Two-thirds of these patients show evidence of right ventricular hypertrophy as indicated by right heart catheterization [12]. Additionally, these cardiac manifestations may also be linked to chronic or intermittent hypoxia-induced vascular remodeling and hyperresponsiveness. The systemic inflammation associated with COPD can also contribute to the development and progression of atherosclerosis. Pulmonary manifestations of COPD (i.e., hypoxemia, systemic inflammation, and arterial stiffness) often exacerbate cardiac manifestations, increasing the cardiovascular risk of disease and further worsening COPD symptoms.

9.1.3 PH

PH is characterized as an increased pulmonary arterial pressure (P_{PA}), $P_{PA} > 20$ mmHg at rest, and is a result of pulmonary vasoremodeling and vasoconstriction of the PA [1, 10, 14]. A high percentage of COPD patients develop pulmonary hypertension [1, 10]. PH is associated with increased exacerbation and decreased survival with COPD. Although this devastating disease is relatively common, the underlying mechanisms are still unknown, with treatments remaining ineffective.

9.1.4 Causes and Risk Factors

9.1.4.1 Asthma

Though asthma is prevalent, affecting 1 in every 13 people, the cause of asthma is not very clear. It is thought to be a combination of environmental and genetic factors. Exposure to irritants and allergens can trigger and exacerbate an asthma attack. These irritants and triggers include airborne allergens (i.e., pollen, dust mites, mold, pet dander), physical activity, cold air, and air pollutants (e.g., cigarette smoke) [3, 5, 15].

Several risk factors may increase the chances of developing asthma, such as having a familial history of asthma, allergies, being overweight, cigarette smoking habits, exposure to secondhand smoke, and exposure to occupational triggers [15].

9.1.4.2 COPD

Several factors can cause COPD; however, chronic obstructive pulmonary disease is ultimately due to long-term exposure to irritants that damage the lungs and airways, thereby promoting inflammation and remodeling of the vasculature and airways [2, 4, 6]. Smoking is recognized as the most important causative factor in developing COPD with nicotine as an active ingredient in cigarette smoke (CS). Studies have shown that approximately 50% of smokers will eventually develop COPD defined by the Global Initiative for Chronic Obstructive Lung Disease (GOLD) guidelines [16]. Although smoking remains the most causative agent in developing COPD, other risk factors such as air pollution, respiratory infections, poor nutrition, and chronic asthma can also promote the development of COPD [2, 4, 7, 17, 18].

In addition to chronic exposure to these irritants, numerous risk factors increase the chances of developing COPD. A hereditary deficiency in alpha-1 antitrypsin (AATD) is a genetic risk factor in COPD [2, 4, 7]. Age and gender also play a significant role in COPD, where those ages 65 or older and females are at an increased risk of developing COPD. People diagnosed with asthma are at a greater risk for COPD due to the pre-existing airflow limitation from airway hyperresponsiveness and remodeling. In addition to childhood asthma, a history of severe respiratory infections has been associated with reduced lung function and an increased risk for respiratory complications in adulthood [7].

9.1.4.3 PH

Although people of all ages, races, and sexes can be diagnosed with PH, certain risk factors make some more likely to get the disease. These risk factors include family history, obesity, gender, pregnancy, altitude, drug use, and cigarette smoking [1, 10, 14]. Obesity alone is not a risk factor; however, if combined with obstructive sleep apnea, it may result in mild PH. Idiopathic and heritable/familial PAH is more common in women with pregnant females, and females of childbearing age are more susceptible to develop PH. Living in high altitudes for years can influence the development of PH. Additionally, other diseases such as congenital heart disease, lung disease, and liver disease can lead to the development of PH [11, 13].

9.1.5 Treatments

There is currently no cure for asthma, COPD, or PH. In many ways, treatments for asthma, COPD, and COPD-associated PH are similar. Management of asthma- and COPD-exacerbating triggers and symptoms is the primary method of improving quality of life and slowing disease progression [2, 4, 7, 14]. For optimal management of the disease, both non-pharmacological and pharmacological treatments are required. In a non-pharmacological treatment, lifestyle changes such as smoking cessation (for smoking COPD patients) and avoiding airborne irritants such as secondhand CS and other air pollutants like dust and noxious fumes [2] are necessary to prevent exacerbating symptoms.

There are several pharmacological treatments for asthmatic and COPD patients. Often, treatments are combinations of different agents, individualized per patient based on the severity of symptoms, exacerbation triggers, and exposure to triggers. Comorbidities of patients must also be considered to avoid worsening conditions and complications.

Pharmacological treatments are aimed at (1) dilators of the airways to increase airflow (FEV_1) and (2) anti-inflammatory agents to reduce inflammation [8, 19, 20]. Bronchodilators are used to increase airflow, working as either β2 agonists or muscarinic receptor antagonists. β2 agonists, either short-acting or long-acting, relax airway smooth muscle by activating β-adrenergic receptors, thus dilating the airways. However, β2 agonists may have some adverse effects in older patients with disturbing cardiac rhythms. Muscarinic receptor antagonists, also known as antimuscarinic drugs, block bronchoconstriction caused by acetylcholine-induced activation of the M3 muscarinic receptors in the airway smooth muscle [6, 8, 19, 20].

Anti-inflammatory agents are used to treat the underlying systemic inflammation associated with asthma and COPD. The maintenance of asthma- and COPD-related inflammation is vital to reduce exacerbations and disease progression. Inhaled corticosteroids are often prescribed in combination with bronchodilators [20]. However, there are several risks in treating COPD with inhaled corticosteroids, which involve the risk of pneumonia, oral candidiasis, hoarseness, and withdrawal symptoms once treatment is ceased [6, 8, 20].

Although treatments have minimized complications and slowed disease progression in asthma and COPD patients, there is no cure for the disease. Further studies must be done to develop a specific treatment that targets the underlying pathophysiology that leads to the development and progression of asthma and COPD.

9.2 Cellular Responses in Asthma, COPD, and PH

9.2.1 Asthma

Airway smooth muscle cells (ASMCs) are seen as the primary effector cells of airway remodeling, contributing to the narrowing seen in asthma [21]. The dominant role of ASMCs may be due to airway hyperresponsiveness (AHR), defined as exaggerated airway narrowing due to nonspecific irritants and agonists, reversible by bronchodilators. ASM cellular processes that exacerbate AHR can have detrimental effects on downstream cellular responses and further worsen asthma symptoms.

9.2.1.1 ASM Hyperresponsiveness

Airway hyperresponsiveness (AHR) is a characteristic feature of asthma, which consists of an increased sensitivity of the airways to an inhaled stimuli that would produce little or no effect in healthy patients [5]. AHR causes excessive narrowing of the airways; thus, its measurement has provided insight into the underlying pathological mechanisms of the disease. AHR is increased in different risk-factor asthmatic groups, including the elderly, obese, and cigarette smoke patients. There are also varying associated pathophysiology with the increased AHR. For example, there are increased neutrophils and decreased elastic recoil in elderly asthmatic patients, whereas cigarette smoking patients display acutely reversible inflammation and structural changes.

9.2.1.2 ASM Remodeling

ASM remodeling is the main contributor to restricted airflow in asthmatic patients [5]. Structural changes correlate with airway wall thickening, reticular basement membrane thickness, and components of the extracellular matrix. The remodeling also includes changes like subepithelial fibrosis, ASM hypertrophy/hyperplasia, angiogenesis, and changes in the extracellular matrix composition [21, 22]. Hyperplasia or ASMC hyperproliferation is often influenced and stimulated by airway inflammation and is believed to be due to an upregulation of inflammatory mediators (i.e., cytokines and chemokines) [5, 23]. These pro-inflammatory cytokines that regulate ASMC proliferation include IL-1β and TNF-α.

9.2.1.3 ASM Cell Migration

ASMC migration is a contributing factor to airway remodeling and pathogenesis in asthma. Cell migration is influenced by chemotaxis or chemokines. It is possible that ASMC migration contributes to the increased smooth muscle mass in asthmatic airways [24]. Migration is composed of synchronized distinct steps of cell polarization, protrusion, adhesion, traction, and contraction [21, 24, 25]. Several molecular regulators control each step in cell migration, including Cdc42, Rac activation, PI3K, Rho family proteins, etc. [25]. Various pharmacological agents have been shown to have an inhibitory effect on ASMC migration and are beneficial in treating asthma [24, 25]. Additionally, traditional medications such as β-agonists and corticosteroids have been shown to reduce ASMC migration.

9.2.2 COPD and PH

Pulmonary arterial smooth muscle cells (PASMCs) are thought to be the main players in the pathogenesis of COPD and associated PH due to the overproduction of ROS and upregulated Ca^{2+} signaling. Regulation of these specific ROS and Ca^{2+} signaling pathways plays a crucial role in maintaining cellular homeostasis. Any disturbance to these processes can have detrimental effects on downstream cellular responses.

9.2.2.1 Vasoconstriction in COPD-Associated PH

COPD often leads to the development of PH, which accounts for the mortality of many COPD patients. Increased pulmonary vascular resistance (PVR) in PH is due to pulmonary artery constriction and remodeling. PASMCs serve as a critical player in vasoconstriction and remodeling through their hyperresponsiveness and increased proliferation, decreased or suppressed apoptosis, and migration.

Hypoxic pulmonary vasoconstriction is an adaptive mechanism to match perfusion and ventilation in response to alveolar hypoxia (a decrease in oxygen levels) in smaller, more resistant pulmonary arteries. Vasoconstriction is highly controlled by Ca^{2+} signaling in PASMCs. Ca^{2+} signaling may occur due to its release from the intracellular store (SR) and/or influx from the extracellular compartment through multiple ion channels. Intracellular Ca^{2+} release and/or extracellular Ca^{2+} influx lead to the increased cytosolic Ca^{2+}, which binds to calmodulin (CaM), activates myosin light chain kinase (MLCK), phosphorylates a 20 kDa light chain of myosin, initiates actin/myosin cross-bridge cycling, and initiates cell contraction.

9.2.2.2 Vascular Remodeling in COPD-Associated PH

Remodeling is characterized by structural changes to either the airway or the vasculature. Often, this involves hyperplasia (hyperproliferation) of airway (epithelial and smooth muscle) cells, thickening of the basement membrane, fibrosis, and collagen deposits [26]. Airway obstruction associated with COPD is a result of small airway remodeling. The vascular remodeling of pulmonary arteries involves hyperproliferation of PASMCs and contributes to COPD-associated PH [26].

Bronchoalveolar lavage fluid (BALF) collected from COPD patients has shown increased levels of matrix metalloproteases (MMPs), proteases that contribute to alveolar destruction and airway obstruction by degrading structural components of the extracellular matrix (ECM) [27]. MMPs are secreted by several inflammatory cell types, including neutrophils and macrophages. Thus, the observed increase in recruitment and infiltration of neutrophils and macrophages in COPD may account for the increased levels of MMPs found in COPD patient BALF [27, 28].

Several studies have shown that cigarette or tobacco smoke-induced ROS generation contributes to airway and pulmonary vascular remodeling in COPD. A study by Zhu et al. [29] has observed that tobacco smoke-induced ROS-mediated calpain activation is necessary for airway or pulmonary artery remodeling, whereas Churg et al. [27, 30] have shown CS induces activation of several growth factors and procollagen synthesis in airways.

9.3 Roles of Reactive Oxygen Species

Reactive oxygen species (ROS) are chemically reactive biomolecules that contain oxygen. Unregulated ROS generation can lead to detrimental effects, such as damage of nucleic acids, proteins, lipid peroxidation, etc. Oxidative stress on cells has been attributed to the development and progression of diseases such as asthma, PH, and other respiratory diseases [31, 32]. It is important to understand ROS signaling since the role of ROS in PASMCs has been shown to be involved in PA vasoconstriction and remodeling that lead to the development of PH.

9.3.1 Generation of ROS

Mitochondria have been noted as a primary and important source of ROS generation in many mammalian cells, including PASMCs [33, 34]. In the oxygen-rich environment of the mitochondria, one-electron reduction of oxygen to superoxide is the major reaction to produce ROS [34, 35]. It has also been shown that mitochondria can produce H_2O_2 [34, 35]. Complexes I and III of the mitochondrial electron transport chain (ETC) are the main contributors to mitochondrial ROS generation [36]. Conditions, such as the increase of electron movement and potential leakage, within these complexes, favor ROS generation [37]. Additionally, a high NADH/NAD+ ratio in the mitochondrial matrix has also been shown to contribute to the favorable ROS-generating environment [34].

Several studies have shown that within the mitochondrial ETC, the Rieske iron-sulfur protein (RISP), a catalytic subunit of complex III, is a significant molecule to ROS generation [38–41], which is evident by the fact that knockdown of RISP in PASMCs has shown to inhibit the

increase in mitochondrial ROS generation associated with hypoxic exposure [39, 41].

Although mitochondria have been noted as a primary source of ROS, there are other sources such as nicotinamide dinucleotide phosphate (NADPH) oxidase (NOX), another well-studied source of ROS. NOX regulation is controlled through the interaction of cytoplasmic and membrane-associated proteins and in response to intracellular stimuli, such as Ca^{2+} signaling [42, 43]. For instance, protein kinase may phosphorylate and then modulate NOX activation [44]. Specifically, protein kinase C (PKC)-mediated phosphorylation can activate NOX [44, 45]. Other enzymes, such as xanthine oxidases, cyclooxygenases, and lipoxygenases, may also play a significant role in cellular responses in certain types of cells [46].

9.3.2 Upstream and Downstream Signaling of ROS

The unregulated overproduction of ROS plays a large role in many cellular processes. ROS can influence Ca^{2+} signaling through oxidizing key residues on several ion channels that allow for the Ca^{2+} influx [42, 47]. Conversely, it has also been shown that intracellular Ca^{2+} can modulate ROS generation as well as ROS scavengers [42, 47, 48]. Besides the mitochondria, Ca^{2+} regulates several enzymes that generate ROS, including NOX and nitric oxide synthase (NOS) [42, 49]. Antioxidant enzymes, such as catalase and GSH reductase, can be activated by Ca^{2+} [42, 50]. Ca^{2+} has also been shown to increase the level of superoxide dismutase (SOD), a key enzyme involved in the catalysis of superoxide into hydrogen peroxide [51]. Mitochondrial Ca^{2+} can activate several dehydrogenases of the citric acid cycle and ATP synthase to increase ROS generation [52, 53] subsequently. The ability of Ca^{2+} to induce ROS generation has been termed Ca^{2+}-induced ROS generation (CIRG). Additionally, the ability of ROS to stimulate the release of Ca^{2+} from the major intracellular Ca^{2+} store (sarcoplasmic reticulum (SR)) has been termed ROS-induced Ca^{2+} release (RICR).

ROS have also been shown to play a regulatory role in many cell signaling pathways, such as nuclear factor (NF)-κB inflammatory signaling, mitogen-activated protein kinase (MAPK) cascade signaling, PI3K-Akt signaling, and Keap1-Nrf2-ARE signaling [49]. ROS-induced oxidation of specific residues of kinases in the NF-κB signaling pathway has been shown to inhibit the activation of NF-κB and its subsequent translocation and transcriptional activity [52]. MAPK cascade signaling is involved in several cellular processes, which include cell growth, differentiation, survival, and death. ROS have been shown to prematurely activate the downstream signaling pathways of MAPK, such as JNK signaling and the ERK pathway [49]. Specifically, H_2O_2 induces the phosphorylation of phospholipase C, resulting in the production of diacylglycerol (DAG) and inositol triphosphate (IP_3) [49]. IP_3 has been shown to increase intracellular Ca^{2+} through the release of Ca^{2+} from the SR by activating its receptors [49, 53]. ROS-induced activation of protein kinase C (PKC) has been shown to increase Ca^{2+} as well as activation of NOX, influencing further ROS production via ROS-induced ROS generation (RIRG) [49, 54].

Keap1-Nrf-ARE signaling plays a critical role in maintaining cellular redox and inducing an adaptive response to oxidative stress. Increased levels of ROS have been shown to disrupt this Keap1-Nrf-ARE-dependent maintenance by influencing the dissociation of regulatory inhibitor Keap1 from Nrf. This dissociation is mediated by the oxidation of essential cysteine residues or activation of kinases such as PKC, MAPK, or PI3K that phosphorylate Nrf [49].

The unregulated generation of ROS plays a significant role in influencing many cellular processes. The oxidation of critical molecules in these pathways leads to unregulated and premature activation of the signaling pathways associated with the development and progression of diseases.

9.3.3 Role of ROS in Asthma

Oxidative stress plays a crucial role in the pathogenesis of asthma. Although accumulation and exposure to ROS can contribute to airway inflam-

mation, it is also speculated that overproduction of ROS occurs after inflammation, post-asthmatic triggers, and attacks. Higher levels of key ROS signaling molecules were found in samples (e.g., breath condensates and sputum) taken from asthmatic patients compared with normal control subjects. In one study, scavenging of ROS prevented an immune response and inflammation in the airways, suggesting that ROS play an essential role in acting as the critical contributor in the initiation of allergic airway inflammation.

9.3.4 Role of ROS in COPD and PH

With a large percentage of COPD patients being smokers, chronic exposure to CS increases the production of ROS [31, 55]. This chronic exposure to cigarette smoke is detrimental for the cellular environment, including an injury to bronchiolar epithelial cells, infiltration of inflammatory cells in the lung, and an increase in the expression of oxidative stress markers and pro-inflammatory cytokines. The chrnoic exposure to CS (you can abbreviate cigarette smoke to CS) [56, 57].

Mitochondrial dysfunction, which can be linked to the increase in ROS generation, is seen in COPD patients compared to healthy patients [58]. Damaged mitochondria from H_2O_2 or CS have been shown to have a decreased mitochondrial membrane potential, impairment in oxidative phosphorylation and ATP production, and altered Ca^{2+} flux [58, 59].

The increase in ROS generation plays a large role in oxidative stress in patients with COPD. Importantly, studies have shown that COPD patients display a reduced anti-inflammatory defense, such as a reduction in glutathione (GSH) as seen in sputum or BAL collection from COPD patients [56], downregulation of SOD [56, 60], reduced catalase activity [56, 61], and reduced levels of GSH peroxidase (Gpx) [56, 61, 62]. Taken together, the reduced anti-inflammatory defense against ROS can contribute to the observed increase in oxidative stress in COPD patients.

Chronic inflammation is a crucial characteristic of COPD. Increased ROS generation has been shown to exacerbate the inflammation seen in COPD patients. ROS promote the recruitment and infiltration of inflammatory cells such as neutrophils and macrophages [7, 31]. ROS have been shown to inhibit the activation of NF-κB through oxidation of its specific residues; however, it has been demonstrated that in COPD patients, NF-κB activity is increased in sputum and BAL samples [63–65]. ROS derived from NOX4, the most abundant isoform of the NOX family in the pulmonary vasculature, has been shown to activate NF-κB and MAPK signaling pathways [66–68]. Thus, ROS can activate as well as repress NF-κB signaling.

COPD is also characterized by vascular remodeling and vasoconstriction. Studies have shown that both COPD-associated remodeling and vasoconstriction can be partly attributed to the increased ROS generation [10, 69]. Specifically, Zhu et al. [29] observed that remodeling is dependent on ERK phosphorylation with ERK activation dependent on ROS. Activation and phosphorylation of ERK influence collagen synthesis and cell proliferation in bronchial and pulmonary arterial SMCs [29]. Both collagen synthesis and cell proliferation of SMCs are critical characteristics of vascular and airway remodeling. TGF-β-induced NOX4-derived ROS generation has also been shown to play a key role in mediating pulmonary arteriolar remodeling, contributing to the development of COPD-associated pulmonary hypertension [70].

A key mechanism in the development of PH is highly associated with chronic hypoxia-induced cellular responses in PASMCs [71, 72]. Studies have shown that in COPD-associated PH, the mitochondria act as an oxygen sensor [31, 39, 73]. Although there is some controversy as to whether ROS generation increases or decreases in hypoxic conditions, the redox theory of hypoxic pulmonary vasoconstriction (HPV) suggests a hypoxia-induced change in ROS inhibits K^+ channels, which causes membrane depolarization and subsequent cell contraction due to the increase in cytosolic Ca^{2+} [74, 75]. Additionally, mitochondrial ETC-derived ROS have also been shown to modulate the mechanisms that mediate vasoconstriction [76, 77]. Sustained hypoxia has also been shown to activate Rho kinase, leading

to Ca^{2+} sensitization and reinforcing vasoconstriction seen in PH [78–80].

Because the generation of ROS plays a large role in mediating several cellular processes associated with the development and progression of COPD, targeting the mechanisms that overproduce ROS will be critical to find effective therapies for COPD.

9.3.4.1 ROS, Nicotine, and Smoking

Nicotine, the main active ingredient in tobacco cigarettes, has been shown to enhance ROS generation in multiple cell types. Cigarette smoke, once inhaled, is divided into two phases: the tar (solid) and the gaseous phase [55]. Both phases contain high concentrations of free radicals, leading to oxidative stress within the cellular environment. Notably, cigarette tar can produce large amounts of H_2O_2 in the aqueous form [55]. Most importantly, CS and nicotine activate intracellular ROS generation systems, causing more ROS production within cells [81, 82].

CS/nicotine inhalation is a potent cellular stimulant that can cause DNA damage. Studies have shown that damage resulting from CS-induced oxidative stress is partially controlled by lack of ataxia-telangiectasia mutated (ATM) protein kinase activity, which in turn may be responsible for apoptosis [83, 84]. CS-induced DNA damage represses ATM protein kinase activity in endothelial cells, decreasing apoptosis. In support, inhibiting ATM protein kinase using pharmacological agent KU60019 increased PASMC proliferation and inhibited cell apoptosis [83].

Several studies suggest the expression of nicotinic receptors (nAChRs) on the mitochondria. Although 17 nAChR subunits have been identified in mammalian cells, mitochondria specifically express α7 nAChRs to regulate Ca^{2+} and cytochrome c release [85]. Apoptogens, such as high Ca^{2+} or oxidants (H_2O_2), stimulate this release of cytochrome c from the mitochondria [85]. Nicotine is detrimental to cells and can induce apoptosis by increasing ROS generation [86]. Additionally, it has been shown that CS activates hypoxia-inducible factor 1 (HIF-1) in a ROS-dependent manner [87].

Thus, studies have shown that CS/nicotine inhalation perpetuates the development of COPD and associated PH mechanistically by the overproduction of ROS.

9.4 Ca^{2+} Signaling

As the most common second messenger, Ca^{2+} signaling plays a significant role in many cellular processes and is critical in maintaining cellular homeostasis. Events that lead to the elevation of intracellular Ca^{2+}, such as chronic or intermittent hypoxia, contribute to PA or airway constriction, hyperproliferation of SMCs, and ultimately airway and pulmonary vascular remodeling and the development of asthma, COPD, and PH.

9.4.1 Important Ca^{2+} Channels

Multiple ion channels control and regulate Ca^{2+} signaling by causing intracellular Ca^{2+} release and extracellular Ca^{2+} influx. The release of Ca^{2+} from the intracellular store (SR) through RyR and/or IP_3R channel may initiate and promote the development of Ca^{2+} signaling [88–90]. All three subtypes of RyRs (RyR1, RyR2, and RyR3) have been shown to play a role in hypoxic cellular responses; however, RyR2 plays a more dominant role in PASMCs [54, 91, 92]. Three subtypes of IP_3Rs (IP_3R1, IP_3R2, and IP_3R3) are also found on the SR in PASMCs. Studies have shown that IP_3R1 plays a large role in mediating Ca^{2+} release in PASMCs, which is associated with PH [90].

L-type voltage-gated Ca^{2+} channels (LTCCs) have been shown to be the source for membrane depolarization-dependent Ca^{2+} influx in PASMCs [40]. Voltage-gated K^+ (K_V) channels are major regulators of the resting membrane potential in PASMCs. The inhibition of K_V channels can depolarize the cell membrane to activate LTCCs [40, 93]. Hypoxia, the main contributor to COPD-associated PH, may also inhibit K_V channels, thus influencing Ca^{2+} influx and vasoconstriction [94]. The increase in cytosolic Ca^{2+} stimulates cell proliferation and inhibits apoptosis, mediating vascular remodeling [91, 95].

The upregulation of transient receptor potential (TRP) channels, a family of nonselective ion channels, has been associated with increased Ca^{2+} influx and has been implicated in PH [96]. Canonical TRP (TRPC) channels include TRPC1–7, are a subfamily of TRP channels, and show mRNA and/or protein expression in pulmonary arteries [97]. Although all seven isoforms are expressed, TRPC1 and TRPC6 are the major players involved in Ca^{2+} responses in PASMCs [97]. Specifically, it has been shown that CS- and nicotine-induced vasoconstriction and remodeling in the PA and development of PH were highly influenced by the upregulation of TRPC1 and TRPC6 [98].

A recent study has shown that nicotine causes proliferation of cultured rat airway SMCs, and the role of nicotine is reliant on TRPC6-dependent Ca^{2+} influx through α7 nAChR on the plasmalemma [99]. Consistent with a report by Wang et al. [98], Hong et al. [99] also showed that CS- and nicotine-exposure increase TRPC6 channel expression. Treatment of human airway SMCs with α7 nAChR antagonists attenuated nicotine-induced proliferation; additionally, treatment of TRPC6 siRNA, with or without nicotine application, significantly affected cell proliferation as measured by EdU-positive staining [99]. Elevated intracellular Ca^{2+} levels have been shown to promote cell proliferation [100, 101]; thus, nicotine-induced increase in TRPC6 expression and Ca^{2+} influx via α7 nAChR may be involved in hyperproliferation characteristic of vasoremodeling seen in COPD-associated PH. Therefore, although CS and its active agent nicotine have been shown to activate α7-nAChR channels to induce Ca^{2+} influx and promote cell proliferation in airway SMCs [99], the role and underlying mechanisms of α7 nAChR have not been well established in PASMCs.

9.4.2 Interaction Between Ca^{2+} and ROS Signaling

It has been shown that K_V channels are hypoxia sensitive, and its activity is mitochondrial ROS dependent in PASMCs [74]. It is interesting to point out that both hypoxic inhibition of K_V channels and activation of TRPC channels may occur due to RyR-mediated Ca^{2+} release [92, 102]. Additionally, the TRP channels are highly modulated by ROS, resulting in the regulation of several Ca^{2+}-mediated cellular processes in PASMCs, including contraction, migration, proliferation, and apoptosis, all of which are associated with COPD and COPD-associated PH [74, 103].

As previously mentioned, ROS have also been shown to influence intracellular Ca^{2+} release and extracellular Ca^{2+} influx. Thus, it is crucial to determine which residues on Ca^{2+} release and influx channels are oxidized by RISP-dependent ROS to play an important role in the development of COPD and associated PH.

The ability for Ca^{2+} to induce ROS generation (CIRG) and for ROS to induce Ca^{2+} release (RICR) in PASMCs, contributing to the development of COPD-associated PH, suggests targeting the underlying mechanisms that cause the upregulation of Ca^{2+} and ROS signaling is necessary.

9.5 Inflammatory Signaling

Three main signaling pathways mediate inflammatory responses, which include nuclear factor (NF)-κB signaling, Janus kinase/signaling transducer and activator of transcription (JAK/STAT) signaling pathway, and mitogen-activated protein kinase (MAPK) signaling pathway. Although all are important, we will focus on the significance of NF-κB signaling, as it has been shown to play a crucial role in lung diseases.

9.5.1 NF-κB Signaling

NF-κB is a family of inducible transcription factors involved in the regulation of inflammatory genes. There are five structurally related family subunits: p50, p51, RelA or p65, RelB, and c-Rel [104]. These subunits mediate target gene transcription through binding a specific DNA element, the κB enhancer [104]. The NF-κB proteins are sequestered in the cytoplasm by inhibitory proteins, which include the IκB family members [104, 105].

There are two major signaling pathways involved in the activation of NF-κB: the canonical and noncanonical pathways, both of which are important in regulating immune and inflammatory responses [65, 104]. In the canonical NF-κB pathway, stimuli such as ligands of various cytokine receptors, TNF receptors, and B-cell receptors induce the degradation of IκBα initiated by site-specific phosphorylation by multisubunit IκB kinase (IKK) [65, 104, 105]. IKK has two catalytic subunits, IKKα and IKKβ, and a regulatory subunit, NF-κB essential modulator (NEMO) or IKKγ [65, 104, 105]. Once IKK is activated, the kinase phosphorylates IκBα at two N-terminal serine residues, which then triggers ubiquitin-dependent degradation of IκBα in the proteasome [65, 104, 105]. Nuclear translocation of canonical NF-κB members, mainly p50/p65 and p50/c-Rel dimers, results from the degradation of IκBα [65, 104, 105].

Innate immune cells, such as macrophages, dendritic cells, and neutrophils, serve important roles as the first line of defense in innate immunity and inflammation. These cells express pattern recognition receptors (PRRs) that detect microbial components, pathogen-associated molecular patterns (PAMPs), and damage-associated molecular patterns (DAMPs), specific molecules released by necrotic cells, and damaged tissues [104, 106]. Specifically, mammalian cells express five PRR families, including toll-like receptors (TLRs) and NOD-like receptors (NLRs) [104]. Each PRR family differs with distinct structural properties and distinct responses to different PAMPs and DAMPs. However, a common event of PRRs is the activation of the canonical NF-κB pathway [104, 106].

The activation of the canonical NF-κB pathway induces the transcription of pro-inflammatory cytokines, chemokines, and other inflammatory mediators such as anti-apoptotic factors, cell cycle regulators, and adhesion molecules [104, 106]. Transforming growth factor-β-activated kinase 1 (TAK1) is a signaling molecule that unites the different PRR pathways for the activation of NF-κB [104, 106]. Once activated, TAK1, composed of subunits TAB1 and TAB2, activates downstream kinase IKK, responsible for IκBα phosphorylation and subsequent NF-κB activation [104, 106]. NF-κB acts as a key transcription factor of M1 macrophages and necessary for the induction of inflammatory genes, including genes for TNF-α, IL-1β, IL-6, and cyclooxygenase-2 [104, 106].

In the noncanonical NF-κB pathway, this pathway selectively responds to a set of stimuli, which includes a subset of TNF receptor ligands, and does not rely on the degradation of IκBα, but on the processing of the p65 precursor protein, p100 [65, 104, 105]. Briefly, NF-κB-inducing kinase (NIK) activates IKKα to mediate the phosphorylation of p100. Phosphorylated p100 induces subsequent ubiquitination and processing, which involved the degradation of its C-terminal IκB-like structure [65, 104, 105]. This degradation generates a mature NF-κB p52 and causes nuclear translocation of noncanonical p52/RelB [65, 104, 105].

9.5.2 Role of Reactive Oxygen Species in Inflammatory Signaling

It has been shown that ROS can affect inflammatory signaling pathways, such as NF-κB signaling [64, 65]. In response to toxic levels of ROS, it is critical for cells to prevent further oxidative damage to maintain cell survival. Based on the severity of oxidative stress, ROS can trigger apoptotic and necrotic cell death [32, 52]. The expression of NF-κB target genes, such as those encoding for antioxidant proteins, promotes cell survival by influencing cellular ROS levels [49, 52].

ROS has also been shown to play a regulatory role in NF-κB signaling. Cytoplasmic thioredoxin, an endogenous small redox protein that maintains protein thiol groups in the reduced state, has been shown to block the degradation of IκB [49, 52, 64]. It has also been shown that ROS can disturb the ubiquitination and degradation of IκB, thus inhibiting the activation of NF-κB [49]. Nucleic thioredoxin has been shown to influence NF-κB activity by enhancing DNA binding abilities [52, 64, 107]. NF-κB heterodimers can also

be modified in increased oxidative stress conditions. Cysteine residue 62 in the Rel homology domain (RHD) of NF-κB p50 subunit is prone to oxidation, which subsequently decreases the ability to bind DNA [64]. However, the RHD has spatial redox regulation with oxidation occurring in the cytoplasm and the reduced form in the nucleus [64]. IKK is also a prime target for ROS, specifically S-glutathionylation of IKKβ on cysteine 179, thus inhibiting the catalytic activity of the IKK subunit and subsequently inhibiting NF-κB signaling [49].

9.5.3 Role of Ca^{2+} Signaling in NF-κB Signaling

Several studies have shown that Ca^{2+} mediates NF-κB signaling [108–112]. Specifically, increased intracellular Ca^{2+} from inherent increased resting intracellular Ca^{2+} [108] or depolarization of muscle cells [111] leads to an upregulation in NF-κB activity [108–111]. Ca^{2+}-induced NF-κB activation increases the transcriptional activity and p65 nuclear localization by mediating the phosphorylation of Ser536 [108, 110].

Intracellular Ca^{2+} can be regulated by several channels; however, only several ion channels are linked to Ca^{2+}-induced NF-κB activation. Release of Ca^{2+} from intracellular stores in the SR is mediated by either ryanodine receptor (RyR) or inositol-1,4,5-triphosphate receptor (IP_3R) channels [109, 111, 112]. Following the release of Ca^{2+} from the intracellular stores, NF-κB activity is increased. Further, the involvement of RyR channels has been confirmed by using ryanodine to inhibit Ca^{2+} release via RyR channels and the subsequent decrease in NF-κB activity [109, 111, 112].

There are several Ca^{2+} signaling pathways involved in the mediation of Ca^{2+}-induced NF-κB activation. Liu et al. showed that non-IκBα degradation-mediated signaling is regulated through Ca^{2+}-dependent PKCα-mediated phosphorylation of p65 [110]. Other studies have further supported the Ca^{2+}-dependent PKCα-mediated activation of NF-κB through pharmacological inhibition [109, 111].

Calmodulin and calmodulin kinases (i.e., CaMKII and CaMKIV) have also been shown to mediate NF-κB activity in a Ca^{2+}-dependent manner [109, 113]. It has been reported that calmodulin inhibitors W7 and calmidazolium decrease the basal activity of NF-κB in primary cultured neonatal cerebellar granule neurons and the role of CaMKII in mediating NF-κB signaling through the activation of IKK [109]. Additionally, it has been shown that CaMKII can induce cardiomyocyte hypertrophy through apoptosis signal-regulating kinase 1 (ASK1)-NF-κB signaling [114]. However, the role of calmodulin and associated kinase Ca^{2+}-dependent signaling is not largely known in PASMCs in the context of COPD and PH.

9.5.4 Role of NF-κB in Asthma and COPD

NF-κB signaling is responsible for mediating inflammatory responses seen in asthma and COPD.

Inflammation of the airways and vasculature is often caused by infiltration by inflammatory cells such as eosinophils, mast cells, monocytes, lymphocytes, and neutrophils. All these cell types contribute to the elevated levels of inflammatory mediators. Studies have shown evidence for upregulated activation of NF-κB and increased inflammatory cells in the bronchial biopsy of asthmatic and COPD patients, observed through bronchial biopsy [63, 115]. Specifically, IκBα levels are significantly lower in tissues and fluids collected from COPD patients than nonsmoking healthy patients [63, 116]. Upstream of upregulated IκBα degradation, IKK activity is increased in COPD patients and smokers [63, 116].

The collection of sputum and bronchoalveolar lavage fluid (BALF) is a common clinical assessment of inflammation in patients with respiratory diseases, such as asthma or COPD. Neutrophils isolated from COPD patient sputum and BALF show increased NF-κB activation following CS exposure, a common irritant and trigger of COPD inflammatory exacerbations [63, 117]. Macrophages isolated from BALF collected from

patients with PH also displayed activated NF-κB [118]. This was further supported in an in vivo COPD model where CS increased NF-κB signaling activity and its subsequent nuclear recruitment to the promoters of several inflammatory genes [63, 117, 119].

Although NF-κB plays a large role in regulating inflammation seen in COPD, ubiquitously targeting this pathway is not an ideal therapeutic target in treating COPD since NF-κB is ubiquitously expressed and involved in other cellular processes. It is necessary to determine a specific and direct target within the NF-κB signaling pathway that contributes to COPD and associated PH.

9.5.4.1 NF-κB in Airway and Vascular Hyperresponsiveness and Remodeling in COPD and PH

Airway and vascular hyperresponsiveness and remodeling play a large role in the development of COPD and COPD-associated PH. Although it has not been well characterized in COPD and PH, NF-κB activity has been shown to be involved in airway hyperresponsiveness and remodeling in the context of asthma [63, 120]. Tully et al. [120] demonstrated that epithelial activation of NF-κB is required for airway remodeling and hyperresponsiveness in dust-mite-induced inflammation, whereas inhibition of NF-κB diminished neutrophil recruitment, remodeling, and hyperresponsiveness.

Additionally, little is known on the role of NF-κB in mediating these processes, specifically in PASMCs. Price et al. [121] showed that NF-κB was activated in PASMCs of the pulmonary vessel in idiopathic PH; however, its role in remodeling or vasoconstriction was not assessed. Another study by Hosokawa et al. [122] demonstrated that an inhibitor of NF-κB, IMD-0354, blocked the hyperproliferation of PASMCs, associated with PH. However, this study of PH was done using monocrotaline, a drug-induced PH model. The role of NF-κB in a hypoxia-induced model of PH in PASMCs was shown to mediate HIF-1α mRNA expression as a hypoxia-regulated transcription factor [123]. The accumulation of HIF-1 has been shown to influence hypoxia-induced apoptosis, which may contribute to vascular remodeling and PH [123, 124].

Further studies investigating the role of NF-κB in mediating cellular processes, such as airway or PA hyperresponsiveness and remodeling, that contribute to the development of COPD and associated PH may prove useful in finding therapeutic targets for the treatment of these devastating diseases.

9.6 Conclusions

We and other investigators have demonstrated that mitochondrial RISP is an essential molecule in ROS generation in PASMCs [38–41, 92], which plays a significant role in mediating Ca^{2+} signaling via RyR2-mediated SR Ca^{2+} release, serving as a significant contributor to PA vasoconstriction and remodeling in COPD-associated PH and possibly COPD as well [54, 91, 92]. In support, we have previously shown that RISP-mediated mitochondrial ROS can activate PKC-ε and then NOX, induce further ROS generation (RIRG), activate RyR2, and cause subsequent Ca^{2+} release from the SR in PASMCs [41, 54, 91, 125]. It is also known that ROS overproduction is a crucial characteristic of COPD, presumably leading to PA inflammation, vasoconstriction, and remodeling [46, 49, 50, 54, 125]. However, it is not known how RISP-mediated ROS generation affects inflammatory signaling pathways and nicotine-initiated signaling pathways.

NF-κB-dependent inflammatory signaling plays a crucial role in mediating multiple cellular responses in COPD [52, 63–65, 126]. Sputum and BALF collected from COPD patients have shown an upregulation in NF-κB activity such as decreased IκBα expression, a characteristic of upregulated IκBα degradation-dependent activation of NF-κB [63, 115, 116]. PASMCs have shown activated NF-κB following inflammatory and proliferative stimuli [121]. NF-κB is also activated in PASMCs of rats with pulmonary hypertension [127].

ROS are known to be the important mediators for NF-κB signaling. The increased ROS production during oxidative stress has shown to affect

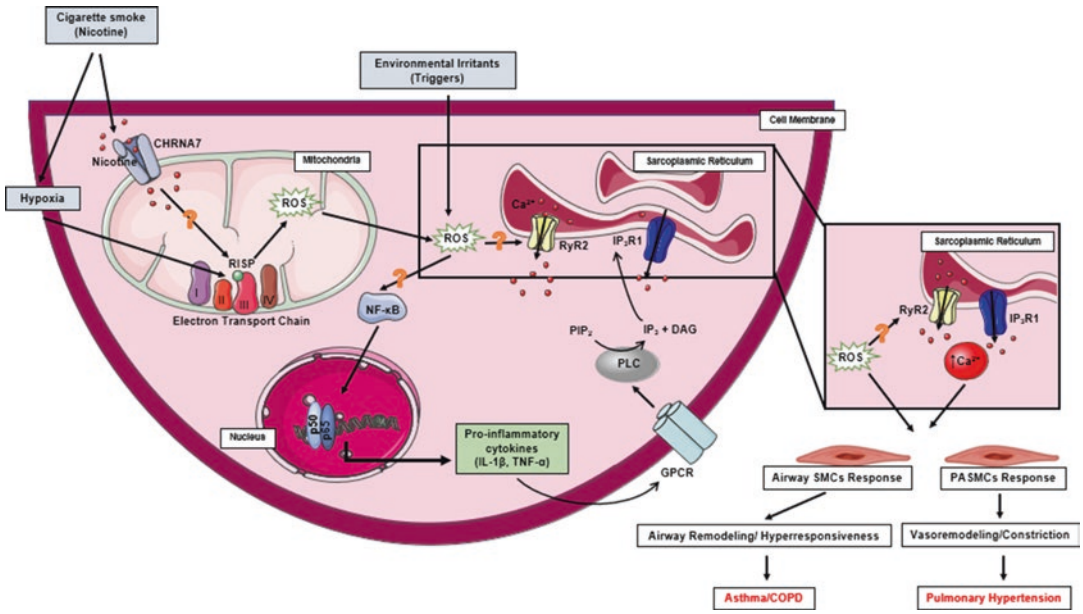
NF-κB function. Inhibition of upstream kinases (e.g., IKK) or phosphorylation of specific residues on NF-κB signaling molecules (e.g., IκBα) has shown to either increase or decrease NF-κB signaling. Because inflammatory signaling can play a role in remodeling and vasoconstriction, an interesting question remains how ROS and NF-κB-dependent inflammatory signaling interact, specifically in PASMCs, to mediate PA vasoconstriction and remodeling, leading to the development of COPD and PH. It is also unclear how ROS are generated to activate NF-κB in PASMCs [34, 46, 49, 56, 57, 128]. As RISP is a primary molecule in ROS generation in PASMCs [39–41, 125], studies proposed to elucidate the role of RISP-mediated mitochondrial ROS in regulating NF-κB activity in PASMCs is of great significance as well.

Intracellular Ca^{2+}, as the downstream signaling factor of ROS signaling in PASMCs, plays a crucial role in PA vasoconstriction and remodeling. Ca^{2+} release from the SR through RyRs and IP_3Rs increases the cytosolic Ca^{2+}, which can activate actin-myosin complexes to induce PA vasoconstriction [88]. Additionally, Ca^{2+} may also mediate PA remodeling, a primary contributor to COPD-associated PH [42, 47, 89, 129]. Targeting readily oxidized residues on RyRs and IP_3Rs in PASMCs may help find more effective and specific therapies for these diseases.

Mitochondrial Ca^{2+} signaling has been attributed to the role of a nicotinamide acetylcholine receptor, α7 nAChR, on the mitochondrial membrane in isolated mitochondria from HEK cells [85]. It is unknown whether α7 nAChR has a role in mediating mitochondrial Ca^{2+} in PASMCs, which may play a role in RISP-mediated CIRG. It is unclear whether and how α7 nAChR contributes to CIRG and upstream calcium-induced calcium release calcium-induced calcium release (CICR) via RyRs and IP_3Rs in PASMCs, contributing to PA vasoconstriction and remodeling, COPD, and COPD-associated PH. Thus, the specific role of CIRG and CICR through mitochondrial ROS and important Ca^{2+} release channels RyRs and IP_3Rs should be the focus of future investigations.

9.6.1 Graphical Conclusions

Schematic of proposed interactions between ROS, Ca^{2+}, and inflammatory signaling in respiratory diseases. Nicotine inhalation (including cigarette smoking) by inducing α7 nAChR-mediated mitochondrial Ca^{2+} release and hypoxia secondary to nicotine inhalation or cigarette smoking induce RISP-mediated ROS generation, oxidizes RyR2, which subsequently enhances its activity and increases Ca^{2+} release from the SR in PASMCs.



Additionally, environmental irritants, such as pollen and pet dander, can trigger ROS production, evident in asthmatic attacks and the development of asthma. Mitochondrial-generated ROS may increase NF-κB activity, increase pro-inflammatory factors, and trigger IP_3R1-mediated Ca^{2+} release from the SR. This Ca^{2+} release may further induce RyR2-mediated Ca^{2+} release, increasing the intracellular $[Ca^{2+}]$, leading to PASM cellular responses (vasoconstriction and remodeling), contributing to the development of COPD-associated pulmonary hypertension. In ASMCs, this increase in intracellular $[Ca^{2+}]$ can lead to ASM cellular responses (airway remodeling and airway hyperresponsiveness), seen in asthma.

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Protein S-Palmitoylation and Lung Diseases

10

Zeang Wu, Rubin Tan, Liping Zhu, Ping Yao, and Qinghua Hu

Abstract

S-palmitoylation of protein is a posttranslational, reversible lipid modification; it was catalyzed by a family of 23 mammalian palmitoyl acyltransferases in humans. S-palmitoylation can impact protein function by regulating protein sorting, secretion, trafficking, stability, and protein interaction. Thus, S-palmitoylation plays a crucial role in many human diseases including mental illness and cancers. In this chapter, we systematically reviewed the influence of S-palmitoylation on protein performance, the characteristics of S-palmitoylation regulating protein function, and the role of S-palmitoylation in pulmonary inflammation and pulmonary hypertension and summed up the treatment strategies of S-palmitoylation-related diseases and the research status of targeted S-palmitoylation agonists/inhibitors. In conclusion, we highlighted the potential role of S-palmitoylation and depalmitoylation in the treatment of human diseases.

Keywords

S-palmitoylation · Depalmitoylation · zDHHC · Protein modification

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Abbreviations

ABHD17s	α/β hydrolase domain-containing 17 proteins
AML	Acute myeloid leukemia
AMPAR	α-Amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptor
APTs	Acyl-protein thioesterases
BMP	Bone morphogenic protein
BMPR1a	BMP receptor 1a signaling
CCN3	Nephroblastoma-overexpressed protein
CCR5	CC chemokine receptor 5
CD-M6PR	Cation-dependent mannose-6-phosphate receptor
CHIKV	Chikungunya virus
CSP	Cysteine-string protein
D2R	D2 dopamine receptor
DR4	Death receptor 4
GPCR	G protein-coupled receptor
α1D AR	α-1 adrenergic receptor
ISO	Isoproterenol
5-HT1AR	Serotonin 1A receptor
IFITM3	Interferon-induced transmembrane protein 3
IRAK4	Interleukin-1 receptor-associated kinase 4
MC1R	Melanocortin-1 receptor
MYD88	Myeloid differentiation primary response protein
NPC	Nasopharyngeal carcinoma
NSPCs	Neural stem/progenitor cells
NTSR-1	Neurotensin receptor-1
NMNAT2	Nicotinamide mononucleotide adenylyltransferase 2
Ncdn	Neurochondrin
NCAM	Neural cell adhesion molecule
PD-L1	Programmed death-ligand 1
PA	Phospholipid acid
PRCD	Progressive rod-cone degeneration
PPHN	Persistent pulmonary hypertension of the newborn
PLCβ1	Phospholipase C β1
PLSCR1	Phospholipid scramblase 1
PPTs	Palmitoyl-protein thioesterases
Rab7α	Ras-related protein Rab-7α
SSTR5	Somatostatin receptor 5
SIRS	Systemic inflammatory response syndrome
TMD	Transmembrane domain
TSP1	Thrombospondin type-1
TLR	Toll-like receptor
TP	Thromboxane prostanoid
TPα	Thromboxane prostanoid α isoforms
β_2AR	β2-adrenergic receptors
VSV-G	Vesicular stomatitis virus

10.1 Introduction of S-Palmitoylation

10.1.1 Concept

Palmitoylation is one kind of common posttranslational lipid modifications of proteins, which was first found about 40 years ago. Protein palmitoylation which generally occurs on cysteine residues is divided into three kinds (N-palmitoylation, O-palmitoylation, and S-palmitoylation) according to different connection modes. S-palmitoylation is a unique, reversible modification with a saturated 16-carbon long-chain fatty acid added to residues of particular cysteine(s); it regulates protein function by altering protein sorting, trafficking, localization, secretion, stability, and protein interaction [1]. A great number of proteins have been reported to undergo S-palmitoylation, including enzymes, receptors, viral glycoproteins, channels, and transporters. Many studies show that cycles of S-palmitoylation and depalmitoylation are pivotal to the occurrence, development, and treatment of diseases [2]. Hence, it is involved in many human diseases including DNA damage [3], neuropsychiatric diseases [4], virus infections [5], Crohn's disease [6], abnormal liver function [7], sepsis [8], alopecia [9], and osteoporosis [10] (Table 10.1).

S-palmitoylation is mainly mediated via a superfamily of 23 mammalian palmitoyl acyltransferases (zDHHCs) that contains a highly conserved domain of zinc finger (Asp-His-His-Cys) rich in cysteine. zDHHCs are membrane

Table 10.1 The characteristics, functions, target proteins, signaling pathways, and miRNAs of zDHHC proteins in related diseases

zDHHC	Intracellular localization	Tissue-specific distribution	Object	Function	Pathway	Disease	Target protein	Modified site	miRNA
zDHHC-1	ER	Brain, placenta, lung, uterus	Rat	Regulate the localization of Ncdn	/	/	Neurochondrin (Ncdn) [15]	Cys-3, Cys-4	/
zDHHC-2	ER/Golgi	Brain, kidney, testis, eye, lung, pancreas	HeLa, 293 T, Huh7.5.1 cells	Promote CHIKV replication	/	Chikungunya virus (CHIKV)	nsP1 [32]	Cys-417, Cys-418, Cys-419	/
			HeLa cells, MDCK cells	Essential for trafficking of CKAP4/p63 from the ER	/	Tumor	CKAP4/p63 [58]	Cys-100	/
			HEK-293, A431, MDA 231 cells	Promote physical associations between CD9 and CD151	/	/	CD9 and CD151 [59]	/	/
			CNE1, TW03, 293 T cells	Regulate cell migration	SOCS1, FOXO3	Nasopharyngeal carcinoma (NPC)	CKAP4/p63 [58]	Cys-100	MiR-155
zDHHC-3	Golgi	Liver, spleen, lung, brain, colon, eye, prostate, placenta	Neuroblastoma N2a cells	Stimulate the neurite outgrowth	/	/	Neural cell adhesion molecule (NCAM) [24]	Cys-18, Cys-295, Cys-297	/
			Rat	Regulate the localization of Ncdn	/	/	Neurochondrin (Ncdn) [15]	Cys-3, Cys-4	/
			C57BL/6	Reduce AMPAR trafficking at synapses	PI3K	Cognitive disorders	AMPA glutamate receptor subunit GluA1 [60]	Cys-585, Cys-811	/
			Human breast cancer	Tumor inhibitor	FAK, STAT3	Breast tumor	ERGIC3 [61]	/	/
			RS cell	Regulate UL20 localization and expression	/	HSV-1 infection	UL20 [42]	/	/
			hRPE1 cells	Regulate protein stability of PRCD	/	/	Progressive rod-cone degeneration (PRCD) [43]	Cys-322, Cys-323	/

(continued)

Table 10.1 (continued)

zDHHC	Intracellular localization	Tissue-specific distribution	Object	Function	Pathway	Disease	Target protein	Modified site	miRNA
			MC38 cells	Stabilize PD-L1	ESCRT-MVB	Colon carcinoma	Programmed death-ligand 1 (PD-L1) [22]	Cys-272	/
			HEK-293 T	Regulate the stability of the D2R	/	/	D2 dopamine receptor [30]	Cys-443	/
			MDA-MB-231, HEK-293, AR230	Important for the homo-oligomerization and raft localization of DR4	/	Cell death	Death receptor DR4 [36]	C261-3S	/
zDHHC	Intracellular localization	Tissue-specific distribution	Object	Function	Pathway	Disease	Target protein	Modified site	miRNA
zDHHC-4	Golgi	Brain, lung, testis, prostate	HEK-293 T	Regulate the stability of the D2R	/	/	D2 dopamine receptor [30]	Cys-443	/
zDHHC-5	Plasma membrane	Prostate, testis, lung, colon, eye	RAW264.7, HCT116 cells	Essential for membrane recruitment and immune signaling	NF-kB, MAPK	Crohn's disease	(NOD1/2) [6]	Cys-557, Cys-567, Cys-952	/
			RPE-1, HeLa, HAP1 cells	Important for the cleavage of the anthrax toxin	/	Intoxication of the cell	Furin and PC7 [62]	Cys-711/ Cys-699, Cys-704	/
			Glioma tissue	Inhibitor of p53-mutated gliomas	/	Glioma	EZH2 [63]	Cys-571, Cys-576	/
			HEK293 cells	Regulate the stability of SSTR5	/	/	Somatostatin receptor 5 (SSTR5) [44]	Cys-319	/
			Neuronal stem cells	Regulate the neural stem cell differentiation	/	/	Flotillin-2 [64]	Cys-4, Cys-20	/
			HT-1080, A549, T98G, HEK 293 T	Regulate CIL56-induced cell death	/	/	Caspase-independent lethal 56 (CIL56) [21]	Cys-134	/
zDHHC-6	ER	Brain, colon, uterus, lung, kidney, thymus	C57BL/6 J	Regulate TLR-induced inflammation	NF-kB	Sepsis	Myeloid differentiation primary response protein (MYD88) [8]	Cys-113, Cys-274	/

zDHHC-7	Golgi	Lung, colon, brain, liver, skin, prostate, kidney	HEK-293T cells	Regulate calcium mobilization and TPα-mediated vasoconstrictor responses	/	PPHN	Gαq [47]	Cys-9, Cys-10	/
			HEK293A cells	Tumor suppression	PI3K, AKT	Cancers	Scribble (SCRIB) [65]	Cys-4, Cys-10	/
			HeLa cells	Affect transport of CCR5	/	HIV-1 infection	CCR5 [13]	Cys-3	/
			HEK-293T, A549, MEFs cells	Increase IFITM3 antiviral activity	/	Virus infections	Interferon-induced transmembrane protein 3[5]	Cys-71, Cys-72, Cys-105	/
			Breast cancer cells	Tumor inhibitor	FAK	Breast tumor	ERGIC3 [61]	/	/
zDHHC	Intracellular localization	Tissue-specific distribution	Object	Function	Pathway	Disease	Target protein	Modified site	miRNA
zDHHC-8	Golgi	Brain, lung, kidney, ovary, pancreas, eye	C57BL/6	Promote the seizures	/	Epilepsy	AMPA receptor [66]	/	/
			Drosophila	Correlate with cancer survival	/	Cancer	Scribble and Ras64B [67]	Cys-46, Cys-120, Cys-147	/
			LgDel/+ mouse	Promote spine stabilization	/	Schizophrenia	cdc42 [68]	Cys-188, Cys-189	/
			HEK293 and HEK-nNOS cells	Important for neuronal connections, contribute to neurodevelopmental deficits	/	Neurodevelopmental deficits	PSD-95[4]	Cys-3, Cys-5	/
			HEK-293 T	Regulate the stability of the D2R	/	/	D2 dopamine receptor [30]	Cys-443	/

(continued)

Table 10.1 (continued)

zDHHC	Intracellular localization	Tissue-specific distribution	Object	Function	Pathway	Disease	Target protein	Modified site	miRNA
zDHHC-9	ER/Golgi	Brain, prostate, lung, kidney, thalamus	MDA-MB-231 and BT549	Regulate PD-L1 stability	/	Breast cancer	Programmed death-ligand 1 (PD-L1) [12]	Cys-272	/
			SD rats	Regulate membrane targeting of H-Ras	/	/	H-Ras [51]	Cys-181, Cys-184	miR-134
			C57BL/6	Regulate N-Ras plasma translocation	/	Leukemias	N-Ras [69]	/	/
			HEK293 cells	Stabilize the receptor	MAPK	/	β2-adrenergic receptors (β_2AR) [28]	Cys-256, Cys-341	/
			HEK293 cells	Functional channel regulation	/	/	STREX [70]	Cys-12, Cys-13	/
zDHHC-11	ER	Testis, brain, lung, placenta, cerebellum	Rat	Regulate the localization of Ncdn	/	/	Neurochondrin (Ncdn) [15]	Cys-3, Cys-4	/
			HEK293, HeLa, THP1 cells	Mediate MITA-dependent innate immune responses against DNA viruses	MITA, STING	Viral infection	MITA [71]	/	/
			COS-7 cells	Regulate gp78 distribution	ERAD	/	Gp78 [72]	Cys-352	/
zDHHC	Intracellular localization	Tissue-specific distribution	Object	Function	Pathway	Disease	Target protein	Modified site	miRNA
zDHHC-12	ER/Golgi	Ascites, skin, lung, prostate, stomach, brain	C57BL/6	Modifies Aβ deposition	/	Alzheimer's disease	β-Amyloid peptides (Aβ) [73]	/	/

zDHHC-13	ER	Uterus, brain, testis, stomach, placenta, colon	C57BL/6 J, HPMs, and B16 cells	Tumor inhibitor	/	Melanomagenesis	Melanocortin-1 receptor (MC1R) [54, 55]	Cys-315	/
			HEK-293 T, Hep1–6, MCF-7	Regulate mitochondrial activity	/	Abnormal liver function	MCAT and CTNND1 [7]	/	/
			C57BL/6NJ	Regulate anxiety-related behaviors	/	Behavioral abnormalities	Drp1 [74]	/	/
			HEK293 and MC3T3E1 cells	Regulator of postnatal skeletal development and bone mass acquisition	/	Osteoporosis	MT1-MMP [10]	Cys-574	/
			C57BL/6	Important for hair anchoring and skin barrier function	/	Alopecia and hyperkeratosis	Cornifelin [9]	Cys-95, Cys-101	/
			YAC128, mouse	Regulate the cell death-signaling pathways	/	Huntington disease	GluN2B [19]	Cys clusters I and II	/
zDHHC-14	ER	Brain, fetal eyes, uterus, prostate	HEK293 cells	Stabilize the receptor	MAPK	/	β2-adrenergic receptors (β_2AR) [28]	Cys-256, Cys-341	/
			TMK-1 cells	Regulate GC cell migration and invasion	/	Gastric cancer	MMP-17[17]	/	/
			K562 cells	Regulate cellular differentiation	/	Acute biphenotypic leukemia	CD61 [18]	/	/
			Serum samples of CAD patients	Promote cell growth of vascular smooth muscle cells	TLR9	Coronary artery disease (CAD)	/	/	miR-574-5p [75]
zDHHC	Intracellular localization	Tissue-specific distribution	Object	Function	Pathway	Disease	Target protein	Modified site	miRNA

(continued)

Table 10.1 (continued)

zDHHC	Intracellular localization	Tissue-specific distribution	Object	Function	Pathway	Disease	Target protein	Modified site	miRNA
zDHHC-15	Golgi	Brain, trachea, cerebellum, ear, eye, kidney	HeLa cells	Affect the transport of CCR5	/	HIV-1 infection	CCR5 [13]	Cys-3	/
			HEK293 and HEK-nNOS cells	Important for neuronal connections, contribute to neurodevelopmental deficits	/	Neuro heteroplasia	PSD-95[4]	Cys-3, Cys-5	/
			PC12, HEK293	Promote CSP stabilization	/	/	Cysteine-string protein [14]	Cys-136	/
zDHHC-16	ER	Brain, placenta, lung, uterus, skin	C57Bl/6	Regulation of DNA damage responses	Atm	DNA damage	C-Abl [3]	/	/
			Zebrafish	Regulate NSPCs proliferation	FGF/ERK	Neurological disorders	Neural stem/progenitor cells (NSPCs) [76]	/	/
zDHHC-17	Golgi	Brain, uterus, eye, lung, thalamus	Zebrafish	Affect TrkA binding to tubulin	ERK1/2	/	TrkA-tubulin [77]	/	/
			YAC128, mouse	Regulate the cell death-signaling pathways	/	Huntington disease	GluN2B [78]	Cys clusters I and II	/
			C57BL/6 JBabr mice	Influence NMNAT2 protein turnover and axon protective capacity	/	Axon degeneration and phenotypic disease	Nicotinamide mononucleotide adenylyltransferase 2 (NMNAT2) [79]	Cys-164, Cys-165	/
zDHHC-18	Golgi	Lung, testis, brain, placenta, carcinoid, kidney, prostate	HEK293 cells	Stabilize the receptor	MAPK	/	β2-adrenergic receptors (β_2AR) [28]	Cys-256, Cys-341	/
			Human GBM specimens	Associated with the malignant development and progression of gliomas	/	Glioblastomas (GBM)	BMI1 [25]	/	/
zDHHC-19	ER	Testis, brain, medulla, placenta	HeLa, 293 T, Huh7.5.1 cells	Promote CHIKV replication	/	Chikungunya virus (CHIKV)	nsP1 [32]	Cys-417, Cys-418, Cys-419	/

zDHHC	Intracellular localization	Tissue-specific distribution	Object	Function	Pathway	Disease	Target protein	Modified site	miRNA
zDHHC-20	Plasma membrane	Placenta, uterus, brain, lung, testis	HEK-293T, A549, MEFs cells	Increase IFITM3 antiviral activity	/	Virus infections	Interferon-induced transmembrane protein 3[5]	Cys-71, Cys-72, Cys-105	/
			PC12, Jurkat cells	Impact the secretion of TAT	/	HIV-1 infections	HIV-1 Tat [37]	Cys-31	/
			HEK-293T, NIH 3 T3, and SW1573	Impact cancer cell survival	ERK/ AKT	Cancers	EGFR [80]	Cys-1025, Cys-1122	/
			Primary mouse neural stem cells	Regulate the localization and trafficking of BMPR1a and alter BMP signaling	BMP	BMP	Bone morphogenic protein receptor 1a (BMPR1a) [35]	Cys-180	/
zDHHC-21	Plasma membrane	Brain, testis, uterus, eye, liver	C57BL/6 J	Regulate depression-like behavior	MAPK	Major depressive disorder (MDD)	Serotonin 1A receptor (5-HT1AR) [52]	Cys-417, Cys-420	miR-30e
			F233Δ mice	Affect vascular function	ERK1/2	/	α1D adrenoceptor [50]	Cys-120	/
			Rats	Regulate endothelial inflammation	GPCR	Endothelial dysfunction	PLCβ1 [49]	Cys-17	/
			Mouse	Regulate hair shaft differentiation	Wnt	Hair loss	Fyn [81]	/	/
			HUVEC, HEK 293 T, COS-7 cells	Regulate the levels of PECAM1 at the cell surface	/	/	PECAM1 [82]	Cys-595	/

(continued)

Table 10.1 (continued)

zDHHC	Intracellular localization	Tissue-specific distribution	Object	Function	Pathway	Disease	Target protein	Modified site	miRNA
zDHHC-22	ER/Golgi	Brain, eye, lung	Neuro2a, HEK293	Regulate CCN3 secretion	/	Cancer	NOV/CCN3 [38]	Cys-241	/
			HEK293 cells	Control BK channel cell surface expression	/	/	S0-S1 loop of BK channels [83]	Cys-53, Cys-54, Cys-56	/
zDHHC-23	ER	Testis, brain, colon, kidney	Human GBM specimens	Regulate the polyubiquitination and accumulation of BMI1		Glioblastomas (GBM)	BMI1 [25]	/	/
			HEK293 cells	Control BK channel cell surface expression	/	/	S0-S1 loop of BK channels [83]	Cys-53, Cys-54, Cys-56	/

"/": Not mention in the chapter

proteins with different subcellular localization, most zDHHCs are located to the secretory pathway such as endoplasmic reticulum and Golgi apparatus, while some are also identified in the cell membrane [11]. Many proteins have been identified as the substrates for zDHHCs, including programmed death-ligand 1 (PD-L1) [12], CC chemokine receptor 5 (CCR5) [13], cysteine-string protein (CSP) [14], and neurochondrin (Ncdn) [15]. When S-palmitoylation happens, zDHHCs first become transient acyl-intermediate by autoacylated, which are then transferred to the target protein. For some special proteins, physical contact between proteins and zDHHCs is essential for the rate and efficiency of S-palmitoylation. For instance, site mutations lead to physical isolation of the CSP from the zDHHCs, further inhibits the S-palmitoylation of CSP [14]. Not all the zDHHCs possess the same enzymatic activity, partly due to the sequence diversity at the C- and N-terminal cytoplasmic tails. Some zDHHCs have substrate specificity, while others do not. Someone attributes it to the different sequence and exterior region of the zDHHCs domain, as well as their subcellular localization, though more studies are needed to confirm this.

As the major enzyme regulating protein S-palmitoylation, zDHHCs are also potentially the targets for the treatment of S-palmitoylation-associated disorders, and the development of agonists/inhibitors of S-palmitoylation is also an alternative solution for disease treatment. In the following, we will review the influence of S-palmitoylation on protein performance, the characteristics of S-palmitoylation regulating protein function, and the potential role of targeted S-palmitoylation agonists/inhibitors in the treatment of related diseases.

10.2 Characteristics of S-Palmitoylation Regulating Protein

10.2.1 Same zDHHC Exerts Opposite Functions in Different Cancers

The same zDHHC has the opposite function in different cancer tissues, overexpress of zDHHC-14 inhibits tumorigenesis [16] but promotes the invasion and migration of scirrhous gastric cancer [17], respectively. The different proteins regulated by zDHHC-14 in different tumors may be responsible for this phenomenon. For example, S-palmitoylation of MMP-17 is regulated by zDHHC-14 in scirrhous-type gastric cancer, and it can promote the growth, invasion, and metastasis of tumor cells, as well as the formation of tumor blood vessels [18]. Besides, S-palmitoylation of CD61 is also regulated by zDHHC-14 in leukemia and related to the inhibition of cellular differentiation [18]. So, if we try to use it as a target for the treatment of related diseases, we need to consider that it has the opposite effect in different tissues.

10.2.2 Same Protein Palmitoylated by Different zDHHCs Has Same/Different Function

One protein can be modified by several zDHHCs; for example, both zDHHC-17 and zDHHC-13 are responsible for the S-palmitoylation of huntingtin [19]. zDHHC-2, zDHHC-3, zDHHC-7, zDHHC-15, and zDHHC-17 are related to SNAP-25 S-palmitoylation [20]. The function of protein palmitoylated by different zDHHCs may be similar. For instance, knockout zDHHC-5 or mutate at its acylated Cys residues decrease the CIL56-induced cell death, overexpression of both zDHHC-5 and zDHHC-8 restore CIL56-induced cell death in 293 T zDHHC-5^{KO} cells [21]. Besides, PD-L1 palmitoylated by zDHHC-9 increases its protein level and cell surface distribution in breast cancer cells, thereby promoting the growth of RAS-activated tumors [12]. Meanwhile, zDHHC-3 can also palmitoylate PD-L1 and inhibit its mono-ubiquitination, thus block its trafficking to the multivesicular body. Consequently, this block increases the protein level of PD-L1 and inhibits T-cell cytotoxicity [22]. However, the same protein regulated by different zDHHCs may also play different roles in diseases. PSD-95 palmitoylated by zDHHC-8 can impact the nitrosylation of PSD-95, while zDHHC-15 can promote the S-palmitoylation of PSD-95 and increase the overall density of excitatory synapses [4].

10.2.3 zDHHC Itself Can Also Undergo S-Palmitoylation

zDHHC-6, as a palmitoyl acyltransferase regulating protein S-palmitoylation, is also palmitoylated by other enzymes. The zDHHC-16 can palmitoylate zDHHC-6, silence or knock out zDHHC-6 in HAP1 cells increases the mRNA level of zDHHC-16, indicating that they may interact physically and genetically [23]. What's more, phosphorylation of zDHHC affects auto S-palmitoylation and S-palmitoylation of target proteins. zDHHC-3 auto S-palmitoylation was increased by abolishing tyrosine phosphorylation, and it further enhanced interplay with neural cell adhesion molecule (NCAM) and promoted NCAM S-palmitoylation [24].

10.2.4 The Impact Between S-Palmitoylation and Other Protein Modifications

When the distance between the S-palmitoylation site and other protein modification sites is close, the two protein modifications may interact with each other. For example, PSD-95 was related to the neurodevelopmental and neurodegenerative diseases, and Cys-3 and Cys-5 are common sites of nitrosylation and S-palmitoylation. The nitrosylation of PSD-95 was influenced by its S-palmitoylation which was regulated by zDHHC-8. At the same time, the S-palmitoylation of PSD-95 was inhibited by NO produced in granule cells of the cerebellum, indicating a competitive cysteine modification between S-palmitoylation and nitrosylation of PSD-95 [4].

The interaction between S-palmitoylation and ubiquitination was observed in many proteins. The overexpression of zDHHC-18 reduced the amount of polyubiquitinated BMI1 and increased the tumor cell survival. Interestingly, the deletion of zDHHC-23 has the same effect as above [25]. It has been also demonstrated that PD-L1 ubiquitination is blocked by its S-palmitoylation on Cys-272, thereby inhibiting the degradation of PD-L1 caused by lysosomes. The ubiquitination of PD-L1 is increased by both 2-BP treatment and depletion of zDHHC-3 [22]. Proteins are more sensitive to ubiquitination when S-palmitoylation is disturbed. S-palmitoylation of lipoprotein receptor-related protein 6 (LRP6) is necessary for its export out of the endoplasmic reticulum and proper cell membrane trafficking. LRP6 deficient in palmitoylation retains in the endoplasmic reticulum, due to ubiquitination at Lys-1403, which locates nearby the palmitoylation sites (Cys-1394 and Cys-1399) [26].

S-palmitoylation of proteins with a weak membrane affinity (e.g., H- and N-Ras) can enhance the strength of their membrane interaction and trap proteins on a proper intracellular membrane. As a consequence, proteins bind to budding vesicles efficiently and do not separate from cell membranes during vesicle transport. S-palmitoylation may enhance protein membrane interaction due to cooperation with other modifications. Farnesylation at the C-terminal of Ras regulates its association with ER and Golgi membranes; however, farnesylation only provides Ras with a weak membrane affinity. When S-palmitoylation occurs, two lipid modifications in tandem can increase the membrane interaction of Ras [27].

Besides, the regulatory effect of S-palmitoylation on phosphorylation was also found in β_2AR. Ser-345/Ser-346 and Ser-261/Ser-262, the phosphorylation sites of β_2AR, are located next to its S-palmitoylation sites, Cys-341 and Cys-265. Studies show that phosphorylation by cAMP-dependent kinase (PKA) is essential for S-palmitoylation of β_2AR at Cys-265. Inhibition of S-palmitoylation by H-89 suppresses isoproterenol-caused, PKA-mediated phosphorylation at both Ser-261/Ser-262 and Ser-345/Ser-346. What's more, S-palmitoylation at Cys-341 restricts the accessibility of a PKA phosphorylation site in the carboxyl tail of the β_2AR and then regulates the phosphorylation state [28].

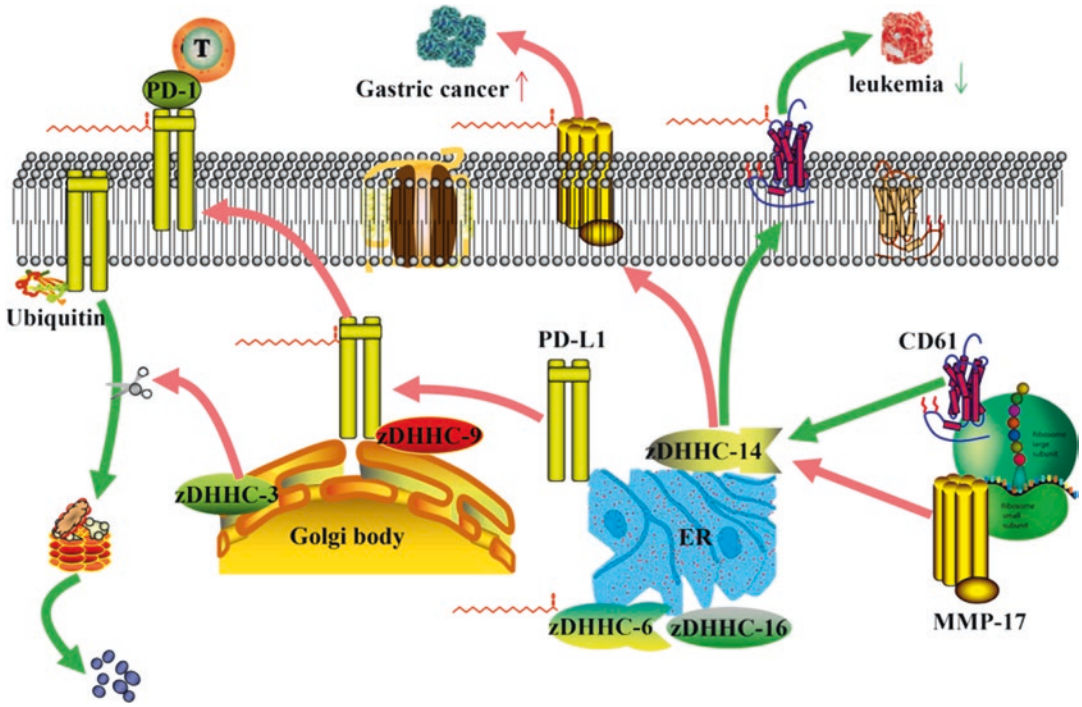

Fig. 10.1 Characteristics of S-palmitoylation regulating protein function

10.2.5 The Interaction Degree of zDHHCs on Different Proteins and S-Palmitoylation Modification Sites Are Various

Different proteins can be palmitoylated by an unequal number of zDHHCs due to their special spatial structure. For instance, interferon-induced transmembrane protein 3 (IFITM3) is a broad-spectrum virus inhibitor that can be palmitoylated by half of the zDHHCs [5]. However, β_2AR can be palmitoylated by zDHHC-9, zDHHC-14, and zDHHC-18 [28]. It is interesting to note that the nucleotide oligomerization domain-like receptors 1 and 2 are only palmitoylated by zDHHC-5 [6]. This phenomenon affects the therapeutic effect of targeting zDHHCs to some extent.

Further studies found that zDHHC has different effects on different S-palmitoylation modification sites. Cys-265 and Cys-341 are S-palmitoylation modification sites of β_2AR, knockdown zDHHC-9, zDHHC-14, zDHHC-18 alone or in combination reduce S-palmitoylation at Cys-265. However, the zDHHC-9/zDHHC-14/zDHHC-18 knockdown shows no obvious influence on S-palmitoylation at Cys-341, indicating the response of Cys-265 and Cys-341 to zDHHC-9/zDHHC-14/zDHHC-18 is different [28]. As a consequence, S-palmitoylation of the same protein at different sites may further exert distinct effects on physiological activity. AMPA receptor subunits (GluR1-GluR4) are palmitoylated at different sites (site 1 and site 2), which are located at various transmembrane domains (TMDs). S-palmitoylation of site 1 increases the accumulation of this receptor in Golgi apparatus and reduces expression levels on the cell surface, while S-palmitoylation of site 2 fails to regulate stable expression levels on the cell surface of the receptor [29] (Fig. 10.1).

10.3 S-Palmitoylation on Protein Function

10.3.1 Effect on Protein Sorting and Trafficking

Many membrane proteins are synthesized on ribosomes and then undergo a variety of processing and modification at the ER. Finally, these proteins with different markers are transported to the destinations via protein sorting and trafficking pathways. S-palmitoylation is certainly important in maintaining the stability of some proteins during sorting and trafficking. D2 dopamine receptor (D2R), a G protein-coupled receptor (GPCR), is indispensable in regulating mood [30]. Cys-443 represents the major amino acid of D2R S-palmitoylation by zDHHC-3 and zDHHC-4. S-palmitoylation of D2R can regulate the receptor proper trafficking to the cell membrane and maintain the receptor stability during the progress. C443 deletion or palmitoylation inhibition caused an obvious decline in D2R expression on the plasma membrane and a contingent increase in the Golgi.

The biophysical properties of many transmembrane and soluble proteins are altered by S-palmitoylation; these changes may affect the protein sorting and trafficking process including the transport rate of proteins across the Golgi. S-palmitoylation has been proved to be an anterograde signal for many proteins at the Golgi membrane interface; it leads to the concentration of curved regions along the Golgi edge by simple physicochemical action. For instance, the S-palmitoylation of G glycoprotein of the vesicular stomatitis virus (VSV-G) and transferrin receptor induced them to concentrate in the most curved regions of the Golgi membranes, thereby they are absorbed by highly curved tubular or vesicular carriers, finally promoted their efficient transport across the Golgi [31].

S-palmitoylation of protein can directly regulate its sorting and trafficking to affect subcellular localization. nsP1 which is one nonstructural protein in the open reading frames of the Chikungunya virus can locate in the plasma membrane and filopodial extensions after palmitoylated by zDHHC-2 and zDHHC-9. When S-palmitoylation is disturbed, nsP1 is degraded without proper localization, leading to reduced nsP1 plasma membrane levels and weakened viral replication [32]. Kim et al. find that S-palmitoylation of MCOLN3/TRPML3 regulates its trafficking between subcellular compartments to maintain its cellular function when autophagy is activated [33]. And some palmitoylated proteins can also regulate other proteins' sorting and trafficking. S-palmitoylation of PSD-95 at Cys-3 and Cys-5 is crucial for the synaptic trafficking of α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptor (AMPAR) [34].

In addition to affect protein proper localization, S-palmitoylation further alters the signaling pathways and related functions involved in these proteins. As a major mediator of the bone morphogenic protein (BMP) signaling, BMP receptor 1a (BMPR1a) in embryonic stem cells and neural stem cells is also palmitoylated. BMPR1a S-palmitoylation at Cys-180 plays an essential role in the appropriate localization and intracellular trafficking of BMPR1a, further selectively alters ERK-dependent BMP signaling and increases the production of oligodendrocytes, ultimately affecting NSC activity and fate choices [35]. A similar phenomenon is also observed in death receptor 4 (DR4), which is palmitoylated by zDHHC-3. The S-palmitoylation of DR4 is required for its localization to lipid rafts, facilitating the efficient transmission of the cell death signal induced by TNF-related apoptosis-inducing ligand [36].

10.3.2 Effect on Protein Secretion

Abnormal protein secretion is related to several diseases and affected by S-palmitoylation. Tat is necessary for viral gene expression and HIV-1 virion production; S-palmitoylation of Tat prevents its secretion by enhancing its combination with the plasma membrane [37]. CCR5 is responsible for the dissemination and establishment of HIV-1 infection; site mutation will weaken the S-palmitoylation and secretion of CCR5. Single-site mutants slightly reduce

the secretion of CCR5, and double- and triple-site mutants lead to a 50% drop in its secretion, which remarkably impairs HIV-1 infection of human macrophages [13]. A recent study shows that excessive secretion of nephroblastoma-overexpressed protein (CCN3) suppresses the neurons' axon growth, and thrombospondin type-1 (TSP1) domain of CCN3 is responsible for its secretion. S-palmitoylation of CCN3 at Cys-241 in its TSP1 domain is regulated by zDHHC-22, and mutation at Cys-241 suppresses the secretion of CCN3, indicating that S-palmitoylation is crucial for the secretion of CCN3 [38]. S-palmitoylation can directly or indirectly affect protein secretion. Wnts is a poorly secreted protein, which is important in the regulation of the growth of embryos and repairing the damaged tissues. There are studies show that Porcupine (PORCN) in combination with Wntless (WLS) regulates the secretion of Wnts, overexpression of PORCN promotes the S-palmitoylation of Wnts, and increase WLS's function of promoting Wnts secretion [39].

10.3.3 Effect on Protein Stability

S-palmitoylation can affect protein stability and alter degradation to cycling. Protein stability directly affects the amount of protein in the cell membrane and its function. As a posttranslational, reversible lipid modification, S-palmitoylation can indeed promote the association between proteins and lipid rafts, partly due to its ability to change the lipophilicity and hydrophobicity of proteins. S-palmitoylation of the D2R at C443 can affect the binding of PDZ-domain-containing proteins such as GIPC. GIPC has been shown to interact with the C-terminal cysteine of D2R and D3R (but not D4R) and prevent their lysosomal degradation. C443 deletion also resulted in decreased expression of D2R protein compared to wild-type D2R. ΔC443-D2R and wild-type receptor exhibited no detectable differences in mRNA expression, whereas the mutant protein showed an increased rate of degradation compared to wild-type D2R [30].

The lysosomal sorting receptor sortilin palmitoylated by zDHHC-15 is a prerequisite for the efficient retrograde trafficking of sortilin and recycling sortilin back to the Golgi. Sortilin fails to be recycled and is rapidly degraded in the absence of S-palmitoylation [40]. Recently study found that Ras is palmitoylated in the Golgi and then transported to the cell membrane, where it undergoes depalmitoylation to release Ras back into the cytosol, allowing Ras rebinds to the Golgi apparatus, and then begins the next cycle [41]. PD-L1 is a famous transmembrane protein that is pivotal for the immune escape of tumor cells. Studies show that S-palmitoylation of PD-L1 at Cys-272 by zDHHC-9 enhances the protein stability and cell surface distribution of PD-L1 and thus prevents the tumor from immune surveillance of T cells. Meanwhile, zDHHC-9 knockout or mutation of Cys-272 sharply abrogates PD-L1 S-palmitoylation, resulting in a lower protein level of PD-L1, and further inhibiting breast cancer cell growth with a better therapeutic efficacy [12]. The effect of S-palmitoylation on protein stability can also be observed in many proteins, including Ncdn [15], UL20 [42], progressive rod-cone degeneration (PRCD) [43], somatostatin receptor 5 (SSTR5) [44], CSP [14], and β2-adrenergic receptors (β_2AR) [28].

S-palmitoylation can gather or separate proteins under specific conditions by regulating the association between membrane proteins and lipid rafts. S-palmitoylation and glycosylation of neurotensin receptor-1 (NTSR-1) promote its trafficking to the structured membrane microdomains, interaction with $G\alpha_{q/11}$, and subsequent NTS-mediated ERK phosphorylation [45]. On the contrary, S-palmitoylation of toxin receptor TEM8 unexpectedly restrains its association with lipid rafts and segregates the receptor from its E3 ubiquitin ligase Cbl and consequently prevents its premature ubiquitination [46].

10.3.4 Effect on Protein Interactions

The biophysical properties of proteins are changed by S-palmitoylation, as well as their interaction with other proteins and the signal

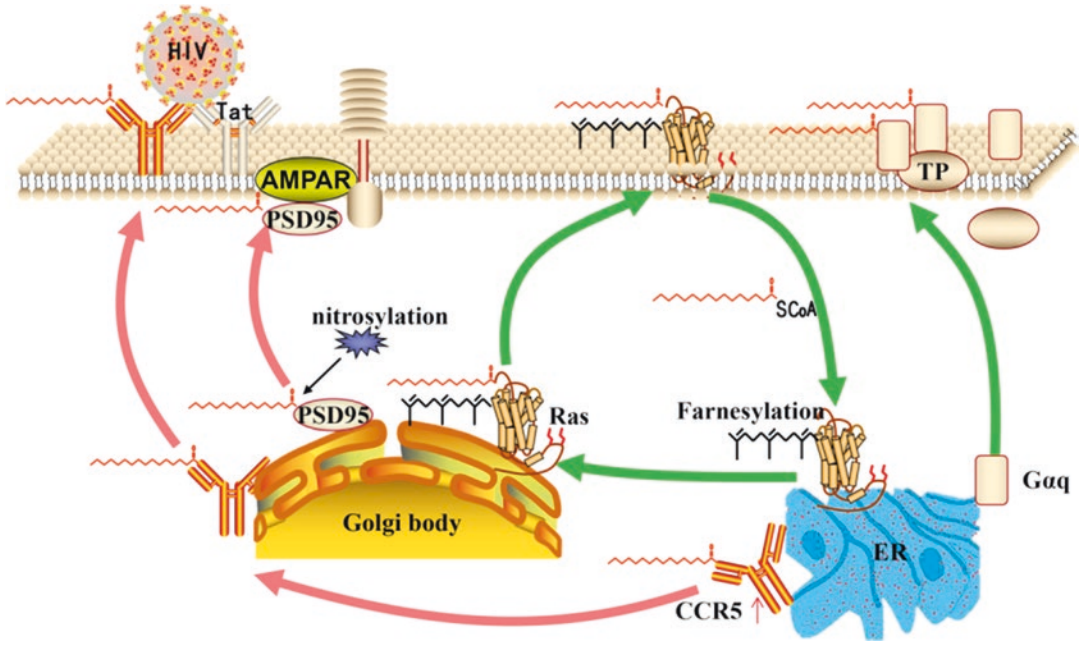

Fig. 10.2 Schematic illustration of S-palmitoylation regulating protein function

pathways they are involved in. A study about sepsis finds that myeloid differentiation primary response protein (MYD88) is responsible for the activation of Toll-like receptor (TLR) signaling by recruiting interleukin-1 receptor-associated kinase 4 (IRAK4). The S-palmitoylation sites of MYD88 (Cys-113 and Cys-274) may be involved in the MYD88-dependent TLR signaling activation. Mutant from cysteine to alanine at position 113 reduces the S-palmitoylation level of MYD88 and blocks the interaction between MYD88 and IRAK4, further inhibits TLR-caused inflammation, and facilitates the survival of mice with sepsis. However, all the phenomena above are rescuable by the CA113C reverse mutant, demonstrating that the S-palmitoylation of MYD88 at Cys-113 plays an important role in recruiting IRAK4 [8].

S-palmitoylation also regulates the interaction between membrane proteins and cytoplasmic proteins. Cation-dependent mannose-6-phosphate receptor (CD-M6PR) which is a type I transmembrane protein takes charge of arranging the new acid hydrolases. The CD-M6PR will return to the Golgi for recycling after it delivers acid hydrolases to endosomes from the trans-Golgi network. This step is under the control of the S-palmitoylation of CD-M6PR, which allows the interaction between cytosolic domain of CD-M6PR and retromer complex [40].

In addition, the degree of protein interaction depends on the level of S-palmitoylation. In pulmonary hypertension of the newborn (PPHN), hypoxia can increase the S-palmitoylation level of Gαq and promote the interaction of Gαq with thromboxane prostanoid (TP). This interaction depends on the S-palmitoylation degree of Gαq, the single-site mutant has little effect on the binding of Gαq and TPα, while double C9A/C10A mutants result in a significant reduction in the association of Gαq with TPα [47] (Fig. 10.2).

10.4 S-Palmitoylation on Pulmonary Inflammation and Disease

10.4.1 S-Palmitoylation and Lung Inflammation

In recent years, inflammatory lung diseases caused by pathogenic microorganisms, such as

SARS and COVID-19, have posed a great threat to human health. Studies have shown that S-palmitoylation is very important in the process of pathogenic microorganisms infecting the lungs. *Legionella pneumophila* was the bacterial pathogen of Legionnaires' disease, it could multiply in human alveolar macrophages and lung epithelial cells, and then cause a severe pneumonia. The virulence of *Legionella pneumophila* is closely related to the Dot/ICM IV type secretion system, which can manipulate the cell signal by carrying more than 300 kinds of effector protein to the host cell protein. This bacterium can build vacuoles (LCV) containing *Legionella* in the endoplasmic reticulum to avoid being decomposed by phagocytic enzymes. The process of localization of effector protein LpdA to LCV requires S-palmitoylation. S-palmitoylation-deficiency LpdA targets the plasma membrane and vesicle, where it hydrolyzes a range of substrates to produce phospholipid acid (PA). The disturbance of cell PA homeostasis will destroy the integrity of Golgi apparatus, thus increasing the virulence of *Legionella pneumophila* in the lung [48].

Endothelial dysfunction is an important sign of systemic inflammatory response syndrome (SIRS). 2-BP treatment can improve the vascular barrier damage in the lung by reducing leukocyte adhesion, microvascular leakage, and ICAM-1 expression. By studying the expression and function of DHHC-PAT in mouse lung microvascular endothelial cells, it was found that only the knockout of zDHHC-5 and zDHHC-21 significantly improved the barrier function. After IL-1b stimulation, the number of adherent white blood cells increased significantly, and inflammation can increase the S-palmitoylation level of phospholipase C β1 (PLCβ1). PLCβ1 is a major signal molecule downstream of GPCR, which mediates the inflammatory effects of thrombin and histamine. Thickening of alveolar capillary membranes and leukocyte infiltration have been noted in the zDHHC-21 group of mice. The overexpression of wild-type PLCβ1 in zDHHC-21$^{dep/des}$ endothelial cells failed to enhance the barrier dysfunction induced by thrombin, indicating that DHHC21-mediated S-palmitoylation of PLCβ1 is pivotal for the dysfunction of endothelial cells during inflammation, because it could activate a series of downstream events including calcium ion and phosphatase mobilization [49].

When the host's response to bacterial infection becomes unbalanced, a systemic inflammation called sepsis occurs. Under such conditions, the uncontrollable activation of inflammatory signals by TLR/MYD88 will damage the bactericidal activity of neutrophils and reduce the apoptosis and chemotaxis activity of neutrophils. zDHHC-6 palmitoylates MYD88 by using the endogenous fatty acids synthesized by FASN and CD36-mediated uptake of exogenous fatty acids. FASN inhibitor (C57) treatment or zDHHC-6 gene knockout can reduce the S-palmitoylation of MYD88 and the activation of TLR/MYD88 stimulated by lipopolysaccharide and further enhance the chemotactic activity of neutrophils and improve the survival of septic mice [8].

10.4.2 S-Palmitoylation and Pulmonary Hypertension

In addition to regulating lung inflammation, zDHHC-21 can also regulate the function of pulmonary blood vessels. zDHHC-21 is expressed in endothelial cells and is responsible for the S-palmitoylation of platelet endothelial cell adhesion molecule-1 and endothelial nitric oxide synthase, which are involved in pulmonary vasodilation and pulmonary vascular remodeling, angiogenesis, and transendothelial cell migration. α-1 adrenergic receptor (α1D AR), a key determinant of vascular tone, was also identified as new substrates for zDHHC-21 recently. zDHHC-21 has been reported to directly interact with α1D AR to form a complex, increasing the steady-state S-palmitoylation of α1D AR and the total expression of α1D AR, finally destroy α1AR-mediated vasoconstriction [50].

The S-palmitoylation of α1D AR is specific because zDHHC-21 cannot palmitoylate Gαq, which can regulate calcium mobilization by interacting with thromboxane prostanoid α isoforms (TPα). zDHHC-7 is responsible for the S-palmitoylation of Gαq in pulmonary hyperten-

sion of the newborn, and this lipid modification of Gαq plays an essential role in receptor-Gαq-phospholipase-C interactions. Hypoxic treatment of HEK-293T cells for 24 hours could promote the S-palmitoylation of Gαq and further increase the generation of inositol-1,4,5-trisphosphate mediated by TP. 2-BP treatment can significantly inhibit the S-palmitoylation of Gαq and reduce TP-mediated calcium mobilization. Cysteine mutations can change the S-palmitoylation and membrane localization of Gαq and have a dose-dependent effect on the calcium response induced by TP [47].

10.5 Treatment Strategies for S-Palmitoylation-Related Diseases

10.5.1 Targeting zDHHC-Related miRNAs

The S-palmitoylation of protein controls its activation and functions, since the most S-palmitoylation of proteins is regulated by zDHHC, it may be a workable plan to regulate protein S-palmitoylation by targeting zDHHC. Present studies show that zDHHC expression can be regulated by miRNAs. miR-134 has been proved to regulate the expression of zDHHC-9 and the S-palmitoylation of H-Ras mediated by zDHHC-9 and further change the subcellular localization of H-Ras [51]. miR-30e can downregulate the expression of zDHHC-21, which further reduce the S-palmitoylation of the serotonin 1A receptor (5-HT1AR) and 5-HT1AR-mediated signaling, eventually lead to depressive symptoms [52].

10.5.2 Regulate the Protein Depalmitoylation

The cycle rates of S-palmitate and depalmitate between different protein types may vary greatly. This dynamic cycle is essential for protein transport, stability, and function. Depalmitoylation can change the location and function of palmitoylated proteins and then deliver them to lysosomes for degradation, indicating the importance of depalmitoylation in protein turnover. AMPA receptor is involved in the higher Ca^{2+} permeability that associates with motor neuron degeneration; PSD-95 can stabilize AMPA receptor at the postsynaptic membrane. GluR2 regulates the trafficking of AMPARs to the cell membrane from the endoplasmic reticulum, and depalmitoylation decreases GluR2 and PSD-95 expressions, leading to reduced mediated toxicity and calcium signaling in motor neurons [53].

Protein depalmitoylation is mainly regulated by the α/β hydrolase domain-containing 17 proteins (ABHD17s), the acyl-protein thioesterases (APTs), and the palmitoyl-protein thioesterases (PPTs). Some drugs targeting these enzymes may exert a positive effect on protein S-palmitoylation-related diseases. The S-palmitoylation of melanocortin-1 receptor (MC1R) regulated by zDHHC-13 was negatively related to the incidence of melanoma. APT2, as the primary MC1R depalmitoylase, can easily abolish these beneficial effects. ML349 and Palm-B are specific and nonspecific inhibitors of depalmitoylation, respectively. Both of them show a surprisingly powerful preventative effect on melanomagenesis by recovering MC1R S-palmitoylation and inhibiting the malignant transformation [54, 55].

Other drugs were also proved to be able to regulate protein depalmitoylation. Wogonoside can significantly induce the depalmitoylation of N-Ras and phospholipid scramblase 1 (PLSCR1), whose abnormal expressions are involved in the acute myeloid leukemia (AML). Depalmitoylation of PLSCR1 controls its trafficking to the cell membrane or the nucleus. Depalmitoylation of N-Ras decreases its ability to bind with phospholipid bilayers in the plasma membrane and thereby suppresses RAF1 phosphorylation and eventually leads to the inactivation of N-Ras/RAF1 pathway. Although the effects of wogonoside on the depalmitoylation of N-Ras and PLSCR1 are different, they all end up having anti-AML effects [56].

10.5.3 Exploit the Agonists of S-Palmitoylation

Since a high level of protein S-palmitoylation exerts a beneficial effect on certain diseases, some agonists are exploited to promote protein S-palmitoylation. Fluoxetine can significantly increase the S-palmitoylation level of GLUT1 and then promote the translocation of GLUT1 to membrane compartments, which increases in transporter activity and cellular glucose uptake [57]. Studies about cell proliferation show that both the S-palmitoylation level of both α-tubulin and Ras-related protein Rab-7α (Rab7α) are increased upon a stimulation of androgen. The regulatory effects of agonists on protein S-palmitoylation are often dose dependent; this phenomenon is observed in the experiment about isoproterenol (ISO) and β_2AR-C341A: 1 nM ISO enhances the S-palmitoylation of β_2AR-C341A to some extent and 10μM ISO greatly increases its S-palmitoylation level [28].

10.5.4 Exploit the Inhibitors of S-Palmitoylation

Until now, there are some nonspecific inhibitors including 2-BP, tunicamycin, and cerulenin that have been identified as the inhibitors of protein S-palmitoylation. However, nonspecific inhibitors may have some potential risks; 2-BP can inhibit protein S-palmitoylation and many other metabolic enzymes including glucose-6-phosphatase and fatty acid-CoA ligase at the same time. So it is a good choice to treat diseases by exploiting specific inhibitor of S-palmitoylation with small molecules. In the past, the intracellular routes of proteins' trafficking were considered too generic to be a therapeutic target. However, recent studies have revealed the diversity of the intracellular routes and tried to regulate protein trafficking with S-palmitoylation. Cadmium chloride and Zn pyrithione were identified as selective inhibitors of CCR5; they could inhibit the S-palmitoylation of CCR5 and further reduce the trafficking of CCR5 to the cell membrane [13].

10.6 Conclusions

S-palmitoylation is a common, reversible post-translational lipid modification of proteins; the balance between S-palmitoylation and depalmitoylation is involved in many human diseases. It provides us a potential way to treat diseases by regulating protein S-palmitoylation and depalmitoylation with selective agonists/inhibitors. However, the exploitation of S-palmitoylation selective inhibitors/agonists has been challenging, partly due to the large number of sequence and structural homology between isoforms, so few new inhibitors/agonists have been reported in recent years. It provides a glimmer of hope for the exploitation of S-palmitoylation selective inhibitors/agonists by targeting the structural heterogeneity in the C- and N-terminal domains of isoforms. However, more experiments are needed to achieve this goal. Even if some small molecules are found to function as potential inhibitors/agonists of S-palmitoylation, their hydrophobicity and poor solubility may become another major challenge in application. Fortunately, the development of using liposomes to transport hydrophobic drugs in recent years may be a potential way out.

It is worth noting that the exploitation of selective agonists/inhibitors of S-palmitoylation opens the door for treating diseases, though many obstacles are needed to conquer. What's more, with the development of cryo-electron microscopy and structural biology, the 3-D structure of many zDHHCs may be revealed in the future. It will be a great help for people to exploit selective inhibitors/agonists with a better physiological understanding of zDHHCs.

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Redox Role of ROS and Inflammation in Pulmonary Diseases

11

Li Zuo and Denethi Wijegunawardana

Abstract

Reactive oxygen species (ROS), either derived from exogenous sources or overproduced endogenously, can disrupt the body's antioxidant defenses leading to compromised redox homeostasis. The lungs are highly susceptible to ROS-mediated damage. Oxidative stress (OS) caused by this redox imbalance leads to the pathogenesis of multiple pulmonary diseases such as asthma, chronic obstructive pulmonary disease (COPD), and acute respiratory distress syndrome (ARDS). OS causes damage to important cellular components in terms of lipid peroxidation, protein oxidation, and DNA histone modification. Inflammation further enhances ROS production inducing changes in transcriptional factors which mediate cellular stress response pathways. This deviation from normal cell function contributes to the detrimental pathological characteristics often seen in pulmonary diseases. Although antioxidant therapies are feasible approaches in alleviating OS-related lung impairment, a comprehensive understanding of the updated role of ROS in pulmonary inflammation is vital for the development of optimal treatments. In this chapter, we review the major pulmonary diseases—including COPD, asthma, ARDS, COVID-19, and lung cancer—as well as their association with ROS.

Keywords

NF-κB · Hypoxia-inducible factor-1 · Leukocytes · Mitochondria

11.1 Introduction

Reactive oxygen species (ROS) are chemically active species containing oxygen. They can be grouped into two subtypes: (1) free radical ROS which have one or more unpaired electrons in the valence shell such as superoxide anion radicals ($O_2^{\bullet -}$) and hydroxyl radicals ($^{\bullet}OH$); iIn an attempt to pair up their own electrons, they extract electrons from a stable molecule and leave this original molecule in an unstable state initiating cellular damage); (2) non-radical ROS which lack the presence of unpaired electrons but are still active and have the ability to generate new radicals (i.e., hydrogen peroxide (H_2O_2)) [1, 2]. In biological systems, ROS

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are mostly generated through endogenous metabolic reactions such as phagocyte activation or mitochondrial electron transport during respiration (Fig. 11.1). ROS can also be derived from exogenous sources like cigarette smoke and contribute to the maintenance of cellular redox homeostasis under physiological conditions [3]. The lungs are exposed to elevated oxygen levels, which together with its large blood supply and surface area make it vulnerable to injury mediated by ROS [4]. Interestingly, ROS can be produced due to mitochondrial damage; thus, mitochondria are regarded as both source and target of these oxidants [5]. Moreover, oxidative stress (OS) results from an oxidant/antioxidant imbalance in favor of oxidants and causes oxidation of DNA, proteins, and lipids [6]. Heightened ROS production during inflammation also induces inhibition of apoptosis and activation of proto-oncogenes by initiation of signal transduction pathways. Therefore, it is conceivable that chronic inflammation-induced pulmonary ROS production may predispose individuals to lung diseases caused by OS-mediated pulmonary damage [7]. Epithelial cells, endothelial cells, and recruited inflammatory cells, such as eosinophils, neutrophils, lymphocytes, and monocytes, generate ROS in response to increased levels of secretagogue stimuli [8]. Activation of these inflammatory cells results in the formation of $O_2^{\bullet -}$, which is rapidly converted to H_2O_2 by superoxide dismutase (SOD). As a secondary reaction, $^{\bullet}OH$ is formed nonenzymatically in the presence of Fe^{2+}. Under pathological conditions when there are large concentrations of cellular ROS, permanent changes in signal transduction and gene expression pathways occur. Thus, OS mediated by ROS plays an important physiological role in inflammation and pathogenesis of various lung disorders such as asthma, acute lung injury (ALI), and lung cancer [9] and contributes to conditions such as hypertension [10].

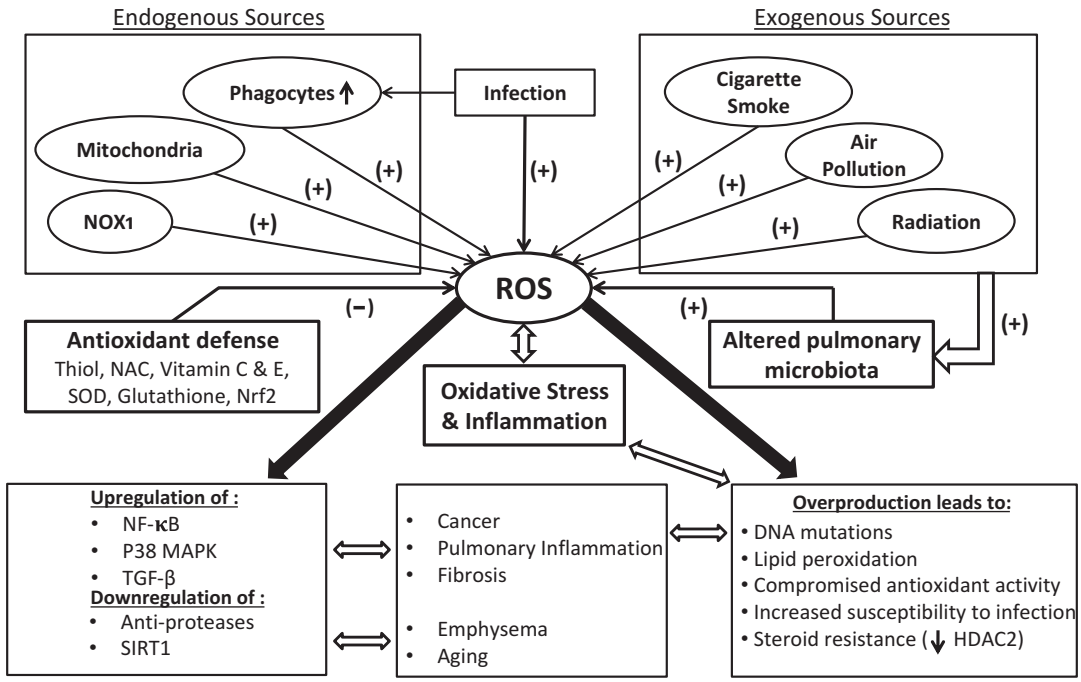

Fig. 11.1 Schematic illustrating key factors of ROS generation in biological and physiological pathways. The level of ROS is regulated by multiple antioxidant defense mechanisms (Thiol; NAC; Vitamin C & E; SOD; Glutathione; Nrf2). Enhanced levels of ROS lead to upregulation of NF-κB associated with cancer, p38 MAPK associated with pulmonary inflammation, TGF-β associated with fibrosis, downregulated anti-proteases with emphysema, and decreased SIRT1 with premature aging. Overproduction of ROS cause DNA mutations, lipid peroxidation and steroid resistance

11.2 Inflammation and Pulmonary Disease

Inflammation is part of the body's defense mechanism to recognize and remove foreign, harmful stimuli to begin the healing process [11]. Leukocytes and mast cells are recruited to the site of damage during inflammation. This causes a boost in the uptake of oxygen which leads to a "respiratory burst" causing an increase in the release and accumulation of ROS at the site of inflammation [12]. This increased inflammatory response exacerbates ROS production via phagocytosis (Fig. 11.1) [13]. Inflammatory cells produce mediators, such as metabolites of chemokines, cytokines, and arachidonic acid, which act by attracting more cells and producing more ROS. These key mediators have the ability to activate signal transduction cascades and induce changes in transcription factors such as nuclear factor-κB (NF-κB), activator protein-1 (AP-1), and hypoxia-inducible factor-1 (HIF-1), which all mediate immediate cellular stress responses. Aberrant expression of inflammatory cytokines such as interleukin-1 (IL-1, IL-6), chemokines (IL-8, CXC chemokine receptor 4 (CXCR4)), and tumor necrosis factor (TNF) have also been reported to play a role in inflammation induced by oxidative stress [14]. The sustained oxidative/inflammatory environment can damage healthy neighboring stromal and epithelial cells over prolonged periods leading to carcinogenesis and pulmonary disease [8, 15].

11.2.1 Nuclear Factor (NF)-κB

NF-κB is a protein transcription factor [16] and modulates gene expression in innate immunity, embryogenesis, cell proliferation, and apoptosis [17]. NF-κB is comprised of a heterodimer with one 50 kDa (p50) and one 65 kDa (p65) polypeptide [18]. NF-κB transcription factors are predominantly regulated by associating with inhibitor IκB proteins. Thus, in most cells, NF-κB is found in the cytoplasm bound to IκB in an inactive complex [19]. ROS molecules can mediate cellular toxicity by reacting with lipids (lipid peroxidation), proteins (especially cysteine residues), and nucleic acids (double strand breaks, histone modifications). Different models of OS have been studied to elucidate their effects on the NF-κB signaling pathway. The archetypal activators of the NF-κB pathway are comprised of TNF-α, lipopolysaccharide (LPS), and IL-1. When stimulated by chemokines such as TNF-α or other cellular stressors, TNF-α binds to TNF receptors. Such binding leads to an interaction with the IκB kinase (IκK) which then leads to the phosphorylation of IκB, subsequently resulting in IκB ubiquitination and degradation. Once degraded, the remaining NF-κB dimer (p65/p50 subunits) translocates to the nucleus, where it binds to various target genes. The selectivity of the NF-κB reaction pathway is based on several factors including cell type, timing, and dimer composition [18].

Endogenous redox regulators like thioredoxin play a role in NF-κB regulation in a model of OS involving UV irradiation. In the cytoplasm, it has been shown that thioredoxin blocks the degradation of IκB in the cytoplasm, while it enhances NF-κB activity in the nucleus by increasing its ability to bind DNA [20]. Antioxidants inhibit NF-κB activity by preventing ROS-induced translocation of this transcription factor into the nucleus. Activation of NF-κB is inhibited by preventing IκB degradation in response to various stimuli [21]. Taken together, these findings indicate that activation of NF-κB by ROS is a critical signaling mechanism for evoking inflammatory responses. NF-κB has also been shown to restrict inflammasome activation by the elimination of damaged mitochondria. Remarkably, in addition to NF-κB being an activator of inflammatory genes, it functions by limiting IL-1β production and NLRP3 inflammasome activation. The The induction of signaling adapter, p62 causes inflammasome inhibitory activity by NF-κB. It can control inflammation in macrophages by promoting p62-mediated removal of damaged mitochondria (mitophagy) after macrophages interact with different NLRP3 inflammasome activators [22].

11.2.2 Hypoxia-Inducible Factor-1

There are many instances, in both physiological and pathophysiological conditions, during which the lungs are subjected to localized or global hypoxia. Adaptation to hypoxia requires the coordinated regulation of a myriad of genes, and this collective response is mostly controlled at the level of transcription. Specifically, the hypoxia-inducible factors (HIFs) have been identified as key mediators of hypoxic conditions [23]. HIF-1α ubiquitination involves hydroxylation at two proline residues, Pro-402 and Pro-564 in human HIF-1α [24]. Under normoxic conditions, prolyl hydroxylase domain proteins (PHD) catalyze the hydroxylation of HIF-1α using molecular O_2 as a substrate. In hypoxic environments, HIF-1α hydroxylation at proline residues decreases due to the absence of sufficient molecular O_2. This causes the PHD activity to decline ensuing protein stabilization. Imminently, HIF-1α translocates into the nucleus where it binds HIF-1β and recruits coactivator proteins to the HIF binding site within the hypoxia response element, activating the transcription of several target genes [25].

HIF-1 is a heterodimeric helix-loop-helix-PAS domain transcription factor. HIF is known to activate hypoxia-responsive genes such as vascular endothelial growth factor (VEGF), an important biomarker of asthma [26]. In a hypoxic ischemia/reperfusion model, increased VEGF levels were associated with upregulation of HIF-1 protein levels resulting in augmented barrier disruption [27]. HIF-1 is composed of two subunits, HIF-1a and HIF-1b. HIF-1a, known to mediate gene expression by intracellular oxygen concentration, has also been found to be activated by nonhypoxic factors such as ROS in a redox-sensitive manner [28]. Furthermore, expression of HIF-1α and HIF-2α occurs in all solid tumors. HIFs represent an important signaling node in the switch to protumorigenic inflammatory responses. In hypoxic environments, antitumor immune responses are suppressed through altered immune cell effector functions and the recruitment of protumor immune cells. Tumor growth is promoted through ROS production, excessive growth-promoting cytokine production, and angiogenesis [29].

Hypoxia may occur as a consequence of acute lung injury (ALI), leading to aberrations in pulmonary function and repair. Initial events in ALI include damage of the alveolar lining layer, apoptosis of alveolar epithelial cells, and lung edema. At advanced phases, reactive hyperplasia of alveolar type II cells is prevalent, leading to fibrosis. During ALI, hypoxia can result in increased vascular permeability. Hypoxia has been reported to induce alveolar type II cell apoptosis via HIF-1α with respect to epithelial cell damage and subsequent fibrotic lung disease [30]. HIF-1α is activated in alveolar type II cells after lung injury and promotes proliferation during repair [31]. Moreover, inflammatory levels of nitric oxide (•NO) upregulate HIF-1 causing the suppression of epithelial cell wound repair [32]. This signifies that increased HIF-1 levels can render the injured, hypoxic lungs which are unable to support an appropriate healing response after epithelial injury. It is proposed that epithelial-mesenchymal transition (EMT) contributes to pulmonary fibrosis in patients with acute lung injuries [33]. This process is related to the hypoxia-induced increases in mitochondrial-derived ROS which stabilizes HIF-1α in multiple cell types, including alveolar epithelial cells [34]. Additionally, cancer cells were found to upregulate HIF-1 activity during metastatic colonization after extravasation in the lungs via ROS-dependent and hypoxia-independent manners. The administration of HIF-1 inhibitor, YC-1, repressed this reprogramming, amplified intratumoral ROS levels, and eventually inhibited the growth of metastatic tumors. These results denoted that HIF-1-mediated metabolic reprogramming is accountable for the survival of pulmonary metastatic cancers by reducing cytotoxic ROS levels [35].

11.2.3 Activator Protein-1

Activator protein-1 (AP-1) is a transcriptional activator composed mainly of the Jun and Fos family members. AP-1 is known to be involved in oxidant signaling, cell proliferation, and apoptosis [36]. TNF-α and transforming growth factor-β_1 (TGF-β_1) are peptides with multiple physiological functions that influence immunologic, neo-

plastic, and fibroproliferative diseases. TNF-α induces TGF-β_1 expression at the transcriptional level in lung fibroblasts via AP-1 activation [37]. It has been shown that many end-stage fibrotic diseases, including idiopathic pulmonary fibrosis, converge in the activation of the AP-1 transcription factor c-Jun in pathologic fibroblasts [38]. Another study analyzed tumor cells grown on an ex vivo 4D lung cancer models. The results show an amplification in components of AP-1, c-Fos, and c-Jun in circulating tumor cells (CTC). Administration of SR11302 (an AP-1 inhibitor) reduced metastatic lesion formation in 4D models [39]. Oxidants also induce AP-1 and AP-1-dependent gene expressions. Pyrrolidine dithiocarbamate (PDTC) inhibits NF-κB specifically. However, PDTC is shown to increase the binding of AP-1 and accumulation of ROS in cancer [40]. Aside from their detrimental effects, ROS function as messenger molecules during physiological processes. Glutamate treatment is also found to increase ROS production and activate AP-1 [41].

11.3 Oxidative Stress and Bronchial Asthma

Bronchial asthma is a chronic inflammatory disease and a serious worldwide health issue affecting 5–10% of people of all ages. Usually characterized by airway eosinophilia, bronchial hyperreactivity, chronic airway inflammation, and bronchoconstriction, its symptoms include recurrent episodes of acute shortness of breath, cough, wheezing, and a feeling of tightness in the chest [42]. According to the Asthma and Allergy Foundation of America (AAFA), over 300 million people suffered from this disorder globally since 2013. In the United States alone, asthma accounts for nine deaths per day and causes a yearly economic loss of $56 billion [43]. I Asthma affected 8.3% of American children in 2019 and is the most common chronic disease observed in childhood [44]. Emerging evidence also suggests that the elderly population is vulnerable to late-onset or even long-standing asthma. Commonly found in the elderly, nanotopic asthma is believed to be related to OS in seniors and vastly affected by ageassociated increases in pathological ROS levels [45].

Several types of asthma have been defined by their phenotypes including allergic asthma, nonallergic asthma, and obesity-related asthma [46]. Most commonly found in childhood, allergic asthma is illustrated by eosinophilic airway inflammation, usually correlated with a familial history of allergic diseases. Allergic asthma is also accompanied by an increase in endogenous ROS formation, OS-induced damage, and mitigated antioxidant defenses [47]. Contrarily, nonallergic asthma is mostly seen in adults. The inflammatory cells present in these asthmatics include eosinophils and neutrophils. Some asthma patients with obesity exhibit significant respiratory symptoms while maintaining low levels of eosinophilic airway inflammation [48]. Excessive ROS can also result in direct oxidant damage and shedding of epithelial cells [49]. There is increasing evidence that inflammation, which is characteristic of asthma, results in increased oxidative stress in the pulmonary tract [50]. Alveolar macrophages from asthmatic subjects show an increased release of $O_2^{\bullet -}$, and other ROS compared with those of healthy controls [51]. The TGF-β-induced activation of the ROS-generating enzyme, NADPH oxidase 4 (Nox4), induces myofibroblast differentiation. This activity is involved in airway smooth muscle (ASM) cell proliferation and hypercontractility in asthma in addition to epithelial ciliary dysfunction in neutrophilic asthma [52].

11.3.1 Role of TLRs in Inflammatory Aspects of Asthma

Emerging data suggest that toll-like receptors (TLRs) may be responsible for the aberrant stimulation of immune responses, feasibly contributing to the long-lasting inflammation seen in asthma [53]. TLRs are a class of pattern recognition receptors (PRRs) that sense conserved molecular patterns for early immune recognition of a pathogen and initiate the innate immune response [54]. Serving as the first line of host

defense, the pulmonary epithelia employ a variety of receptors including TLRs to detect antigens of numerous pathogens. The lung and respiratory tracts are particularly vulnerable to allergens and pathogens due to continuous contact with inhaled air. In addition, TLRs recognize exogenous pathogen-associated molecular patterns (PAMPs) and host-derived damage-associated molecular patterns (DAMPs) [55]. The activation of TLRs through PAMPs and DAMPs selectively induces cytokine release, inflammatory cell recruitment, and inflammation. Specifically, TLR-2 and TLR4 are identified to be the major TLRs responsible for sustaining the immune responses in both asthma and COPD. TLR4 detects gram-negative bacteria via their LPS, while TLR-2 recognizes gram-positive bacteria. Th2 cells, mast cells, and eosinophils are associated with the innate and adaptive immune responses in asthma.

The recognition of allergens activates TLR4 which consequently activates allergen-specific Th2 cells. TLR-2 stimulates Th2-biased immune responses, which may be correlated to the Th1/Th2 discrepancy in asthma. There are two major pathways in TLR signaling that is crucial to the innate immune response: myeloid differentiation factor 88 (MyD88) dependent and MyD88 independent. MyD88 and Toll/IL-1 receptor domain-containing adapter-inducing interferon-β (TRIF) bind autonomously to TLRs. This leads to the release of cytokines such as TNF-α, IL-1β, CXCL10, IL-6, and IFN-γ [56]. During acute asthmatic events, the cleavage products of proteinases, such as fibrinogen, bind to TLR4s resulting in allergic inflammation. Asthmatic patients who eventually died had increased expression of TLR-2, TLR3, and TLR4, suggesting their potential role in the advancement of severe or even fatal asthmatic exacerbations [57].

11.3.2 Clinical Aspects of Asthma

There is an increased oxidant production in patients with asthma compared to healthy subjects. Both EPO and MPO levels are increased, and many markers of OS such as glutathione disulfide, malondialdehyde, and thiobarbituric acid are found in the sputum, peripheral blood, and bronchoalveolar lavage (BAL) fluid of patients with asthma. Levels of these markers correlate with the severity of asthma [58]. At the onset of an asthma attack, an increased production of $^{\bullet}NO$ is paired with an increase in inducible NO synthase (NOS) activity. In the course of an allergic inflammatory response, $^{\bullet}NO$ and $O_2^{\bullet-}$ form peroxynitrite, which exerts damaging effects in the respiratory tract. Reactive nitrogen species (RNS) directly heighten cytotoxicity and airway inflammation through nitrosative stress. Evidence suggests that examination of RNS in the pathobiology of asthma by monitoring the use of fractional exhaled nitric oxide (FE_{NO}) measurements can markedly contribute to asthma diagnosis. Peripheral airway inflammation correlates with an increase in alveolar FE_{NO} in patients with mild asthma. Hence, alveolar FE_{NO} can be used to evaluate the level of eosinophilic inflammation in the distal lungs. FE_{NO} measurement also presents a valuable clinical tool to gather information related to steroid responsiveness in patients with asthma [59]. In a recent study, an inverse correlation was observed between FE_{NO} and Asthma Control Test (ACT) score as well as between FE_{NO} and spirometry indicators of airway obstruction [60]. Therefore, FE_{NO} is a useful tool in asthma management.

11.3.3 Antioxidant Therapies for Asthma

Nutritional supplementation on chronic bronchial asthma plays an important role in the management of the disease. Antioxidant vitamins A, C, and E help counteract oxidants and reduce external attacks by bacteria, viruses, toxins, and xenobiotics in the lungs [61]. Thiol antioxidants that are metabolically converted to glutathione precursors, are also popular options for therapeutics. For example, *N*-acetylcysteine (NAC) is a common thiol precursor. Eosinophils, alveolar macrophages, and neutrophils from asthmatic patients produce more ROS than those from healthy specimen. In mice treated with NAC

which was used as a ROS scavenger, there was a reduction in inflammatory cells in the lungs. Other antioxidants such as diphenyleneiodonium (DPI) and NAC can reduce eosinophil peroxidase (EPO), pro-inflammatory cytokines, NF-κB p65 immunocontent, and OS in the lungs, showing that these antioxidants are alternatives for reducing airway inflammation in asthma [62]. Other therapeutic strategies including inhibition of AP-1 and NF-κB have been developed in the signaling of airway inflammation. MOL 294 can be used to reduce airway hyperreactivity and inflammation in asthmatic mice by yet again inhibiting the activity of NF-κB and AP-1 [63]. The application of PNRI-299, a potent and specific inhibitor of AP-1, significantly attenuated both IL-4 release and airway eosinophil infiltration [63]. SOD and glutathione peroxidase mimetics are also effective antioxidants [64]. A study showed that ferroxidase enzymes such as ceruloplasmin are able to reduce active oxygen form (AOF) levels and improve immunity in patients with bronchial asthma [65]. Nontypeable *Haemophilus influenzae* (NTHi) is found in the upper respiratory tract of healthy individuals. It is also one of the most common strains found in the lower respiratory tracts of neutrophilic asthma patients. Recently, it was found that NTHi may cause the aggravation of neutrophilic asthma. Therefore, targeted treatment of NTHi with the use of antibiotics, anti-inflammatory drugs, or IL-17, has been shown to effectively reduce the symptoms of neutrophilic asthma [66].

11.4 Cigarette Smoke, Inhaled Oxidants, and COPD

Chronic obstructive pulmonary disease (COPD) is the most prevalent chronic respiratory disease in the world. According to the Centers for Disease Control and Prevention (CDC), in the United States, it is the third leading cause of death by disease after heart disease and cancer in 2020. Inhalation of volatile substances in cigarette smoke and air pollutants like O_3 and sulfur dioxide (SO_2) activates inflammatory responses and causes lung damage while increasing ROS levels in the lungs (Fig. 11.1) [67]. Cigarette smoke is a complex mixture of thousands of chemical compounds, including two different populations of free radicals, one in the tar and one in the gas phase. The primary radical is a quinone/hydroquinone (Q/QH2) complex held in the tarry matrix capable of reducing molecular oxygen. This reduction process produces $O_2^{\bullet-}$, eventually forming H_2O_2 and $^{\bullet}OH$. These gas-phase radicals are produced by the oxidation of $^{\bullet}NO$ to NO_2, which reacts with active species in smoke such as isoprene [68]. Cigarette smoke induces damage to DNA in alveolar macrophages and suppresses the expression of important phagocytic activity antigen such as CD11b, TLR-2, and CD14 [69].

Emphysema and chronic bronchitis are the most common conditions for COPD. COPD causes irreversible damage to the lungs and is characterized by airflow blockage leading to difficulties in breathing. Its major features include chronic inflammation throughout the airways, parenchymal vasculature with increased numbers of macrophages, neutrophils, and T lymphocytes (especially $CD8^+$). Markers of oxidative stress like $^{\bullet}NO$ and H_2O_2 have been found in the urine, epithelial lining fluid, breath of patients with COPD, and cigarette smokers [70]. Disease development is associated with a protease/antiprotease imbalance [71] that leads to a lack of protection against elastolytic enzymes [72]. This imbalance creates an accumulation of endogenous ROS released by inflammatory cells like macrophages, neutrophils, and epithelial and endothelial cells [73].

Oxidants exacerbate inflammation by activating NF-κB, facilitating the expression of multiple inflammatory genes such as IL-8 and TNF-α which are thought to be important in COPD [74]. Furthermore, H_2O_2 narrows airway smooth muscle in vitro. Isoprostane F2a-III, formed by free radical peroxidation of arachidonic acid, is a potent constrictor of human airways and an important biomarker of pulmonary oxidative stress in vivo. There is an increased $O_2^{\bullet-}$ production and upregulation of adhesion molecules in circulating neutrophils from patients with COPD. Lipid peroxidation products such as F2-isoprostane, conjugated dienes of linoleic

acid, and thiobarbituric acid reactive substances are notably higher in the plasma of healthy smokers and patients with acute exacerbations of chronic bronchitis compared with healthy nonsmokers. Thus, the products of lipid peroxidation formed by ROS also trigger signals that enhance pulmonary inflammation [75]. COPD is known to induce respiratory muscle dysfunction caused by constant resistive breathing. Respiratory muscle contractions increase significantly, resulting in ROS formation and OS. ROS activate molecules such as NF-κB and mitogen-activated protein kinases which stimulate cytokine release causing damage to the diaphragm and sarcomeric disruptions [76]. ROS play a vital role in vascular homeostasis; however, excessive ROS can impair lung function and alter pulmonary vasculature as implicated in COPD. Increased endothelial dysfunction and inflammatory cell infiltration contribute to the severity of the disease. Pulmonary hypertension caused by vascular remodeling reduces the long-term survival rate of patients [77]. COPD is commonly observed in the elderly population. Recently, it was proposed that a chronic state of inflammation associated with aging known as inflammaging is inflicted in COPD. A major aspect of inflammaging is the overabundance of ROS leading to OS, cellular damage, enhanced inflammation, and activation of apoptotic pathways [78].

11.4.1 COPD Therapeutics

COPD is a global health issue linked with high morbidity and mortality, especially in elderly patients. Several factors associated with aging include OS, shortened telomere length, and cellular senescence, closely related to chronic inflammatory responses in COPD [79]. Previous studies have shown that increased levels of biomarkers of OS (8oxodG, NT, F2-IsoPs, and AGEs) strongly correlate with the severity of airflow restriction in elderly patients with COPD [80]. A recent study showed that a combination of antioxidants, anti-inflammatory drugs, and mesenchymal stem cell treatments are a possible therapeutic strategy to treat elderly COPD patients [81]. Preclinical studies and clinical trials have shown that small thiol molecules such as NACs [82], antioxidant enzymes such as glutathione peroxidases [83], activators of the Nrf2-regulated antioxidant defense system such as sulforaphane [84], and vitamins, for example, C, E, and D [85], can all reduce oxidative stress and boost the endogenous antioxidant system while slowing the progression of COPD [72].

11.5 Acute Lung Injury, Acute Respiratory Distress Syndrome

Acute respiratory distress syndrome (ARDS) is clinically characterized by the abrupt onset of severe hypoxemia and the presence of bilateral diffuse pulmonary infiltrates [86]. These infiltrates appear on a radiograph as pulmonary edema resulting from increased pulmonary vascular permeability. ARDS affects patients of all ages. The disproportionate generation of ROS under pathological conditions such as ALI and its most severe form, ARDS, leads to boosted endothelial permeability. Loss of junctional integrity in vascular microvessels and increased myosin contractions are hallmarks of ALI and ARDS. These stimulate the migration of polymorphonuclear leukocytes (PMNs) and the changeover of solutes/fluids in the alveolar lumen. Exacerbated ROS production by the injured endothelium/epithelium as well as recruited leukocytes play an important role in ARDS pathogenesis and lung damage. OS causes endothelial and epithelial barrier dysfunctions resulting in massive neutrophil penetration across barriers followed by secretion of cytotoxic agents. ROS upregulate the expression of proinflammatory cytokines and adhesion molecules amplifying tissue damage and pulmonary edema. A proper oxidant/antioxidant balance is critical for vasculature homeostasis [87]. Therefore, such biological generators for excessive ROS production such as leukocytes can be therapeutic target options in ARDS treatments [88]. Platelets are known to play an important role in the inflammatory cascade leading to the pathophysiology of

ARDS and are a vital component of regular homeostasis. Antiplatelet therapy (APT) functions by interfering with platelet activation that include adhesion, release, and aggregation [89]. New studies show that prehospital APT is associated with a reduced rate of ARDS [90].

Additionally, ROS contribute to cellular injury by various mechanisms including lipid peroxidation with formation of pro-inflammatory thromboxane molecules and direct damage to DNA resulting in strand breaks and point mutations. It also oxidizes proteins (predominantly at sulfhydryl groups) and alters their activity. Protein oxidation leads to the release of proteases and inactivation of antioxidant enzymes. In addition, ROS-mediated alteration of transcription factors such as AP-1 and NF-κB leads to enhanced expression of pro-inflammatory genes [91, 92]. To minimize the detrimental effects of ROS generated during cellular respiration, cells express a number of endogenous antioxidants such as catalase, superoxide dismutase, and glutathione peroxidase. Yet these antioxidants are rapidly overwhelmed during an acute inflammatory response [93]. In the context of ALI/ARDS, sources of ROS may include leukocytes, parenchymal cells, oxidant-generating enzymes, and inhaled gases with high concentrations of oxygen during mechanical ventilation. Patients with ARDS have increased levels of H_2O_2 in exhaled breath condensate. Moreover, BAL fluid from these patients usually contains an excess of oxidized proteins combined with a relative deficiency in antioxidant molecules such as glutathione. Thus, in ALI/ARDS, there is extensive overproduction of ROS to the extent that endogenous antioxidants are overwhelmed, leading to OS and oxidative cell damage [91, 94].

11.6 ROS-Induced Lipid Peroxidation and Protein Oxidation

Lipid is the main component of cellular, nuclear, and mitochondrial membranes in the lungs. Lipids, especially polyunsaturated fatty acids, are vulnerable to any damage mediated by ROS [95]. In polyunsaturated fatty acids, a hydrogen moiety of unsaturated carbon can be easily attacked by ROS to form water, leaving an unpaired electron which can be converted into a peroxyl radical [96]. These peroxyl radicals eventually produce malondialdehyde (MDA), 4-hydroxynonenal (4-HNE), and other toxic by-products [97]. It has been suggested that MDA is the major mutagenic and carcinogenic product of lipid peroxidation, while 4-HNE is less mutagenic but more toxic [98]. Peroxided lipid reacts with polyunsaturated fatty acids leading to further oxidation, ultimately disrupting plasma membranes [99]. It has been shown that ROS initiate protein oxidation directly as well as indirectly through lipid peroxidation and glycosylation [100]. Cytotoxic roles of lipid peroxidation include inhibition of gene expression and induced cell death in pulmonary tissue leading to lung cancer and hyperoxic lung injury [101]. Lipid peroxidation through TNF-induced ROS formation causes alterations in mitochondrial membrane properties such as permeabilization, acting as a key regulator in cell death [102]. Protein oxidation includes carbonyl group formation while cross-linking and fragmentating the proteins [103]. It is notable that surface-exposed cysteine and methionine residues of proteins are particularly sensitive to oxidation by ROS. Protein oxidation is known to affect cell survival via disrupting the active site of enzymes and subsequently interrupts both protein-protein and protein-DNA interactions [104]. Cellular injury mediated by radiation causes oxidative damage to DNA and proteins. While DNA damage can be fixed by highly efficient mechanisms, repair of oxidized proteins is limited. Oxidized proteins lead to endoplasmic reticulum stress and inflammation, eventually destined for programmed cell death [105]. Hence, cellular apoptosis and protein oxidation are associated with pulmonary diseases such as asthma, COPD, ARDS, and cystic fibrosis [106].

11.7 ROS-Induced DNA Oxidation

ROS are a persistent threat to DNA as they modify bases with the risk of inducing genome instability, as well as disrupting genome function and

mutation. Such risks are primarily due to oxidative DNA damage and the repair process. The cell has to either repair the damaged base at a specific genomic site or leave it unrepaired. Persistent DNA damage can disrupt genomic function, but, conversely, it can also contribute to gene regulation by serving as an epigenetic marker. When such processes are out of balance, pathophysiological conditions get accelerated since oxidative DNA damage and resulting mutagenic processes are tightly linked to aging, inflammation, and the development of cancer [107]. It is known that $^{\bullet}OH$ can bind with DNA molecules leading to oxidation of both bases and the deoxyribose backbones [108]. The key product of DNA oxidation is 8-hydroxy-2 deoxyguanosine (8-OHdG), which results in transcriptional mutagenesis [109]. Remarkably, mitochondrial DNA (mtDNA) oxidation by ROS causes mtDNA abnormality and subsequently triggers the expression of aberrant mitochondrial proteins and mitochondrial dysfunction, collectively exacerbating ROS production. Therefore, there is a vicious cycle between mtDNA oxidation and increased ROS production, which ultimately leads to lung damage and ARDS pathogenesis [110].

11.8 COVID-19

The novel coronavirus disease (COVID-19) caused by severe acute respiratory syndrome coronavirus (SARS-CoV-2) spread throughout China in the year 2020 and received worldwide attention. The emergence of SARS-CoV-2 marks the third introduction of a highly pathogenic coronavirus into the human population in the twenty-first century. The first two included the Middle East respiratory syndrome coronavirus (MERS-CoV) in 2012 and SARS-CoV in 2002. According to the US Centers for Disease Control and Prevention, SARS-CoV-2 has infected more than 47 million people worldwide with an estimated 1.2 million deaths by November 2020. COVID-19 was declared a public health emergency of international concern on January 30, 2020, by the World Health Organization (WHO) and a pandemic on March 11, 2020 [111]. SARS-CoV-2 is an enveloped, positive-sense, and single-stranded 29.9 kb RNA beta-coronavirus [112]. The first symptoms present as fever, dry cough, tachypnea, and shortness of breath [113], and latest studies report the occurrence of a cytokine storm [114]. Lung inflammation is the main cause of life-threatening respiratory disorders at the severe stages of a SARS-CoV-2 infection, characterized by the so-called cytokine release syndrome (CRS). Patients mostly die from acute respiratory distress syndrome, whereas in many cases the disease has a mild or even asymptomatic progression [115].

Moreover, a common factor in all conditions associated with COVID-19 appears to be the imbalanced redox homeostasis responsible for ROS accumulation. The inflammatory response can be traced back to the pathway of viral entry through its receptor, angiotensin-converting enzyme 2 (ACE2). ACE2 is a protease that takes part in the renin-angiotensin system (RAS) with its companion ACE. Located at the cell surface, they compete for the same substrates, angiotensin I and II (ANG). ACE2 counters the activity of ACE by reducing ANGII levels and increasing the amount of ANGI-7 peptide. The downstream effects of the two enzymes are antagonistic: ACE2 activity leads to vasodilatation, angiogenesis, anti-inflammatory, anti-oxidative, and anti-apoptotic effects, while ACE causes vasoconstriction, OS, inflammation, and apoptosis [116]. OS generated by ACE activity is due to the effects of its product, ANGII, which increases the production of ROS through the activation of NADPH oxidase and the generation of peroxynitrite anions. Contrarily, ACE2 synthesizes the ANG1-7 peptide leading to downregulation of pro-oxidant pathways, which attenuates cellular damage induced by OS. Each person has a distinctive balance between ACE and ACE2 and thus can be more prone to inflammation if ACE prevails. When this happens, an infection by SARS-CoV-2 further downregulates ACE2 prevalence on cell surfaces [117]. This results in the overaccumulation of toxic ANGII, exacerbated inflammation, and ARDS. One approach for the treatment of COVID-19 could be reducing OS

secondary to the imbalance between ACE and ACE2. OS is a result of the failure of antioxidation defense systems to keep ROS and RNS in check. Hence, glutathione (GSH), a crucial endogenous antioxidant, is critical in extinguishing the exacerbated inflammation that triggers organ failure in such a disease [118].

Additionally, another aspect of COVID-19 involves induction of mitochondrial ROS functions in pulmonary host cells to promote viral replications [119] since cellular ROS levels are markedly increased in SARS-CoV $3CL^{pro}$-expressing cells [120]. Mitochondrial ROS are an important factor for SARS-CoV 3a-induced NLRP3 inflammasome activation [121]. Underlying molecular mechanisms such as Nod-like receptor family and pyrin domain-containing 3 (NLRP3) have been reported to be activated by virus infection. This causes lung injury, dysregulation of inflammatory cytokines [122], and release of ROS from damaged mitochondria [123] leading to pathogenesis of SARS-CoV in the respiratory system. Activation of the NLRP3 inflammasome demonstrates significant dependency on ROS generation [124]. The mitophagy/autophagy blockade results in the buildup of damaged, ROS-generating mitochondria which activates the NLRP3 inflammasome. Thus, all known NLRP3 activators generate ROS, which results in the secretion of IL-1β in an NLRP3-ASC-caspase-1-dependent manner in THP-1 human macrophages [125]. Testing for COVID-19 includes nucleic acid amplification tests, direct viral antigen tests, and serological tests [126]. Fresh sputum contains plenty of virus-ridden lung epithelium [127]. Electrochemical diagnostic systems have also been developed to detect ROS levels in the sputum of candidates for COVID screening [128].

11.9 Lung Cancer

OS plays an essential role in the regulation of a variety of physiological processes, such as apoptosis, proliferative signaling pathways, and the pathogenesis of cancer. According to the 2018 global cancer statistics, lung cancer (LC) is considered the most common cancer worldwide and is also the leading cause of death related to cancer [129]. There are two histologic types of lung cancer: small-cell lung cancer and non-small cell lung cancer (NSCLC). Particularly, NSCLC is further subdivided into three classifications: adenocarcinoma, squamous cell carcinoma, and large-cell carcinoma [130]. Cigarette smoking is a well-known environmental risk factor for LC, enhancing lung carcinogenesis by free radical-mediated pathways associated with OS [1]. It has been shown that the two main components of tobacco (nitrosamine 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone and polyaromatic hydrocarbons) are considered the predominant risk factors for LC [131]. Other inhaled carcinogens such as environmental pollutants and microorganisms can promote tumorigenesis through production of ROS and OS, leadsing to LC [132]. ROS induce DNA damage through oxidation of nucleobases. Repair of these altered bases can result in errors leading to mutagenesis. Consistently, radiation is one of the most well-known sources of ROS and has long been linked to tumor-initiating events [133].

ROS can also alter cellular processes through their effects on protein oxidation. Mild oxidation promotes cellular signaling and is usually reversible (e.g., conversion from disulfides to sulfenic or sulfinic acid and vice versa), allowing prompt changes in protein activity and signaling networks. On the contrary, excessive oxidation leads to terminal oxidation (formation of sulfonic acid) and a complete loss of protein function. Reversible modifications can be protective during stress, while irreversible cysteine modifications can be detrimental to protein function. Protein modifications play a key role in adaptation to OS by activating antioxidant (KEAP1) or metabolic (GAPDH, PKM2) pathways [134]. Other reversible modifications include CoAlation [135] and glutathionylation [136]. Several studies have reported that ROS act as a double-edged sword in cancers. Their role is dedicatedly governed by the amount, type, duration, and site of ROS production. Moderate amounts of ROS have been found to promote tumor survival, while excessive levels serve to suppress tumors and

enhance tumor cell death [137]. Also, NOX-derived ROS in the cytoplasm in response to TNF-α promote tumor cell survival, while mitochondrial-derived ROS stimulate apoptosis [138]. In prostatic carcinoma, inhibition of ROS by antioxidants or NOX inhibitors is associated with an increase in apoptosis. This dual role of ROS in cancers provides a challenge for the development of different targeting therapeutic modalities for cancers [139].

11.9.1 Key Pathways of Lung Cancer Metastasis

Metastasis implicates the spread of cancerous cells from the primary tumor to neighboring tissues as well as distant organs. Metastasis of cancers is the primary cause of morbidity and mortality [140]. Tumor metastasis is not an independent program but a complex and multifaceted process. Metastasis mainly occurs due to the intrinsic mutational burden of cancerous cells and bidirectional interaction between nonmalignant and malignant cells [141]. It occurs due to the upregulation of several transcriptional factors such as NF-κB, ETS-1 (ETS proto-oncogene 1, transcription factor), Twist, AP-1, and Zeb (zinc finger E-box binding homeobox). ROS play a vital role in the migration and invasion of cancerous cells. Epithelial-mesenchymal transition (EMT) is the major cause of tumor metastasis, where epithelial cells lose their polarity and cell-cell adhesion and gain mobility [142]. Multiple studies show ROS to be a key source of EMT [143]. TGF-β1 regulates uPA (urokinase-type plasminogen activator) and MMP-9 to facilitate cell migration and invasion through ROS-dependent mechanisms. ROS also increases tumor migration by inducing hypoxia-mediated MMPs [144]. Mitochondrial dysfunction can lead to increased ROS production, which further upregulates C-X-C motif chemokine 14 (CXCL14) expression through the AP-1 signaling pathway and enhances cell mobility by elevating cytosolic Ca^{2+} levels [145]. ROS activate Nrf2 that then stimulates protein coding gene, Klf9 (Kruppel-like factor 9). This in turn activates ERK1/2 resulting in an increased ROS production in cancer cells. Hence, a premalignant growth can be suppressed by using topical antioxidants that target Klf9 [146].

Mitochondrial Ca^{2+} also plays an important role in cancer metastasis. MCUR1 (mitochondrial calcium uniporter regulator 1) is upregulated in hepatocellular carcinoma (HCC) which promotes EMT by activating ROS/Notch1/Nrf2 pathways. Accordingly, MCUR1 can be a potential target for the treatment of HCC [147]. NOX2 generates ROS, which influence metastasis by downgrading the function of natural killer (NK) cells (Fig. 11.1). NOX2 inhibition restores the NK cell-mediated clearance of myeloma cells [148]. A protein named vimentin plays a crucial role in cancer initiation and progression such as EMT and metastasis. OS caused by HIF-1 regulates vimentin gene transcription, aiding in the formation of invadopodia during cancer cell invasion and migration [149]. Suppression of vimentin expression by RNAi can reduce cell metastasis and hence decrease tumor volume [150]. ROS also induces epigenetic changes in the promoter region of E-cadherin and other tumor suppressor genes, resulting in tumor progression and metastasis. It causes hyper-methylation of the promoter gene by increasing the expression of transcriptional factor—Snail. This factor induces DNA methylation with the help of histone deacetylase 1 (HDAC1) and DNA methyltransferase 1 (DNMT1) [151]. •NO plays a role in angiogenesis and intravasation. Therefore, it has been clinically connected to a poor cancer prognosis. •NO donors inhibit cell proliferation and anti-apoptotic pathways, suggesting a novel therapy for various cancer treatments [152].

11.10 Conclusion

Over decades, studies have attempted to resolve the complex roles of ROS in pulmonary diseases. Physiological levels of ROS are produced by mitochondria as defenses to maintain pulmonary homeostasis. However, ROS overproduction causes inflammation and damage to the lungs. ROS play a critical role in inflammatory responses

through the upregulation of redox-sensitive transcription factors. The resulting OS induce pro-inflammatory gene expression causing pulmonary diseases. antioxidants However, further studies are required to understand the molecular mechanisms of ROS-mediated pathophysiological pathways. ROS suppression by various antioxidants may aid in the design of novel therapies that target specific molecular pathways.

Conflict of Interest The authors confirm that this chapter content has no conflict of interest.

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Semaphorin3E/plexinD1 Axis in Asthma: What We Know So Far!

12

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Abstract

Semaphorin3E belongs to the large family of semaphorin proteins. Semaphorin3E was initially identified as axon guidance cues in the neural system. It is universally expressed beyond the nervous system and contributes to regulating essential cell functions such as cell migration, proliferation, and adhesion. Binding of semaphorin3E to its receptor, plexinD1, triggers diverse signaling pathways involved in the pathogenesis of various diseases from cancer to autoimmune and allergic disorders. Here, we highlight the novel findings on the role of semaphorin3E in airway biology. In particular, we highlight our recent findings on the function and potential mechanisms by which semaphorin3E and its receptor, plexinD1, impact airway inflammation, airway hyperresponsiveness, and remodeling in the context of asthma.

Keywords

Semaphorin3E · PlexinD1 · Asthma · Airway biology · Inflammation · Airway hyperresponsiveness · Tissue remodeling

12.1 Introduction

Asthma is one of the most common chronic diseases affecting 300 million people of all ages, with 250,000 annual deaths [1, 2]. Epidemiological studies have shown that asthma prevalence is more significant in high-income countries than low- and middle-income countries. In Western countries, asthma affects approximately 14% of children and 8% of adults [3–6]. The clinical symptoms of asthma are repeated wheezing episodes, shortness of breath, chest tightness, and nighttime or early morning coughing [7, 8].

From the pathological perspective, asthma is defined as a heterogeneous chronic disorder of the airways characterized by airflow obstruction, airway inflammation, airway hyperresponsiveness, and tissue remodeling [9–12].

Recent studies have implicated semaphorins and plexins in many airway diseases, including acute lung injury, allergic asthma, and pulmonary fibrosis [13]. This review summarized our recent work on the semaphorin3E (Sema3E)/plexinD1

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axis on various aspects of asthma. Our studies' results using in vitro and in vivo approaches inform us that while critically important, the Sema3E/plexinD1 pathway is highly complex and touches upon all aspects of asthma. Further detailed understanding of the kinetics, cellular distribution, binding partners, and intracellular signaling networks of Sema3E/plexinD1 will help develop novel immunomodulatory strategies to target this pathway better and improve asthma outcomes.

12.2 Semaphorins

Semaphorins were initially discovered as axon guidance molecules in the nervous system [14, 15]. They are ubiquitously expressed in cardiovascular, endocrine, gastrointestinal, musculoskeletal, immune, and respiratory systems. Semaphorins play an essential role in regulating morphogenesis, angiogenesis, cell differentiation, adhesion, proliferation, and migration [16].

Semaphorins are phylogenetically categorized into eight classes. Classes 1 and 2 are found exclusively in invertebrates, whereas classes 3, 4, 6, and 7 are expressed in the vertebrates [17]. Class 5 semaphorins are found in both vertebrates and invertebrates, and class 8 is specific to viruses. Vertebrate-secreted semaphorins form class 3.

The semaphorins' structural hallmark is the N-terminal "Sema domain," which consists of ~500 amino acids with a seven-blade β-propeller fold conformation. Semaphorins function through binding to their receptors called plexins. Plexins are classified into four subfamilies based on the sequence similarity of their ectodomains [17]. In addition to plexins, neuropilins, tyrosine kinases, and integrins interact with semaphorins [18].

Binding of semaphorins to their receptors triggers diverse signaling pathways involved in the pathogenesis of various diseases [13]. These effects are mediated by shaping the immune system [22], regulating cell trafficking, and cell-to-cell interactions [19–21]. Semaphorins are involved in various phases of the immune response, including the activation of T cells [22] and dendritic cells [23], the regulation of T helper cell differentiation, and the navigation of immune cell trafficking [24].

12.3 Semaphorin3E and PlexinD1

12.3.1 Sema3E

Sema3E is a secreted protein originally known as a regulator of axonal growth of neurons [25]. Sema3E is biosynthesized as 85–90 kDa protein and can undergo cleavage by furin convertase giving rise to P61 kDa fragment [26]. Similar to other Sema3s, Sema3E comprises of Sema domain, PSI (plexin-semaphorin-integrin), Ig (immunoglobulin) domains, and a basic C-terminus tail. Sema3E exerts a significant role in immune responses [27], cell migration [28], and proliferation [29].

Recent studies demonstrated that Sema3E has a significant impact on macrophages and thymocytes. In the thymus, Sema3E is mainly expressed in the medulla and binds to plexinD1 receptors of $CD69^+$ cells. Sema3E binding causes the inhibition of $CD69^+$ cell migration toward the cortex via the repression of CCL25-CCR9 chemokine signaling. Thus, Sema3E plays a crucial role in thymocyte development by aiding the migration of $CD69^+$ to thymic medulla [30].

Sema3E/plexinD1 axis is also involved in the process of inflammation and migration of macrophages. Sema3E is upregulated in macrophages when stimulated with oxidized low-density lipoprotein (LDL), LPS, and hypoxia. These stimulations convert macrophages toward M1 phenotype, which exerts pro-inflammatory action predominantly [31]. Sema3E also attracts monocytes via induction of p53 into adipose tissue, which eventually becomes pro-inflammatory macrophages [27]. In contrast, Sema3E also causes retention of M1 macrophages in atherosclerotic plaque by blocking CCL19 and CCL21 [31]. Also, Sema3E deficiency is associated with a reduction of macrophages and production of pro-inflammatory cytokines without any effect on vascularity

in adipose tissue [27], thus highlighting the context-dependent manner of Sema3E function.

12.3.2 PlexinD1

PlexinD1 is considered the main binding partner of Sema3E. PlexinD1 is dynamically expressed in many embryonic tissues, and after development, in the endothelial cells, the podocytes, adrenal and mammary glands, osteoblastic cells and bone tissues, the lung mesenchyme, the smooth muscle of the small intestine, and immune cells [32]. Human *PLXND1* is located on chromosome 3 (3q22.1) which encodes a 1925 amino acid (212.07 kDa) protein. PlexinD1 expression is essential for cardiovascular development wherein the mice with genetic deletion of its gene will succumb 2 days postnatal because of cardiovascular defects [33]. On the other hand, *Sema3e*-deficient mice are viable after birth, and developmental cardiovascular defects are recapitulated suggestive of additional plexinD1 ligand(s) [34, 35]. Sema3E/plexinD1 axis has a significant contribution to many biological systems such as vascular and neuronal development [36, 37] and hormonal control [38]. It also exerts various functions in pathological conditions such as cancer metastasis [39], immune cell migration [28] and proliferation [29], insulin resistance, and release of pro-inflammatory cytokines [27].

Sema3E is recognized as the canonical ligand for plexinD1 [35], and it does not bind to other plexins. This situation is an exception to the typical pattern of class 3 semaphorin interaction with Nrp-Plexin complexes [40]. Binding of Sema3E to plexinD1 is an Nrp-independent process that leads to plexinD1-mediated endothelial cell repulsion [35]. In tumor models, Sema3E-plexinD1 signaling could be affected by ErbB2 [41, 42]. However, Nrp1 [34] and VEGFR2 [43] are the only known co-receptors that could be associated with plexinD1. Gating of Sema3E by these co-receptors is functionally crucial because it switches the repulsive effect of Sema3E-plexinD1 signaling into an attractive outcome. Nrp1 expression determines the functional pattern of Sema3E in neuronal cells in axon guidance. The absence of Nrp1 in the neurons ensures the repelling function of Sema3E, which is evident in the cortifugal and striatonigral tracts. In contrast, the subiculo-mammillary tract neurons express Nrp1, which leads to attraction by Sema3E [34]. Altogether, the precise mechanism underlying the Sema3E-plexinD1 function is not entirely understood, and the ultimate functional outcome more likely follows a cell- and context-dependent fashion. It should be defined in each cell/disease model.

In humans, expression of Sema3E was significantly suppressed in the airways of severe asthmatic patients [44] and an allergen-challenged mouse model of the disease. Interestingly, the surface expression of the Sema3E high-affinity receptor, plexinD1, was also reduced in ASM cells from asthmatic patients [29], suggesting that Sema3E/plexinD1 axis is dysregulated in allergic asthma.

12.4 Sema3E/plexinD1 Axis in Allergic Asthma

12.4.1 Airway Inflammation

Airway inflammation is a cardinal feature of many chronic airway diseases. Exposure to an allergen, a virus, or air pollutants, smoke, and cold air can induce inflammatory cell recruitment to the airway [12]. In asthma, chronic inflammation is associated with airway hyperresponsiveness that leads to recurrent episodes of wheezing, breathlessness, and coughing. These episodes are usually associated with widespread, but variable, airflow obstruction within the lung that is often reversible either spontaneously or with treatment [12].

Airway inflammation in asthma is mainly characterized by an increased number of eosinophils in most patients' peripheral blood and airways, which correlates with disease severity [44–46]. Eosinophils exert their functions by releasing preformed granular cytotoxic mediators, such as eosinophil peroxidase and major

basic protein (MBP), oxygen radicals, and lipid mediators and cytokines and chemokines that aggravate allergen-induced airway inflammation and remodeling [47]. However, there are non-eosinophilic cases of asthma distinguishable from eosinophilic ones. The non-eosinophilic asthmatics are associated with clinical and pathological manifestations, for the most part, neutrophilia [48, 49]. Neutrophil number is increased in severe but not mild or moderate asthmatics [50–52]. In addition, neutrophilic inflammation is predominantly associated with asthma exacerbations [53], fatal asthma [53–55], occupational asthma [56], nocturnal asthma [57, 58], and childhood asthma [59–61].

Airway Neutrophilia and Eosinophilia One of our in vivo study's key findings is that *Sema3e*$^{-/-}$ mice displayed an enhanced pulmonary granulocytosis (i.e., eosinophils and neutrophils) at the steady state [22, 62]. This phenotype may account for the exacerbation of the allergic response upon HDM challenge. These data also suggest that Sema3E pathway may be a predisposing factor for human asthma and some asthmatics may have dysregulated Sema3E expression at the baseline that need further investigation. Furthermore, lung neutrophilia is a hallmark of subtypes of asthma [47]. In particular, severe asthmatics that are refractory to glucocorticoid therapies are characterized by massive recruitment of neutrophils to their lungs, where they accumulate due to higher migration or survival compared to normal conditions [63–65]. In acute and chronic HDM-induced models of allergic asthma, lung neutrophils were significantly higher in *Sema3e*$^{-/-}$ mice than those of wild-type littermates [62, 66]. These data suggest a regulatory role for Sema3E in pulmonary neutrophil extravasation. Besides, Sema3E intranasal treatment reduced HDM-induced recruitment of neutrophils into the lungs, associated with improved lung function, decreased IgE synthesis, and airway inflammation. It further suggests Sema3E as a potential treatment option for severe refractory asthma that deserves more mechanistic studies. Taken together, our data point out the importance of Sema3E endogenous defect as a predisposing factor for pulmonary neutrophilia and provide evidence of a previously unknown mechanism that regulates neutrophil migration in airway inflammatory disorders.

Dendritic Cell Function In allergic asthma, the most common form of the disease, inhalation and subsequent presentation of allergens by dendritic cells (DCs) induce Th2 immune deviation and recruitment of inflammatory cells into the lungs, which lead to tissue damage in atopic individuals [67]. Allergen-specific pulmonary Th2 cells producing interleukin (IL)-4, IL-5, and IL-13 play critical roles in IgE synthesis, eosinophil recruitment, mast cell growth, and AHR. Considering the essential role of DC in the induction of Th2 and Th17 responses [68], interference with their pro-allergic functions is regarded as a potential new therapeutic strategy in allergic asthma [69, 70].

In the lung, five lung DC subsets have been defined that include conventional DCs (cDCs), monocyte-derived DCs (Mo-DCs), and plasmacytoid DCs (pDCs) [71]. The cDCs could be further divided into CD11b^{+} and CD11b^{-} [72]. CD11b^{+}CD103^{-} cDC (cDC2) are endowed with the ability to prime effector CD4 Th cells in both homeostatic and asthmatic conditions, whereas CD103^{+}CD11b^{-} cDC (cDC1) play a crucial role in the development of tolerogenic protective response upon allergen inhalation [73]. cDCs and Mo-DCs contribute to HDM-induced airway inflammation, with lung CD11b^{+} cDC2s being necessary and sufficient to induce allergic sensitization [74]. DC functional behavior is dictated by many local factors, including the presence of semaphorin 3 family members [75].

Sema3E plays an essential role in pulmonary DC composition in the HDM mouse model of allergic asthma. Sema3e-deficient mice revealed higher DC recruitment into the airways both at the baseline and after HDM sensitization. In particular, a higher frequency of pulmonary CD11b^{+} DC observed in Sema3e-deficient mice is consistent with previous studies where CD11b^{+} DC induced Th2 response upon HDM exposure [74],

whereas $CD103^+$ DC induced pulmonary tolerance to inhaled allergens [73] and Th1 deviation [2]. The higher frequency of pulmonary $CD11b^+$ DC from *Sema3e*$^{-/-}$ mice was also accompanied by privileged secretion of Th2/Th17 cytokines in our adoptive transfer model in vivo. This finding implies that Sema3E plays a role in regulating Th2/Th17 response in allergic airway inflammation. Also, adoptive transfer of $CD11b^+$ pulmonary DC from HDM-sensitized *Sema3e*$^{-/-}$ into WT recipients induces higher airway inflammation compared to those of WT mice, suggesting an essential role of Sema3E in allergic asthma via modulating $CD11b^+$ pulmonary DC function.

12.4.2 Airway Hyperresponsiveness

AHR is a major clinical facet of allergic asthma [76]. Sema3E-Fc Ig, performed in prophylactic and therapeutic regimen, prevented HDM-induced airway resistance, tissue resistance, and elastance considered the characteristic parameters of AHR [66, 77]. Interestingly, in the chronic model of HDM challenge, Sema3E-Fc Ig effect was significant followed another week of HDM challenge that mimic life time scenario [66]. Conversely, we also showed that Sema3E-deficient mice have an exaggerated AHR upon HDM challenge [22]. A decreased level of IL-4 upon Sema3E-Fc Ig administration or after recall stimulation may explain, at least in part, the diminished AHR, since IL-4 and its signaling pathways such as STAT6 are required for the development of sustained AHR in mouse models of allergic asthma [78–80]. Downregulation of IL-4, as a key player for Ig class switching, by Sema3E treatment may further explain the reduction of pro-allergic antibody, IgE, considered a central driver of AHR [81, 82]. Also, a reduced TNF and IL-1β and possibly their direct effects on smooth muscle may be responsible for the decreased AHR upon Sema3E treatment which is in line with the important role of these pathways in AHR [12, 47]. In fact, TNF and IL-1β have been shown to induce impaired receptor-coupled airway relaxation in isolated segments of tracheal smooth muscle [83] and increased ASM contractility [84].

12.4.3 Airway Remodeling

In chronic asthma, airway remodeling involves alterations in structural cells in all of the layers of the airway wall. These include epithelial injury and repair, an increased number of goblet cells, deposition of extracellular matrix protein, increased development of myofibroblasts, neoangiogenesis, and thickness of the muscle bundles [47]. All these features seem to be enhanced in Sema3E-deficient mice subjected to challenge with HDM allergen and attenuated upon treatment with Sema3E-Fc prophylactically or in a therapeutic regimen [22, 66, 77].

Mechanistically, Sema3E significantly reduces growth factor-induced human ASM cell proliferation and migration that was associated with suppression of F-actin polymerization, Rac1 GTPase activity, ERK1/2, and Akt signaling [29]. In vivo, acute or chronic intranasal HDM exposure induces higher mucus overproduction and collagen deposition in the airways of Sema3E-deficient mice compared to the control littermates. Enhanced overexpression of *Col3a1* and *Muc5a genes* was observed in both naïve and upon HDM-challenged *Sema3e*$^{-/-}$ mice compared to WT littermates [66], and exogenous treatment with Sema3E-Fc significantly reduced mucus overproduction and collagen deposition [77]. Altogether, these findings support the notion that Sema3E could modulate airway smooth muscle and mucus hyperplasia.

It is clearly known that Sema3E/plexinD1 interaction has a crucial role in vascular development [37]. The inhibitory effect of Sema3E/plexinD1 axis on endothelial cells culminates on inhibition of vessel growth and branching. This inhibition operates through various mechanisms that include the suppression of VEGF and Dll4/Notch signaling pathway [85–88] and the induction of soluble VEGFR-1 (sFlt-1) that suppresses VEGF-induced angiogenesis [89–92]. Consistent with these data, we recently showed that Sema3E

has the ability to inhibit new blood vessel formation in the airways of HDM-challenged mice by shifting the ratio of VEGF/VEGFR2, enhancing the soluble VEGFR-1 production, and downregulating von Willebrand factor and CD31 expression [93], providing the first evidence that Sema3E modulates angiogenesis in allergic asthmatic airways via modulating pro- and antiangiogenic factors.

12.5 Conclusion

RNA-Seq data of normal human tissues has revealed that Sema3E is highly expressed in the lung and airway epithelial cells (AECs) are among the primary sources of Sema3E (www.lungmap.net). Furthermore, a genome-wide association study (GWAS) of African-American children, SAGE II (Study of African Americans, Asthma, Genes, and Environments; 812 asthma cases and 415 controls), revealed a *Sema3e* single-nucleotide polymorphism (SNP) genotype as a truly indicative of "direct" asthma associations [94]. AEC gene expression from 155 subjects with asthma and 26 healthy controls in the Severe Asthma Research Program (SARP) was analyzed by weighted gene co-expression network analysis to identify gene networks and profiles associated with severe asthma and its specific characteristics (i.e., pulmonary function tests, quality of life scores, urgent healthcare use, and steroid use). The authors found that gene modules linked to epithelial growth, repair, and neuronal function were markedly decreased in severe asthma. Further, *Sema3e* was among the top 25 genes correlated with asthma while adjusting for potential confounders, mainly age, sex, race, inhaled corticosteroids (ICS), and oral corticosteroids (OCS) [95]. Taken together, these data combined with our studies [22, 29, 62, 66, 77, 96] suggest that Sema3E functions as a critical factor in maintaining airway homeostasis and should be considered as therapeutic for the severe asthma.

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Serine Protease Inhibitors to Treat Lung Inflammatory Diseases

13

Chahrazade El Amri

Abstract

Lung is a vital organ that ensures breathing function. It provides the essential interface of air filtering providing oxygen to the whole body and eliminating carbon dioxide in the blood; because of its exposure to the external environment, it is fall prey to many exogenous elements, such as pathogens, especially viral infections or environmental toxins and chemicals. These exogenous actors in addition to intrinsic disorders lead to important inflammatory responses that compromise lung tissue and normal functioning. Serine proteases regulating inflammation responses are versatile enzymes, usually involved in pro-inflammatory cytokines or other molecular mediator's production and activation of immune cells. In this chapter, an overview on major serine proteases in airway inflammation as therapeutic targets and their clinically relevant inhibitors is provided. Recent updates on serine protease inhibitors in the context of the COVID-19 pandemic are summarized.

Keywords

Lung · Airway inflammation · Serine proteases · Clinical inhibitors · Respiratory viruses · Repurposing

Abbreviations

ALI	Acute lung injury
ARDS	Acute respiratory distress syndrome
COPD	Chronic obstructive pulmonary disease
COVID-19	Coronavirus disease 2019
HNE	Human neutrophil elastase
KLK	Kallikrein-related peptidase
PARs	Proteinase-activated receptors
TMPRSS2	Transmembrane protease, serine 2

13.1 Introduction: Overview on Serine Proteases

In humans, serine proteases exert their activities at various cellular levels and are responsible for the coordination of many physiological functions including digestion, cell cycle, coagulation, immunity, and reproduction [1, 2].

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Furthermore, serine proteases are key elements of the inflammation response due to their release from activated leukocytes and mast cells or generation through the coagulation cascade [3, 4]. Serine proteases which possess similar structures and catalytic properties are grouped into clans. The four main clans are clan PA represented by chymotrypsin, clan SB by subtilisin, and clans SC and SF which encompass various proteases [1, 5]. The specificity of cleavage of a given protease is based on the interaction of a protein or peptide substrate with the residues of the protease at the active site. The surface of the protease that is capable of hosting a side chain of a single substrate residue is referred to as the "subsite" [6–8]. The subsites are numbered from either side of the cleavage site: S_1–S_n to the N-terminus and S_1–$S_{n'}$ to the C-terminus of the substrate. The corresponding residues on the substrate are numbered P_1–P_n and P_1–$P_{n'}$, respectively [6, 9]. The structure of the active site of the protease thus determines the nature of the residues of the substrate which can bind specifically to the enzyme [9]. Depending on their specificity for cleaved residues (P_1), serine proteases can be classified as trypsin, chymotrypsin, or elastase analogs. This specificity is guided by the size and nature of the residue involved in the catalytic pocket of the enzyme. Trypsin or trypsin-like (TL) analogs cleave after a positively charged residue (lysine or arginine), their pocket S_1 being narrow, deep, and negatively charged. The S_1 pocket of "chymotrypsin-like (CTL)" is broad and hydrophobic in nature; this results in a specificity for the medium or large hydrophobic residues (tyrosine, phenylalanine, and leucine) [7, 8]. Elastase-like (EL) has a reduced pocket that receives short and uncharged residues [7]. For example, those which have a digestive role, such as chymotrypsin, generally have few requirements with respect to the substrate, and a large hydrophobic residue in position P_1 is sufficient. The activity of other proteases can be also based on the recognition of a complete peptide portion, such as enterokinase, which requires the binding of an Asp-Asp-Asp-Asp-Lys sequence in the S_1–S_5 subsites to operate properly [10].

Inflammation is a classical well-recognized essential step for the control of microbial invasion or tissue injury as well as for the maintenance of tissue homeostasis under various noxious conditions [11–13]. The causes of inflammation are numerous and varied: infectious agent, inert foreign substance, physical agent, post-traumatic cytotoxic injury, etc. Inflammation begins with a "recognition" reaction involving specific cells of the body (monocytes, macrophages, lymphocytes) or circulating proteins (antibodies, complement proteins, Hageman factor, etc.). The recognition phase follows the sequential activation of a whole set of cells and mediators whose order of intervention is complex and variable. Some mediators, such as prostaglandins and cytokines, are produced by different cell types, act on several cell types, and control sometimes their own production by retroactive regulation. Moreover, inflammation and coagulation constitute two host defense systems with complementary roles in eliminating invading pathogens, limiting tissue damage, and restoring homeostasis [12]. Infection leads to the production of pro-inflammatory cytokines that, in turn, stimulate the production of tissue factor. Conversely, activated coagulation proteases may affect specific receptors on inflammatory cells and endothelial cells and thereby modulate the inflammatory response [13]. Serine proteases are key actors of inflammation responses, both in physiological and pathophysiological contexts [2, 3]. In particular, in the microenvironment of inflammatory tissues, extracellular serine proteases (e.g., HNE or KLKs) can modulate cell signaling via the regulation of PARs. PARs (proteinase-activated receptors) (PAR-1, PAR-2, PAR-3, and PAR-4) belong to the superfamily of receptors coupled to G proteins and are involved in a number of pathways for physiological and pathological signaling in a wide variety of tissues [14]. These receptors are irreversibly activated by the action of proteases mainly from the class of serine proteases having a specificity of the trypsin-like substrate, cleaving following the arginine or lysine residues. A multitude of works suggest that the mechanism of this cleavage occurs within the extracellular domain of the

receptor following an arginine or lysine residue, with the generation of a new N-terminus. This unmasked end (tethered ligand) binds as a ligand on the extracellular loops of the receptors causing allosteric changes followed by the coupling of receptors to heterotrimeric G proteins and signal transduction. Biased cleavage, namely, proteolytic processing outside this region, can occur and mediates various cellular responses especially in inflammatory context [15].

13.2 Lung Diseases and Serine Proteases: (Physio) pathological Implications and Overview

Lung inflammation is associated with a wide set of diseases and still represents a real challenge to public health. The airway epithelium is indeed the first site of contact with inhaled agents. Its epithelial cells secrete a variety of substances such as mucins, defensins, lysozyme, lactoferrin, and nitric oxide, which nonspecifically shield the respiratory tract from microbial attack [16]. For example, inflammation is an important feature of many pulmonary diseases such as pneumonia, ARDS (acute respiratory distress syndrome), asthma, and COPD (chronic obstructive pulmonary disease) [17]. COPD is a global epidemic, affecting nearly 300 million people worldwide and killing 3 million individuals each year. It is the only major cause of mortality that is increasing such that by 2030 the mortality rate will reach 7–8 million per annum. COPD which mainly affects cigarette smokers is characterized by lung inflammation, which intensifies with disease progression and is characterized by abnormal inflammatory response, ECM and age-related changes, structural changes in the small airways, and the role of sex-related differences [18]. Proteolytic enzymes also have a prominent role in particular in the emphysematous phenotype [19]. Varied and disparate strategies have been adopted to intervene in pulmonary inflammatory responses. In addition to looking at the cytokines, cytokine receptors, and cell-surface molecules, cellular signal transduction and gene activation have been targeted for therapy [17]. Neutrophil proteases, especially HNE, have been early and extensively investigated as therapeutic target of prime importance in the above-cited lung diseases [20, 21]. Other selected serine proteases emblematic of lung inflammation processes are summarized in Table 13.1 and Fig. 13.1, namely, plasma kallikrein, kallikrein-related peptidases, and transmembrane serine protease 2, TMPRSS2, for which significant efforts have been recently put in the context of the COVID-19 pandemic.

13.3 Development of Serine Protease Inhibitors to Treat Inflammation in Lung Diseases

13.3.1 Neutrophil Elastase (HNE)

Neutrophils, key immune cells for protection against microbial infection, are also associated with a range of pathologies, including auto-inflammatory diseases, such as systemic lupus erythematosus (SLE) and psoriasis [22, 23]. Neutrophil infiltration is a common pathological feature in acute inflammatory diseases. Furthermore, neutrophils are a rich source of proteolytic enzymes, including serine proteases and their inhibitors involved in neutrophil programmed cell death pathways [24]. Four active serine proteases, neutrophil elastase (HNE), cathepsin G (CatG), proteinase 3 (PR3), and neutrophil serine protease 4 (NSP4), as well as azurocidin, an enzymatically inactive serine protease homolog, were characterized in neutrophils [25, 26]. Human neutrophil elastase (HNE) belongs to the chymotrypsin-like family of serine proteases stored in the azurophilic granules of the neutrophil cytoplasm. A very efficient HNE is necessary to many biological processes that necessitate structures breakdown, such as dynamics of extracellular matrix and tissue remodeling (elastin, collagens), host defense by the disabling of bacterial invasion (cell wall proteins) and in initiation steps of inflammation [27, 28]. Indeed, HNE is a key regulator by its inter-

Table 13.1 Serine proteases involved in lung inflammatory diseases selected in this chapter

Serine protease	Substrates in lung	Implication in lung inflammatory disorders	References
Neutrophil elastase	Elastin, collagens	COPD, ALI, ARDS	[22, 31, 39, 42, 92]
Plasma kallikrein	Kininogen, plasminogen	ARDS, asthma, COVID-19	[43, 93–95]
Tissue kallikreins	PARs, HA proteins	Asthma, influenza infections	[96]
TMPRSS2	AC2, spike SARS-CoV-2, hemagglutinins	Viral infections: influenza, SARS, MERS, SARS-CoV-2	[55, 64, 69, 97]

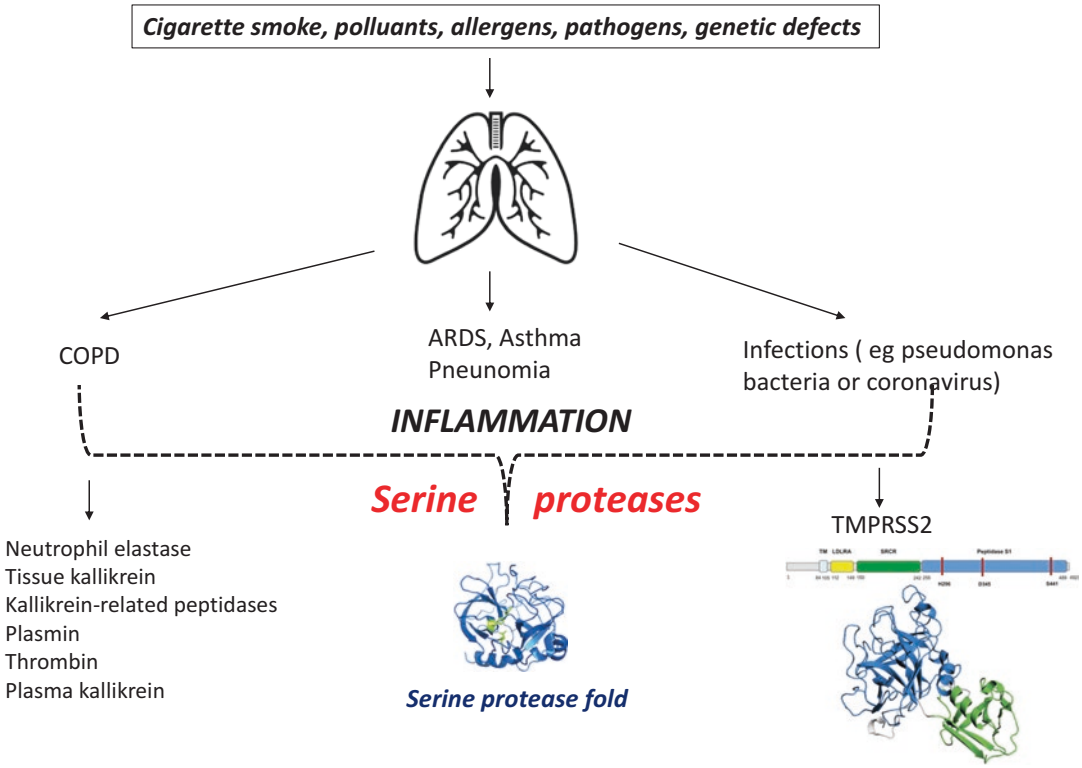

Fig. 13.1 General scheme illustrating lung inflammation in major diseases that imply serine proteases, constituting thus a key duo

vention in the activation of bioactive proteases like MMPs, release of growth factors, shedding of cell-surface-bound receptors, and degradation of endogenous protease inhibitors or virulence factors [20, 29]. The activity of HNE is tightly regulated by compartmentalization in storages granules and phagolysosomes, as well as by the intervention of endogenous serine protease inhibitors such as SERPINs (e.g., α-1 antitrypsin). Unopposed activity of HNE is implicated in the onset and progression of many inflammatory diseases especially of the cardiopulmonary system such as lung emphysema, chronic obstructive pulmonary disease (COPD), pulmonary arterial hypertension (PAH), and pulmonary fibrosis. Various rodent knockout models modulating either HNE or antiprotease expression revealed a significant decrease of phenotypic aspects of pulmonary diseases like emphysema. Elastase knockout mice are particularly sensitive to Gram-

negative bacterial infection [30]. Thus, HNE constitutes an attractive target for drug discovery in the pharmaceutical industry by developing inhibitors [22, 31]. Despite the importance of HNE in the clinic (see cited pathologies), only few inhibitors reached the clinic. Only few chemical scaffolds showed profiles suitable for clinical development. The first potent HNE inhibitors to reach clinical investigations were biologicals such as elafin (tiprelestat) [32]. Among small-molecule inhibitors, bearing electrophilic properties like serine acylator sivelestat [33, 34] or transition state analog such as freselestat are very effective [35]. Therapeutic inhibition of HNE holds promise with powerful treatment effect in various preclinical models of lung, bowel, and skin inflammation and ischemia-reperfusion injury relevant to myocardial infarction, stroke, and transplant medicine [23]. Furthermore, sivelestat significantly attenuated LPS-induced acute lung injury (ALI) during recovery from neutropenia [36]. These findings suggest that HNE inhibition could be a promising way to decrease lung inflammation without increasing susceptibility to infection in ALI/ARDS during neutropenia recovery. Recently, phase II studies are in progress by the AstraZeneca firm on a reversible inhibitor AZD9668 (alvelestat) for patients with pulmonary diseases [37, 38]. Interestingly, HNE inhibitors demonstrated innovative strategies to cure lung inflammation [39].

Neutrophil elastase (HNE) plays also an important role in neutrophil extracellular traps (NETs) that contribute to the pathogenesis of acid aspiration-induced ALI/ARDS. NETs may contribute to ALI/ARDS by promoting tissue damage and systemic inflammation. Targeting NETs by inhibiting HNE using alvelestat was proposed as potential therapeutics [40].

The recent identification of BAY 85-8501, led to a very modern inhibitor which binds HNE via an induced fit with a frozen bioactive conformation leading to a significant increase in potency, selectivity, and stability [41]. This compound entered phase II clinical trials for patients with non-CF (cystic fibrosis) bronchiectasis [42]. Moreover, AZD9668, another HNE potent reversible inhibitor, with IC_{50} 12–50 nM, already succeeded in preclinical studies and is now under phase II clinical trial for bronchiolitis obliterans syndrome (BOS) that is a complication for patients after hematopoietic stem cell transplant.

13.3.2 Plasma Kallikrein

Plasma kallikrein is a trypsin-like serine protease that proteolytically cleaves high molecular weight kininogen to generate the potent vasodilator and pro-inflammatory peptide, bradykinin [43, 44]. Unregulated plasma kallikrein activity is responsible for excessive and potentially fatal edema like hereditary angioedema with C1-inhibitor deficiency [43, 45]. Inhibitors of plasma kallikrein with an optimized selectivity profile were generated as therapeutics and diagnostic tools [46]. The potential of plasma kallikrein was recently explored in the context of the actual SARS-CoV-2 pandemic. SARS-CoV-2 enters cells employing angiotensin-converting enzyme 2 (ACE2) as a receptor, which is highly expressed in lung alveolar cells. ACE2 is one of the components of the cellular machinery that inactivates the potent inflammatory agent bradykinin, and SARS-CoV-2 infection could interfere with the catalytic activity of ACE2, leading to accumulation of bradykinin which induces vasodilation, lung injury, and inflammation [47].

In an open-label, randomized clinical trial, two pharmacological inhibitors of the kinin-kallikrein system that are currently approved for the treatment of hereditary angioedema were tested, icatibant and inhibitor of C1 esterase/kallikrein, in a group of 30 patients with severe COVID-19. Icatibant (Firazyr) is a synthetic peptidomimetic drug consisting of ten amino acids and acts as an effective and specific antagonist of bradykinin B2 receptors. Neither icatibant nor inhibitor of C1 esterase/kallikrein resulted in significant changes in disease mortality and time to clinical improvement. Icatibant may also improve oxygenation in patients with coronavirus disease 2019 (COVID-19) [48]. Both molecules rather

promoted significant improvement of lung computed tomography scores and increased blood eosinophils, which has been reported as an indicator of disease recovery. Hence, in this small cohort, pharmacological inhibition of the kinin-kallikrein system seems to improve disease recovery [49].

13.3.3 Kallikrein-Related Peptidases

Multiple studies have revealed the crucial role of kallikrein-related peptidases in the pathophysiology of a number of chronic, infectious, and tumor lung diseases [50].

Among the relatively new serine proteases, "tissue" kallikreins or kallikrein-related peptidases – as distinct from "plasma" kallikrein – form a family of proteases present in at least six orders of mammals. In humans, tissue kallikreins (KLKs, hKLKs, or hKs for human kallikreins) are coded by 15 structurally similar genes (KLK) which co-locate in tandem on chromosome 19q13.4, thus representing the largest cluster of contiguous protease genes in the human genome [51–53]. They include human kallikrein KLK1 and the other 14 kallikrein-related peptidases (KLK2-KLK15). The first member of this family, KLK1, was characterized in the pancreas almost a century ago and named "kallikrein" in reference to this organ (καλλικρεας in Greek). With KLK3 or "PSA" (prostate-specific antigen), discovered in the 1960s, and KLK2, whose gene was isolated in the 1980s, KLK1 belongs to the subfamily of "classical kallikreins." These three proteases are more closely related to each other than the 12 "new kallikreins" (KLK4-15) whose progressive assignment to the KLK family only began in the late 1990s. Thus, the KLK family was best known for the role of KLK1 in the kallikrein-kinin system or for the use of KLK3 or "PSA" (and, to a lesser extent, KLK2) as a biomarker in screening for prostate cancer. However, during the last decade, great progress has been made in understanding the cellular and tissue localization and in vivo logical physio(patho)regulation of most KLKs [54].

KLK1, KLK3, and KLK14 are involved in asthma pathogenesis, and KLK1 could be also associated with the exacerbation of this inflammatory disease caused by rhinovirus. KLK5 was demonstrated as an influenza virus-activating protease in humans, and KLK1 and KLK12 could also be involved in the activation and spread of these viruses. KLK1 (tissue kallikrein 1) is a member of the tissue kallikrein family of serine proteases and is the primary kinin-generating enzyme in human airways. DX-2300 is a fully human antibody that inhibits KLK1 via a competitive inhibition mechanism (Ki = 0.13 nM). Proteolytic cleavage of the hemagglutinin (HA) of influenza virus by host trypsin-like proteases is required for viral infectivity [55]. Some serine proteases are capable of cleaving influenza virus HA, whereas some serine protease inhibitors (serpins) inhibit the HA cleavage in various cell types. Kallistatin, a serpin synthesized mainly in the liver and rapidly secreted into the circulation, forms complexes with KLK1 and inhibits its activity [56]. Kallistatin and other kallikrein inhibitors may be explored as antiviral agents against respiratory viruses [57].

13.3.4 TMPRSS2, a Key Trypsin-Like Protease in Viral Respiratory Diseases

The transmembrane protease serine type 2 (TMPRSS2), also known as epitheliasin, belongs to the hepsin/TMPRSS subfamily [58, 59] and was first largely investigated in the context of prostate cancer where its expression is upregulated by androgens [60, 61]. TMPRSS2 is a 492-amino acid protein organized in functional domains as follows: residues 1–84 constitute the cytoplasmic region; 85–105, the transmembrane region; and 106–492, the extracellular one; LDL receptor (LDLR) class A (residues 112–149), the scavenger receptor cysteine-rich domain 2 (SRCR-2) (residues 150–242), and the peptidase S1 C-terminal domain (residues 256–489), with the catalytic triad (H296, D345, and S441), two potential glycosylation sites (positions 213 and

249), as well as a cleavage site (residues 255–256) that may allow the shedding of the TMPRSS2 extracellular region [62]. TMPRSS2 was proven to be crucial for the activation of hemagglutinin of several human influenza viruses [55, 63]. In December 2019, a new coronavirus named SARS-CoV-2 was identified in the Hubei province of central China. This new coronavirus induces COVID-19, a severe respiratory disease with high death rate. Recently, validated *TMPRSS2* SNPs were proposed to be predictive biomarkers and to be incorporated in the CDC's current list of clinical biomarkers for COVID-19 disease severity [64]. TMPRSS2 protein has a key role in severe acute respiratory syndrome (SARS)-like coronavirus (SARS-CoV-2) infection. SARS-CoV-2 was reported to enter cells via binding to AC2 followed by priming of the virus's spike (S) protein by TMPRSS2 through trypsin-like activity [65–67] (Fig. 13.2). Hence, blocking its proteolytic activity appears as a valuable strategy. Recent systematic studies on the expression of AC2 and TMPRSS2 performed using different cell types of lung tissue from donors have shown that AC2 and TMPRSS2 co-expressed in bronchial and lung cells [68, 69] and underlined that both proteases were expressed in bronchial transient secretory cells [70]. In inflammatory common diseases like asthma, a study with patient cohorts showed that IL-13, a cytokine associated with type 2 asthma, suppresses *ACE2* expression and increases *TMPRSS2* expression in airway epithelial cells from participants with type 2 asthma and atopy; hence, AC2 and TMPRSS2 are modulated in type 2 inflammation in the upper and lower airways [71].

Moreover, naturally occurring genetic variations resulting in defective activity of TMPRSS2 may explain why some populations develop only weak symptoms [72, 73]. In murine models after coronavirus infection, it has been suggested that TMPRSS2 contributes to virus spread and immunopathology in the airways while its genetic inhibition reduces the severity of lung pathology after SARS-CoV or MERS-CoV infections [74]. All these literature data, although not exhaustive, underline that TMPRSS2 is a potential therapeutic target for the cure of respiratory viral infections. Since the beginning of the sanitary crisis, various research programs and clinical trials have been conducted to examine whether TMPRSS2 inhibitors may be useful therapeutics [75, 76]. Early researches have given rise to the design of the first synthetic subnanomolar inhibitors using classical medicinal chemistry to prevent influenza virus activation [77].

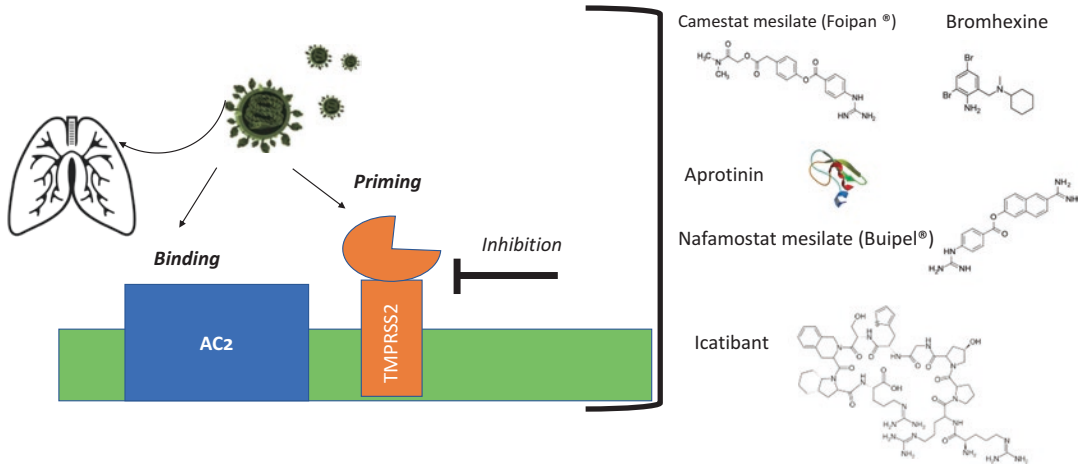

Fig. 13.2 Targeting TMPRSS2 to prevent viral infection and to attenuate COVID-19 symptoms. SARS-CoV-2 was reported to enter cells via binding to AC2 followed by priming of the virus's spike (S) protein by TMPRSS2 through trypsin-like activity [65–67]. Chemical structure of inhibitors under clinical consideration is given (see text for details)

Different strategies have been used to identify TMPRSS2 inhibitors including virtual screening on homology structural models of TMPRSS2 peptidase domain [78, 79], high-throughput screening, or drug repurposing [80].

Clinical serine protease inhibitors, namely, aprotinin, camostat, and nafamostat, are under consideration as TMPRSS2 inhibitors in several clinical trials: camostat (NCT04321096, NCT04338906, NCT043532284), nafamostat (NCT04352400), as well as bromhexine that is revealed as a TMPRSS2 inhibitor [81–83] (NCT04273763, NCT04340349, IRCT20200317046797N4); their chemical structure is given in Fig. 13.2 and their target in Table 13.2. Bromhexine is a bioflavonoid plant-derived mucolytic medication used to decrease viscosity of mucosal pulmonary secretions and was recently shown to inhibit TMPRSS2 in metastatic prostate cancer. The main active metabolite ambroxol of bromhexine was shown to have an anti-inflammatory effect through a decrease of the expression of various pro-inflammatory mediators (IL-1β, IL-6, IL-8, TNF-α) and antioxidative property [84, 85].

Aprotinin is a small protein bovine pancreatic trypsin inhibitor (BPTI), or basic trypsin inhibitor of bovine pancreas, that is part of antifibrinolytic arsenal [86]. Through its ability to inhibit kallikreins, thrombin, and plasmin, it contributes to attenuate inflammation, coagulation, and fibrinolytic pathways. Aprotinin aerosol were early shown to display a positive impact on influenza and paramyxovirus bronchopneumonia of mice [87]. In combination with furin inhibitors, aprotinin used as a TMPRSS2 inhibitor was shown to provide enhanced antiviral effect in human airway epithelial cells [88].

Camostat is an oral serine protease of plasmin, kallikreins, and thrombin used in the treatment of chronic pancreatitis. Hoffman et al. have shown in the recent report that camostat mesylate inhibits SARS-CoV-2 activation through TMPRSS2 and its metabolite GBPA exerts antiviral activity [89]. Nafamostat is another broad-spectrum synthetic serine protease inhibitor that displays anticoagulant and anti-inflammatory properties by inhibiting trypsin-1, kallikrein-related peptidase 1 (KLK1), coagulation factor XII, and coagulation factor X.

Nafamostat mesylate inhibits SARS-CoV-2 infection in the nanomolar range, making it an interesting candidate for clinical trials [90, 91].

13.4 Concluding Remarks

Lung inflammation is a physiological part of the complex biological response of tissues to counteract various harmful signals including pollutants and viruses. Respiratory diseases constitute an important and prioritary public health issue. Inflammatory processes involve diverse actors such as immune cells, blood vessels, and other molecular mediators to eliminate initial events of cell injury. Among them, serine proteases are key elements in both physiological and pathological inflammation; this was particularly emphasized by the recent and current COVID-19 epidemic. The active research programs have given the opportunity to repurpose well-established serine protease

Table 13.2 Summary of serine protease inhibitors that demonstrated potential therapeutic value or in clinical use

Target serine protease	Inhibitors	Targeted diseases	References
HNE	Sivelestat AZD9668	COPD, ARDS, ALI	[33]
Plasma kallikrein	Lanadelumab, icatibant	Lung inflammation, asthma, COVID-19, pulmonary edema	[47, 49]
Tissue kallikrein (kallikrein-related peptidase 1, KLK1)	Kallistatin	COPD, asthma, COVID-9, influenza	[57]
TMPRSS2	Camostat, nafamostat, gabexate, bromhexine, aprotinin	MERS, COVID-19, influenza, ARDS	[80, 89, 91]

inhibitors, illustrating common pathological pathways. Uncertainties around the development of a vaccine against SARS-CoV-2 make it essential to develop distinct and complementary therapeutic solutions. In this objective, serine proteases, namely, inhibitors of trypsin-like proteases, seem to be a valuable strategy to counteract at the same time virus entry, associated coagulopathy, and enhanced fibrinolysis. Several recent reports and ongoing clinical trials have shown that repurposing of already clinically used inhibitors constituted very appropriate strategies; however, definitive conclusions have not been yet established.

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Sex and Gender Differences in Lung Disease

14

Patricia Silveyra, Nathalie Fuentes, and Daniel Enrique Rodriguez Bauza

Abstract

Sex differences in the anatomy and physiology of the respiratory system have been widely reported. These intrinsic sex differences have also been shown to modulate the pathophysiology, incidence, morbidity, and mortality of several lung diseases across the life span. In this chapter, we describe the epidemiology of sex differences in respiratory diseases including neonatal lung disease (respiratory distress syndrome, bronchopulmonary dysplasia) and pediatric and adult disease (including asthma, cystic fibrosis, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, lung cancer, lymphangioleiomyomatosis, obstructive sleep apnea, pulmonary arterial hypertension, and respiratory viral infections such as respiratory syncytial virus, influenza, and SARS-CoV-2). We also discuss the current state of research on the mechanisms underlying the observed sex differences in lung disease susceptibility and severity and the importance of considering both sex and gender variables in research studies' design and analysis.

Keywords

Sex · Gender · Lung disease · Hormones · Chronic disease

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14.1 Introduction

Sex-related differences exist in many lung diseases throughout the life span [36, 277]. In neonates, the male disadvantage is a well-established clinical fact, especially in the preterm population [16] to the point that guidelines to predict outcomes from the *Eunice Kennedy Shriver* National Institute of Child Health and Human Development (NICHD) and Neonatal Research Network (NRN) for extremely preterm birth outcomes include sex as a critical biological variable [225]. In children and adults, some lung conditions are more commonly found in women and men, respectively, and can present with different degrees of severity and symptoms.

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Overall, the literature shows that most lung diseases are more commonly found or present with higher degree of severity, exacerbation rate, hospitalizations, and mortality in women than in men [89]. These include asthma, chronic obstructive pulmonary disease (COPD), pulmonary hypertension, and some types of lung cancer such as adenocarcinoma [211, 228, 316]. Furthermore, some rare and less-understood lung conditions such as lymphangioleiomyomatosis (LAM) are almost exclusively found in women [309].

Although the terms sex and gender are commonly used interchangeably, they represent different concepts. According to the National Institutes of Health (NIH) Office of Research on Women's Health (ORWH), "sex" refers to the biological differences between females and males, including chromosomal, anatomical, hormonal, and other physiological and functional differences. "Gender," on the other hand, refers to the characteristics that a society or culture delineates as masculine or feminine, including social, environmental, cultural, and behavioral factors and choices that influence an individual's self-identity. As opposed to sex, gender is a social construct and not defined biologically. Importantly, an individual's gender does not necessarily need to be consistent with their biological sex given at birth nor be fixed or binary. However, because the health of men and women is influenced by both sex and gender, including these variables in research studies is crucial. In basic science, this means including both male and female cells and/or experimental animal models in study designs, as well as examining the influence of sex hormones down to the molecular level. For clinical, behavioral, and outcomes research, this means considering gender-specific social influences and their impact on health and disease. Only when we incorporate sex and gender factors in research studies, we will be able to understand the mechanisms underlying the numerous sex disparities observed in lung disease prevalence and severity and provide more efficient and personalized sex- and gender-specific medicine.

14.2 Sex and Gender Differences in Respiratory Disease

It is not possible to talk about sex differences in respiratory disease without discussing first sex differences in lung biology. From the 16th week of gestation to adult life, significant differences exist in the male and female lung. In addition, changes in sex hormone levels throughout development, puberty, and physiological events such as pregnancy and menopause also influence lung function and health. Early in life, while female sex hormones are beneficial, promoting lung development and maturation, androgens appear to exert the opposite effect [245]. After puberty, the opposite occurs in diseases such as severe asthma, where improvement is observed with increasing androgen levels, and fluctuations in female hormones throughout the menstrual cycle promote asthma exacerbations. Overall, the available body of research shows that the effect of sex hormones on lung health appears to depend on the timing of exposure and thus differentially affects disease prevalence and severity in males and females throughout the life span. Table 14.1 summarizes the information available on some of the most common lung diseases affecting men and women disproportionately. In the sections below, we describe the epidemiological information available as well as the status of the research aiming to understand the mechanisms behind the observed sex differences for each disease.

14.3 Neonatal Lung Disease

Infants born prematurely are at higher risk for cardiopulmonary and neurological comorbidities such as retinopathy, pulmonary hypoplasia, respiratory distress syndrome (RDS), bronchopulmonary dysplasia (BPD), intraventricular hemorrhage (IVH), and chronic neurocognitive developmental disorders [190]. Many of these comorbidities exhibit significant sex disparities that could be a consequence of differences in lung development and/or caused by a complex interaction between immunological, hormonal, and genetic factors earlier in life [189]. Overall,

Table 14.1 Sex differences in neonatal, pediatric, and adult lung disease prevalence

Disease	Population	Sex differences	References
Asthma	Children	Boys > girls	[3, 36, 185]
	Adults	Women > men	
Bronchopulmonary dysplasia (BPD)	Neonates	Boys > girls	[17, 85, 276]
Chronic bronchitis	Adults	Women > men	[11]
Chronic cough	Children	Boys > girls	[27]
Chronic obstructive pulmonary disease (COPD)	Adults	Women > men	[2, 111]
Cystic fibrosis	Children	Girls > boys[a]	[92, 289]
	Adults	Women > men	
Coronavirus disease 19 (COVID-19)	Adults	Men > women	[234]
Emphysema	Adults	Men > women	[160]
Idiopathic pulmonary fibrosis	Adults	Men > women	[213, 314]
Lung cancer	Adults	Women > men	[209, 252]
	Adults	Women > men	[309]
Pulmonary arterial hypertension	Adults	Women > men	[170]
Obstructive sleep apnea	Adults	Men > women	[144, 184]
Respiratory distress syndrome (RDS)	Neonates	Boys > girls	[17, 85, 276]
Respiratory syncytial virus infection (RSV)	Neonates/children	Boys > girls	[182]

[a]Infection rates and outcomes worse in girls than boys, but no sex differences in incidence

male infants are presumed to have an intrinsic disadvantage and to be more sensitive to adverse environmental exposures during development and after birth [181]. This sex-related disparity is particularly manifested during the neonatal period and is more pronounced in prematurely born infants.

14.3.1 Sex Differences in Lung Development

The development of the male and female lung is a highly regulated process controlled by genetic, epigenetic, hormonal, and environmental factors. This process is divided into five stages: embryonic, pseudoglandular, canalicular, saccular, and alveolar (Table 14.2). Each stage is characterized by specific cellular and structural events that are controlled by the expression of multiple developmental genes [296, 297]. Sex differences in structural, mechanical, and functional aspects of lung development, as well as in its control by sex hormones, have been widely documented [36, 37, 163]. These differences are thought to be associated with the sexual dimorphism observed not only in neonatal lung disease but also later in life [245]. Respiratory diseases such as RDS and BPD contribute to a large proportion of the morbidity and mortality of prematurely born infants [276]. Importantly, even late preterm infants, born at gestational ages of 34–36 weeks, have been found to be greater risk for adverse respiratory morbidity and mortality than infants born at term [87].

During the fetal period, male lung maturation is usually delayed in comparison to female maturation. Pulmonary surfactant production initiates later in the male vs. the female lung [36, 235]. Consequently, male neonates are at increased risk of developing respiratory distress syndrome (RDS) and a higher risk of morbidity and mortality due to RDS compared with female neonates of similar gestational age [107, 269]. Furthermore, sex differences in overall neonatal survival and pulmonary outcomes have been described with a significantly higher incidence in males versus females [96]. One example is the high incidence observed in males for the development of bronchopulmonary dysplasia (BPD), a pulmonary pathology of the neonate for which RDS is not always an anterior event [207]. Differences in gene expression, particularly at the late developmen-

Table 14.2 Stages of human lung development

Developmental stage (gestational age)	Main events	Sex differences	References
Embryonic (3–6 weeks)	Lung buds emerge (foregut), and trachea and bronchial buds form	None reported	–
Pseudoglandular (6–16 weeks)	Bronchial development, airway branching	Fetal growth and breathing movements are detected earlier in the female fetus. AMH delays branching by promoting apoptosis in males	[41, 98]
Canalicular (16–26 weeks)	Subdivision of distal airways into canaliculi, vascularization Differentiation of type I and II cells, surfactant production	Surfactant secretion and phospholipid maturation are inhibited in males (androgens) and promoted in females (estrogens)	[207, 235, 274]
Saccular (26–36 weeks)	Cell differentiation, type II cell maturation, surfactant secretion Formation of sacs and primary septa	Surfactant production and phospholipid profile remain more advanced in females	[71]
Alveolar (36 weeks–adolescence)	Alveolar multiplication, enlargement, and maturation Lung growth continues and lung function increases with age and peaks in adolescence	Faster alveolarization in females. Higher flow rate per lung volume, but smaller lung size in girls. Better response to surfactant therapy in female newborns with RDS. FEV1 peaks earlier in females than males	[23, 30, 231, 271]

AMH Anti-Müllerian hormone, *FEV1* Forced expiratory volume in 1 minute

tal stages, have been shown to play significant roles in this sex disparity in lung health outcomes [6, 23, 85].

14.3.2 Respiratory Distress Syndrome

Respiratory distress syndrome is a condition of the premature born characterized by a deficiency in pulmonary surfactant [9]. Infants presenting with RDS show widespread alveolar atelectasis and a reduction in lung compliance, with secondary complications such as pneumothorax. Prior to the introduction of antenatal corticosteroids and postnatal surfactant replacement therapy, RDS was a major contributor to neonatal mortality, particularly in male newborns [194].

The main factors involved in the pathophysiology of RDS are surfactant deficiency and dysfunction in the immature lung, which occur at higher rates in males than females of the same gestational age [181]. Thus, the less developed or mature the lung, the higher the chance of disease manifestation after birth. As mentioned earlier, pulmonary surfactant is produced earlier in females than males during gestation, and its production is stimulated by female sex hormones, and inhibited by male sex hormones [263, 278]. A meta-analysis of data from over 500,000 preterm newborn infants found that RDS was between 1.56 and 1.84 times higher to occur in newborn males than females [145]. This report indicated that males were also at higher risk for other diseases of the newborn, such as BPD, as well as lower respiratory tract infections, bronchiolitis, and pneumonia.

Preventative and treatment options for RDS include postnatal surfactant administration and antenatal corticosteroid therapy [276]. For a long time, corticosteroids (e.g., betamethasone) have been reported to have sex-specific effects on placental oxidative balance and microvascular blood flow [254, 255], as well as to improve the subsequent response of infants to surfactant administration [120], with more beneficial effects in females than males [194]. However, a more recent systematic review and meta-analysis on the topic did not find sex-specific differences, although the type of antenatal glucocorticoid

used (betamethasone vs. dexamethasone) displayed a sex-specific effect [221].

14.3.3 Bronchopulmonary Dysplasia

Bronchopulmonary dysplasia is a lung disease of the prematurely newborn, characterized by an arrest in alveolarization and aberrant pulmonary vascular development [17, 113]. The disease diagnosis is performed by assessing the need for mechanical ventilation and oxygen respiratory support at 36 weeks' postmenstrual age [16] and displays a higher incidence in extremely low birth weight neonates [38].

The widespread use of antenatal corticosteroids, neonatal exogenous surfactant, and protective ventilation strategies has led to increased survival of more extremely preterm infants, with a consequent increase in BPD incidence in the past few decades [112, 113]. While mortality from the disease has declined significantly in the past several decades, children diagnosed with BPD still display long-term complications in lung health ranging from the need for tracheostomy and mechanical ventilation to pediatric pulmonary arterial hypertension and poor neurodevelopmental outcomes [55, 219]. Recent studies have also reported that adults who were born preterm display a higher incidence of airflow obstruction, gas trapping, and reduced gas exchange than those born term [310] and that worsening of lung function persists throughout childhood, particularly in males [93].

Multiple clinical studies have reported sex differences in BPD, including a higher incidence in males vs. females that persists after adjusting for other confounders. Moreover, males display higher death and oxygen dependency rates, as well as pulmonary hemorrhage and use of postnatal steroids [28, 112, 113]. Male sex is considered not only an independent major risk predictor of BPD but also to worsening of lung function during the neonatal and early childhood periods [268]. However, despite the well-established sexual dimorphism in the incidence of BPD, the mechanisms associated with these disparities are not completely understood. Recent studies in animal models have suggested a role for microRNAs (miRNAs) in mediating sex biases in BPD [138, 210, 317]. Others have related the sexual dimorphism of PBD to sex-specific differential activation of hypoxia-inducible factors and genes related to angiogenesis, supporting the pulmonary angiogenesis dysregulation in the pathobiology of BPD [49, 138].

14.4 Pediatric and Adult Lung Disease

Sex differences in lung and airway development persist throughout infancy and early childhood [270, 293]. While females display larger airways than males, the number of alveoli per unit area and the alveolar size do not differ between sexes. The age- and height-adjusted lung volume, however, is higher in boys than girls, which may result in a larger alveolar surface area and a higher diffusion capacity of carbon monoxide (DLCO) in males [20, 233, 270]. With age, differences in lung volumes, as well as in lung size and shape, become more evident [270, 275]. Together with differences in the distending forces of the lungs, these result in differences in the recoil pressure between males and females [51]. This sexual dimorphism in human lung morphometrics and function, together with physiological differences observed by pulmonary function testing, spirometry, and other techniques, has been used to partially explain the observed sex disparity in multiple pulmonary conditions.

Overall, while the majority of lung diseases presented below affect more adult women than men, several conditions are observed at higher rates in men than women and/or show opposite trends in childhood vs. adult life. A multitude of intrinsic factors, such as sex hormones, genetic and epigenetic factors, and comorbidities, along with other extrinsic factor,s have been suggested to contribute to these trends. In the next sections, we summarize the recent epidemiological data, as well as research aiming to understand the mechanisms behind sex disparities in lung disease throughout the life span.

14.4.1 Asthma

Asthma is a heterogeneous disease characterized by chronic airway inflammation. Some of its symptoms are wheezing, shortness of breath, chest tightness, cough, and airflow limitation [83]. Asthma is one of the most prevalent inflammatory diseases of the lung, affecting a significant portion of the world's population. The World Health Organization reported that more than 339 million people suffer from asthma, resulting in more than 400,000 deaths per year [42].

While asthma imposes a substantial public health burden in terms of impaired quality of life and mortality in men and women, clear sex differences exist in its risk, prevalence, and severity across life span [66, 89, 180, 237]. Depending on the sex and age of the patient, striking differences are observed in asthma incidence, prevalence, and severity [162]. An interesting fact is that asthma in children is more prevalent in boys than girls, and studies in adult populations frequently report more negative lung health outcomes for women than men, suggesting an involvement of sex hormones in mediating these effects [129, 228].

Epidemiological studies of childhood asthma have shown that prepubertal boys have more asthma than girls, especially at younger ages [75, 143]. Chronic cough in early childhood, whether from asthma or other causes, is also more common in boys than girls [27]. According to the Centers for Disease Control and Prevention, in the United States, it is estimated that 8.3% of boys and 6.7% of girls under 18 years old currently suffer from asthma. Interestingly, these patterns are reversed after puberty, where asthma prevalence rates for women are almost twice as those for men (5.5% vs. 9.8% for women and men over 18 years of age, respectively) [42]. These statistics have led investigators to hypothesize that hormonal changes starting in puberty contribute to asthma development. This notion is further supported by studies showing that girls who undergo menarche at an earlier age have a higher risk of developing asthma after puberty than girls in which menarche occurs later [226].

Studies showing variations in asthma symptoms and hospitalization rates throughout the menstrual cycle and a decline in asthma incidence in women after menopause also support this hypothesis [33, 204]. Also, women are more susceptible to asthma induced by air pollution and show worse adverse pulmonary health outcomes than men [141, 147]. In this regard, clinical studies and experimental evidence from mouse models have reported that female hormones such as estrogen can trigger lung inflammatory and allergic reactions, while male hormones such as androgens play the opposite role [76, 186, 307]. Interestingly, the severity of asthma in men increases later in life when androgen levels decrease [35]. Overall, more research is needed to elucidate the mechanisms underlying the observed sex differences in disease susceptibility and progression.

Sex differences in asthma have been linked to immunological factors, lung physiology and growth, and behavioral factors [74–130], as well as exposure to air pollutants [88, 86]. Human studies and in vivo models of asthma have shown that female hormones can trigger lung inflammatory and allergic reactions, and male hormones usually play the opposite role [77]. Interestingly, researchers have discovered that sex hormones can alter macrophage polarization and other immune-related cells such as the group 2 innate lymphocytes (ILC2s) and airway smooth muscle cells [22]. ILC2s that lack a killer cell lectin-like receptor G1 accumulate in the lungs of females after they have reached reproductive age but not in males [115]. Others have found that estrogen and testosterone increase and decrease Th2-mediated airway inflammation, respectively [78]. The authors of this study also concluded that females have augmented IL-17A-mediated airway inflammation compared to males [78].

Genetic associations with asthma have also been reported and found to be sex specific [105]. Two single nucleotide polymorphisms (SNPs) in the thymic stromal lymphopoietin (TSLP) gene (rs1837253 and rs2289276) have been associated with asthma in a sex-specific manner. Specifically, rs1837253 is associated with a lower risk for asthma in men, and rs2289276 is associated with

a higher risk of asthma in women. While the underlying mechanisms for these sex-specific associations have not been elucidated, these genetic variants have been associated with changes in immunoglobulin E (IgE) levels, which in children are correlated with higher airway resistance and exacerbations triggered by dust, pollen, and pets [94].

14.4.2 Exercise-Induced Bronchoconstriction

Exercise-induced bronchospasm/bronchoconstriction (EIB) is a phenomenon of acute airway narrowing that occurs during or after exercise or physical exertion. As such, EIB can occur in the presence or absence of asthma. Traditionally, the terms exercise-induced asthma (EIA) and (EIB) have been used interchangeably. However, the current consensus is that EIB represents a more accurate reflection of the underlying pathophysiology of the condition, since exercise is not an independent risk factor for asthma but rather a trigger of bronchoconstriction in patients with underlying asthma [175, 196, 258].

As mentioned above, asthma prevalence is higher in boys than in girls; however, after puberty the prevalence is around 20% higher in women than men, indicating a potential contribution of hormones after puberty [195]. Moreover, sex and gender differences in response to exercise have clear implications for understanding gender-specific adaptations to exercise for athletic performance and overall health [188].

The estimated prevalence of EIB varies from approximately 5% to 20% in the general population to an estimated 30% to 70% in elite winter athletes and athletes who participate in summer endurance sports, and at least 90% in individuals with persistent asthma [298]. This condition has been reported in a range of sporting activities but is most common in participants of cold weather sports (e.g., Nordic skiing) and indoor sports (e.g., ice-skating and swimming) [224]. Shinohara et al. investigated whether sex differences influence the prevalence and severity of EIB in prepubertal children aged 5–6 years. They found that the prevalence of EIB was higher in girls than in boys. In addition, the time to maximal bronchoconstriction was slower in girls than in boys, and the pattern of recovery after exercise was also faster in females than males [243]. Therefore, it is recommended that when evaluating the prevalence and severity of EIB in prepubertal children, the influence of sex is considered.

The pathogenesis of EIA is not fully elucidated. Minute ventilation, the volume of air inhaled or exhaled from a person's lungs per minute, rises with exercise. It is believed that EIB probably results from changes in airway physiology triggered by the large volume of relatively cool, dry air inhaled during vigorous activity [8, 167]. One of the major triggers for bronchoconstriction is water loss during periods of high ventilation. Strenuous exercise creates a hyperosmolar environment by introducing dry air into the airway with compensatory water loss, leading to transient osmotic changes in the airway surface. This hyperosmolar environment leads to mast cell degranulation and eosinophil activation with consequent release of inflammatory mediators, including leukotrienes. This process triggers bronchoconstriction and inflammation of the airway, as well as stimulation of sensory nerves and release of neurokinin and mucins [299]. All this is supported by several research findings concluding that it is not the type of exercise but the ventilation demand and humidity of the inspired air that are the main determinants of the occurrence and degree of bronchoconstriction [58, 119]. Therefore, the diagnosis of asthma in athletes should be confirmed by lung function test, usually with bronchial provocation testing [166] in association with a history consistent with EIB, because self-reported symptoms are not adequate. Varsity athletes show a high incidence of EIB when objectively diagnosed by a variety of pulmonary function criteria. The use of symptoms to diagnose EIB is not predictive of whether athletes have objectively documented EIB [197].

Management of EIB should be based on the understanding that EIB susceptibility varies widely among asthmatic patients, and it could

also be present in individuals without underlying asthma. A study by Parsons et al. found that 36 out of 42 EIB-positive athletes (86%) had no prior history of EIB or asthma [197]. In patients with asthma, EIB can also be an indicator of poorly controlled disease, and underlying asthma should be treated prior to controlling EIB [299]. As mentioned above, asthma can deteriorate during the peri-menstrual period, a phenomenon known as peri-menstrual asthma (PMA) which is usually much more severe and troublesome than the reported periovulatory worsening of asthma [246]. In this context, Stanford et al. demonstrated for the first time that the menstrual cycle phase is an important determinant of the severity of EIB in female asthmatic athletes [253]. This study reported deterioration in the severity of EIB during the mid-luteal phase accompanied by worsening asthma symptoms and increased bronchodilator use [253]. Aiming that exercise is not avoided by patients with EIB, general measures and pharmacologic interventions can be assessed subjectively in terms of symptom control and exercise tolerance, considering the fact that sex hormones play an important role in lung inflammation. Thus, medical evaluation and medication adjustment would likely be based on the understanding of sex differences.

14.4.3 Chronic Obstructive Pulmonary Disease

Chronic obstructive pulmonary disease (COPD) affects an estimated 174 million people worldwide (104.7 million males and 69.7 million females) [53]. For many years, it was considered a disease of older men [211]. However, over the past 20 years, its prevalence and rates of hospitalization have increased among women, closing this prevalence gap [11, 56]. This phenomenon is due in part to increased rates of tobacco use – the single largest risk factor for the development of COPD – among women, together with recent evidence demonstrating that first- and secondhand tobacco smoke has more severe effects in women than men [26, 89]. Moreover, there is an increased recognition that the clinical presentation of COPD is different in women than men, which has led to better and more accurate diagnosis in women in the past few decades [111, 137]. It has been shown that women with COPD have different disease burden, symptoms, and clinical trajectory than men [89, 199] and that women tend to develop COPD earlier in life and have more frequent respiratory exacerbations than men [199].

While asthma remains the most prevalent respiratory disease in the world, COPD is the fourth leading cause of death in the United States and the eighth leading cause of disability worldwide [248]. Recently, the World Health Organization has projected that COPD will be the third leading cause of death worldwide by 2030. Moreover, although the overall prevalence of COPD is increasing in both men and women [249], recent data from US Center for Disease Control's National Center for Health Statistics has shown that COPD prevalence in the United States not only is higher in women but also increasing at a higher rate among women than men [2]. Epidemiological data show that since the year 2000, the number of women in the United States dying from COPD has surpassed the number of men [10, 157]. Some studies have suggested that both asthma and the so-called asthma-COPD overlap syndrome (ACOS), which are more common among adult women than men, can predispose women to develop COPD [61, 272].

It is possible that the increased prevalence of COPD in women is not only due to increased tobacco use but also related to longer life expectancy for women in general, as well as changes in women's occupational exposures over the past few decades [10]. Historically, professions that predispose to lung disease were predominantly held by men. However, due to the reassignment of sex roles and more single-parent households in recent decades, a higher number of women are found in these jobs [11]. This may play a role in the increasing prevalence of the disease among women. It is estimated that 15% of COPD is work-related. In addition, it has long been theorized that indoor air pollution resulting from smoke from biomass fuel combustion for cooking and other purposes also contributes to the development of COPD in never smokers, with

women being disproportionately exposed [284] and affected [202]. It is estimated that 50% of deaths from COPD are associated with indoor air pollution in developing countries, and about 75% of these are in women [227].

In recent years, there have been several clinical and experimental studies aiming to understand the contribution of sex to the biologic pathogenesis of COPD [18]. Levels of pro-inflammatory cytokines, including C-reactive protein, interleukin-6 (IL-6), tumor necrosis factor alpha (TNFα), matrix metalloproteinase 9 (MMP-9), pulmonary and activation-regulated chemokine (PARC), and vascular endothelial growth factor (VEGF), have been theorized to contribute to the development of COPD. VEGF helps regulate growth of new vessels and vascular leak and was found to be elevated in patients with COPD compared to healthy controls. In patients with COPD, statistically significant higher levels of VEGF and IL-6 have been found in men vs. women [10]. Additionally, studies in mouse models of chronic cigarette smoke have indicated that sex hormones may be contributing to the greater COPD susceptibility in females. Exposure to cigarette smoke in female mice results in higher peripheral airway obstruction and airway remodeling and less emphysema than male mice, an effect that is mediated by estrogens [267]. It was also found that in female mice, cigarette smoke was associated with activation of transforming growth factor-β (TGF-β), decreased expression of antioxidant genes and the transcription factor Nrf2 (nuclear factor erythroid-derived 2-like 2), as well as increased oxidative stress [267]. Overall, more research is needed to better understand the mechanisms behind sex differences in COPD susceptibility, as well as in the response of men and women to COPD available therapies.

14.4.4 Cystic Fibrosis

Cystic fibrosis (CF), an autosomal recessive multiorgan disease caused by mutations in the cystic fibrosis transmembrane conductance regulator (CFTR) gene, also displays sex differences. Epidemiological studies have reported a sex-based disparity in CF outcomes, where females experience higher rates of pulmonary exacerbations and a shortened life expectancy than males [289]. While the etiology of this disparity is not fully elucidated, it appears to be multifactorial. Studies have associated the sexual dimorphism in CF outcomes to bias in diagnosis [136], anatomical differences between males and females [60], socioenvironmental factors [218], medication adherence [239], physical activity level [229], and actions of male and female sex hormones [1, 264]. A combination of poor perception of disease prognosis, withdrawal, anxiety, decreased adherence to therapies, and decrease in physical activity after puberty has been associated with increased morbidity and mortality in CF females [236]. Moreover, despite reported earlier referral to lung transplantation in females than males, survival time after transplantation does not show sex differences. Not only females with CF experience higher rates of infection and exacerbations than males, they also require more intensified treatment regarding antibiotics, macrolides, steroids, and days of hospitalization than their male counterparts [171, 193]. However, despite earlier referral to lung transplantation in females than males, survival time after transplantation does not show sex differences.

As with other lung diseases described earlier, the sexual dimorphism in CF outcomes is also age dependent. In females, the predisposition to worse outcomes in CF has been found at a young age, where girls are more susceptible to bacterial infection than boys [50]. Females not only show higher lung bacterial colonization with *Pseudomonas aeruginosa*, *Burkholderia cepacia*, and *methicillin-resistant Staphylococcus aureus* than males [54, 103, 161, 217] but also earlier colonization in life, which is a predictor of negative outcomes and decline in survival for females [59]. Females have also been found to acquire *methicillin-sensitive Staphylococcus aureus*, *methicillin-resistant Staphylococcus aureus*, *Haemophilus influenzae*, *Achromobacter xylosoxidans*, *Aspergillus species*, and nontuber-

culous mycobacteria at earlier ages than males and often even prior to puberty [92].

During puberty and reproductive years, the predisposition to infection is enhanced in females, as well as an increased risk for pulmonary exacerbations and extrapulmonary complications [161]. Females also show a steeper decline in lung function, one of the key predictors of long-term health in CF patients, than males [50]. Because of the reduced life expectancy of patients with CF, little is known about the influence of menopause in the course of the disease [187]. A study in long-term survivors (older than 40 years old) showed that females with CF are also less likely to live to the age of 40 than males [187].

While the mechanisms underlying these sex-disparities have not been fully elucidated, a role of sex hormones in mediating inflammatory processes [101], and types of pathogens colonizing the lung has been suggested [280]. A study by Chotirmall et al. showed that the female hormones 17β-estradiol and estriol can induce conversion of *Pseudomonas aeruginosa* from a non-mucoid to mucoid phenotype in females with CF. The same study suggested that high levels of 17β-estradiol in females result in higher capture of more mucoid strains of *Pseudomonas aeruginosa* and subsequent pulmonary exacerbations [48]. In addition, not only postpubertal increases in pulmonary exacerbations are reported in females [261], but also women display cyclical symptoms in relation to their menstrual cycle, with higher lung function measures during the luteal phase than other cycle phases [114]. Studies in bronchial epithelial cells also showed that 17β-estradiol reduces expression of proinflammatory cytokines via upregulation of the secretory leucoprotease inhibitor (SLPI), which could contribute to the higher infection rate observed in females vs. males [48]. In mouse models of CF, 17β-estradiol stimulates expression of toll-like receptor 2, IL-23, and IL-17A and results in higher lung inflammatory infiltrates and mucin [295]. Abid et al. showed that female mice inoculated with *Pseudomonas aeruginosa* died earlier and showed slower bacterial clearance than male mice [1]. This effect was reversed by treatment with the estrogen receptor (ER) antagonist ICI 182,780 and ovariectomy and recapitulated in ovariectomized females treated with exogenous 17β-estradiol [1].

Very few studies have evaluated the role of progesterone and testosterone in mediating sex differences in CF infection rates and outcomes. One study in human tracheal epithelial cells showed that exposure to progesterone results in decreased cilia beat frequency, an effect that was attenuated with the addition of 17β-estradiol [109]. While women with CF are able to carry on pregnancies, the role of progesterone in lung function and CF outcomes has not been studied in detail [191]. With regard to androgens, a few reports have indicated that adolescent and adult males with CF have lower salivary and serum levels of testosterone than healthy controls [29, 139], as well as higher rates of male infertility [312]. In rodent studies, testosterone was found to enhance expression and functional activity of epithelial sodium channels [174]. Overall, the direct impact of sex hormones on disease progression in patients with CF remains unknown.

14.4.5 Idiopathic Pulmonary Fibrosis

Idiopathic pulmonary fibrosis (IPF) is a specific form of chronic, progressive fibrosing interstitial pneumonia of unknown cause, occurring primarily in older adults, and limited to the lungs [212]. With a median survival of 3–5 years following diagnosis, IPF is characterized by a progressive worsening of dyspnea and decline in lung function and quality of life in most patients [68]. Sex discrepancies in this disorder have been suggested for some time. The incidence and prevalence of disease have been reported in multiple studies to be higher in males than in females, with ratios ranging from ~1.6:1 to 2:1. Prior reports have also suggested that female sex is associated with better survival [90].

Although our current understanding of the pathogenesis of IPF is incomplete, recent advances have delineated specific clinical and pathologic features. Epithelial cell dysfunction and aberrant epithelial-mesenchymal signaling lead to the activation of fibroblasts and extracel-

lular matrix deposition and remodeling. This chronic activation appears to lead to profibrotic, pathologic changes in IPF fibroblasts. The myofibroblast is the classic pathologic fibroblast phenotype described in IPF lungs. Several mediators, including TGF-β, can elicit the differentiation of fibroblasts to myofibroblasts. Compared with resident lung fibroblasts, myofibroblasts secrete excessive amounts of matrix, including type I collagen. This excess matrix deposition may lead to pathologic lung fibrosis and remodeling [303]. Although these mechanisms have provided significant advances in our understanding of the disease, there is limited information on the molecular basis underlying the observed sex disparities in IPF. A study by Smith et al. suggested that estrogen may modulate the expression of genes involved in chromatin remodeling pathways, as well as the expression of genes in extracellular matrix turnover [247]. However, results from animal studies have provided mixed results. Genome-wide association studies have pointed to genetic influences mediating sex differences, including SNP polymorphisms in mucin 5B, near A-kinase anchoring protein 13, and desmoplakin genes [7].

Sex differences in IPF have been studied in the clinic. Han et al. studied whether the rate of increase in desaturation during serial 6-min walk testing, as well as survival, displayed sex differences. They noted several important observations: (1) males with IPF demonstrate more rapid deterioration in exertional desaturation over time when compared with females; (2) survival was worse in males than females; and (3) better survival for females persisted after additional adjustment for relative change in exertional desaturation and forced vital capacity (FVC) [90].

Among the clinical conditions that have been associated with a worse IPF prognosis is the presence of comorbidities and complications such as emphysema, pulmonary hypertension, cardiovascular diseases, and bronchogenic carcinoma [68]. As mentioned in other sections, some of these conditions also present a sexual dimorphism, which could potentially influence the progression and outcomes of IPF. Finally, prompt treatment of IPF is critical to preserving the patients' lung function, reducing the risk of acute exacerbations, and improving outcomes [149]. Currently, two drugs are approved for the treatment of IPF in the United States and Europe: nintedanib and pirfenidone. In vitro studies have shown that by inhibiting signaling mediated via tyrosine kinases, nintedanib inhibits fundamental processes of fibrosis, such as the recruitment, proliferation, and differentiation of fibroblasts and fibrocytes and the deposition of extracellular matrix. Data from animal models of fibrosis suggest that nintedanib may also act to normalize the distorted microvascular architecture in the lungs. The mechanism of action of pirfenidone is less well defined, as its target remains unknown, but nonclinical studies suggest that it inhibits profibrotic behaviors in fibroblasts and fibrocytes. Both drugs have been shown to slow the disease progression but not significantly impact mortality [149]. However, studies have not addressed sex differences in the effectiveness of these and other therapies for IPF. Current efforts are directed at identifying key biomarkers that may direct more customized patient-centered healthcare to improve outcomes for these patients in the future, and it is essential that they address sex-specific mechanisms [19].

14.4.6 Lung Cancer

Lung cancer is a major public health problem worldwide and is the world's leading cause of cancer death [21]. Approximately 95% of all lung cancers are classified as either small cell lung cancer (SCLC) or non-small cell lung cancer (NSCLC) [242, 260]. This distinction is essential for staging, treatment, and prognosis. Lung cancer is relatively rare before the fifth decade of life, and risk increases with age thereafter. Over the past decade, the cancer incidence rate (2005–2014) has been found stable in women and declined by approximately 2% annually in men, while the overall cancer death rate (2006–2015) declined by about 1.5% annually in both men and women [165]. Lung adenocarcinoma is also more common among women than men [315].

Environmental risk factors for lung cancer include smoking cigarettes and other tobacco products, as well as exposure to secondhand tobacco smoke, occupational lung carcinogens, radiation, and indoor and outdoor air pollution [4, 132, 201]. However, lung cancer incidence patterns reflect trends in sex behaviors associated with cigarette smoking [220]. Generally speaking, any form of smoking exposure increases the lung cancer risk [4, 311]. A recent US report indicated that lung cancer incidence and death rates among women have increased in 18 states. Interestingly, the states with higher prevalence of smoking among adult women had the highest rates of lung cancer. This report showed that only one state had decreasing lung cancer incidence and death rates in women [110]. Currently, lung cancer incidence rates are declining about twice as fast in men as in women, reflecting historical differences in tobacco uptake and cessation, as well as upturns in female smoking prevalence in some birth cohorts [64]. In addition, the implementation of widespread lung cancer screening holds promise for the future.

Zang et al. found that the odds of developing major lung cancer types are consistently higher for women than for men at every level of exposure to cigarette smoke [315]. This sex difference, however, cannot be explained by differences in baseline exposure, smoking history, or body size, but it is likely due to the higher susceptibility to tobacco carcinogens in women [198, 26]. In this regard, higher levels of polycyclic aromatic hydrocarbon-derived DNA adducts have been reported in female smokers vs. male smokers [177]. A potential mechanism associated with these outcomes is related to the fact that estrogen synergizes with some tobacco compounds through the induction of CYP1B1, an enzyme responsible for estrogenic metabolism, which leads to enhanced reactive oxygen species formation and carcinogenesis [102]. Moreover, Kure et al. found a higher frequency of G:C-->T:A mutations and a higher average hydrophobic DNA adduct level in female patients than males, even though the level of exposure to carcinogens from cigarette smoke was lower among females than males [131]. These findings lend support to epidemiological evidence that women are at greater risk than men of contracting tobacco-induced lung cancer.

As mentioned earlier, there is considerable evidence indicating that sex hormones can influence respiratory function throughout life [24, 277]. As with other lung diseases, sex hormones have also been implicated in lung cancer [176]. For example, estrogen, known to be a risk factor for the development of adenocarcinoma of the breast, ovary, and endometrium, has been postulated to contribute to lung cancer development and progression [244, 315]. Furthermore, estrogen has also been implicated in lung cancer therapy [13]. Women with advanced NSCLC survive longer than men after adjustment for other prognostic factors in the modern chemotherapy era, suggesting that estrogen levels may interact with the efficacy of current chemotherapy prescriptions or other as yet undefined factors. This finding, if validated, could be potentially exploited in designing new therapies [230, 294].

Regarding estrogen receptors (ERs), Kadota et al. reported that stage I lung adenocarcinoma cells express higher levels of ERα in females than males (19% vs. 14%) and that ERα expression correlates with smaller tumor size. The authors concluded that nuclear ERα expression is an independent predictor of recurrence in pT1a stage lung adenocarcinoma (i.e., tumor size of 2 cm or less) and correlates with poor prognostic immune microenvironments [118]. In addition, non-small cell lung cancer lines (both squamous cell and adenocarcinoma) have been found to express estrogen receptors [192].

Hormone replacement therapy (HRT) is a common treatment used in postmenopausal women. To date, there are several controversies in the relationship between the HRT and lung cancer. The Women's Health Initiative trial concluded that treatment with estrogen plus progestin in postmenopausal women did not increase the incidence of lung cancer. However, HRT was found to increase the number of deaths from lung cancer, in particular deaths from non-small cell

lung cancer [47]. These findings should be incorporated into risk-benefit discussions with women considering combined hormone therapy, especially those with a high risk of lung cancer.

In summary, there is accumulating evidence to support the notion that the risk of development of lung cancer is different among women than among men. As expressed earlier, women may be more susceptible to the effects of carcinogens in tobacco and tobacco smoke as a result of hormonal, genetic, and metabolic differences between the sexes. Thus, the significance of sex as a separate contributing factor shall be considered in prognosis and therapeutic management.

14.4.7 Lymphangioleiomyomatosis

Lymphangioleiomyomatosis (LAM) is a rare progressive lung disease that occurs almost exclusively in women [309]. The incidence of LAM is estimated to range between 1 and 8 per million women, and the disease mostly affects women of childbearing age [91]. The average age of symptom onset among LAM patients in the United States and Europe ranges between 34 and 37 years of age [52]. LAM is characterized by infiltration of specific dysregulated smooth muscle-like cells (LAM cells) in various organs and tissues, including lymph nodes, kidneys, and the lungs. As a result, LAM patients experience a progressive decline in lung function due to parenchymal destruction and development of cysts in lung tissue.

The mechanisms underlying LAM development, and the marked sex disparity in its incidence, have not been fully elucidated [89]. However, the neoplastic phenotype of LAM cells is known to occur as a consequence of constitutive activation of the mechanistic target of rapamycin (mTOR) due to loss of heterozygosity in the tuberous sclerosis genes (TSC1 or TSC2) [97]. Advances in the understanding of TSC biology have provided critical clues to LAM pathogenesis and treatment and led to the use of the mTOR inhibitor sirolimus (i.e., rapamycin) as an effective suppressive therapy. Alternatively, lung transplantation is also an established option for women with severe pulmonary impairment due to LAM.

The striking sex disparity observed in LAM has led multiple investigators to consider a role of sex hormones, and specifically estrogen, in the development, progression, and severity of LAM disease [63]. LAM clinical presentation occurs after puberty, accelerated progression is frequently observed during pregnancy, and menopause is associated with attenuated progression [154]. Animal models and in vitro studies have also shown that estrogen increases cell proliferation and migration [313]. Moreover, LAM cells are known to express both estrogen and progesterone receptors. However, definitive evidence is lacking regarding manipulating sex hormones as a potential therapeutic approach, and additional efforts are needed to develop strategies for disease prevention and treatment.

14.4.8 Obstructive Sleep Apnea

The prevalence of OSA is similar between the sexes before puberty but becomes more common in boys than girls after puberty [216]. This sexual dimorphism persists throughout adulthood, where both the rate and severity of OSA are higher in men compared to women. These differences have been attributed to anatomical differences in the upper airway and increased accumulation in the neck of fluid displaced from the legs during recumbency while sleeping [122, 155]. Other risk factors include craniofacial abnormalities, genetic conditions, and neuromuscular disorders. Studies in hypogonadal men and obese adolescents with low testosterone levels have suggested a role of male sex hormones in the observed sex differences in OSA [164, 172]. In females, progesterone has been found to increase the tone of upper airway muscles and stimulate ventilation via chemoreceptor responses to hypoxia and hypercapnia [203, 238]. These sex hormone-mediated mechanisms have been proposed to contribute to the lower risk and severity of OSA observed in girls and women after puberty.

14.4.9 Pulmonary Arterial Hypertension

Pulmonary arterial hypertension (PAH) is a progressive and devastating disease of the pulmonary vasculature characterized by extreme elevation of pulmonary arterial pressure and subsequent right ventricular failure [72]. PAH is also characterized by progressive obstruction of the pulmonary arterial circulation due to formation of vaso-occlusive lesions arising from vigorous proliferation and migration of endothelial cells [214]. As a result of the increased pulmonary vascular resistance, higher right ventricular (RV) afterload causes adaptive RV hypertrophy that often progresses to maladaptive RV hypertrophy and fibrosis, leading to eventual premature death from RV failure. Despite improvements in the diagnosis and management of PAH, the disease continues to have a poor prognosis. A recent analysis showed that the 5-year survival for PAH is approximately 60% [169].

Accumulating evidence shows that more females than men are diagnosed with PAH; however, epidemiological data show that survival among females is better than among males, especially in older patients [12, 104, 108, 135, 159]. Interestingly, the survival benefit for females appears to decline with age [240] and correlate with declines in estradiol levels [285]. This discrepancy in incidence and disease outcomes in men and women is commonly referred to as the PAH "estrogen paradox" and has prompted research into the sex-based differences and hormonal regulation mechanisms in PAH. While the mechanisms behind the sex disparity are far from being understood, they likely involve contributions of genetics, as well as sex hormones and their metabolites.

A few studies have suggested a genetic component in PAH. Mutations in the gene encoding for the bone morphogenetic protein (BMP) receptor type 2 (BMPR2) have been shown to increase PAH penetrance and severity in mouse models [69]. Moreover, mutations in the *BMPR2* gene are the most common genetic cause of familial PAH [65, 148]. By using the "four core genotypes" mouse model [57], it was found that the Y chromosome, and specifically upregulation of Y chromosomal genes in the lung, was protective against pulmonary vascular remodeling [281] irrespective of gonadal sex. More recent studies have investigated whether genes encoding for enzymes that mediate estrogen metabolism, such as CYP1B1, are associated with PAH in males and females. West et al. found that CYP1B1 expression was markedly downregulated in female but not male patients with PAH due to BMPR2 mutations [301].

Regarding sex hormones, there are multiple studies demonstrating that estrogens exert complex and context-dependent effects on the pulmonary vasculature [62, 133, 168, 208, 308]. Microarray analyses in animal models identified diverse set of pathways regulated by estradiol, including steroid metabolism, immune response, cytoskeletal function, extracellular matrix composition, bone morphogenetic protein (BMP), Notch, Wnt, and calcium signaling [73]. Studies in vascular cells have shown that estradiol affects proliferation [151, 152, 302]. In a rescue approach experimental animal model, it was shown that estradiol treatment reversed pulmonary vascular remodeling, fibrosis, and inflammatory signaling [282]. Overall, while some studies in animals have demonstrated that both exogenous and endogenous estradiol can be protective against PAH, others have suggested a more causative role [123, 134, 151]. Collectively, these studies demonstrate that both endogenous and exogenous estradiol can act as potent regulators of pulmonary vascular homeostasis and greatly impact the progression or resolution of vascular injury. However, these models do not display sex differences nor point to a female predisposition, indicating that more research is needed to fully understand the roles played by hormones in PAH in men and women. Accumulating evidence indicates that estrogen metabolites can also modulate PAH pathogenesis [273]. Thus, it is important to consider the role of metabolites when investigating the effects of estrogen in PAH. Interestingly, low levels of dehydroepiandrosterone (DHEA), a precursor for estrogens that can bind estrogen

receptors, are associated with PA development in men [286]. A recent study in postmenopausal women also showed that women with PAH had lower levels of DHEA and higher levels of estradiol than those without cardiopulmonary disease [14]. In patients with PAH, low DHEA and high estradiol were also associated with worse prognosis and increased risk for death [14], as well as fluctuations in pulmonary function throughout the menstrual cycle [15]. Whether DHEA is a marker or mediator of PAH remains under investigation. Overall, more research is needed to understand the mechanisms mediating sex differences in PAH, in order to develop sex-specific therapies to prevent and treat this devastating disease.

14.4.10 Respiratory Infection

Respiratory infection remains a leading cause of morbidity and mortality across all age groups. While, overall, males are disadvantaged in the occurrence and severity of lower respiratory tract infections, females appear to be more susceptible to upper respiratory infections [67]. Multiple studies have suggested that a complex interplay of genetics, sex hormones, host immunity, anatomical and physiological differences, as well as sociocultural and behavioral is likely to underlie the observed sex differences in infection rates and severity [25, 45, 106, 117]. In the following sections, we describe the epidemiology and current knowledge on respiratory diseases that present with a sexual dimorphism.

14.4.10.1 Respiratory Syncytial Virus

During infancy and early childhood, infection with respiratory syncytial virus (RSV) occurs more frequently in boys than girls, especially those born prematurely [150]. Resulting from RSV infection, bronchiolitis is also more frequent and severe in male infants and young children and is often associated with higher risk of wheezing and childhood asthma, as well as higher risk of hospitalization [95, 183].

Sex differences in RSV infection and bronchiolitis have been attributed to anatomical and immunological factors, including smaller airway diameter in males than females [40], and sex differences in the Th2/Th17 response to viral infection [128, 124]. Animal mouse models of RSV infection show that infected female mice display better viral control than males, via mechanisms involving interferon-β expression. In addition, male mice show persistent immune alterations in Th2/Th17 cells, dendritic cells, and ILC2 responses that result in delayed control of viremia [156]. Similar studies have indicated that sex hormones and their receptors can also mediate these mechanisms, although their contributions to infant and pediatric infectious disease remain unclear [116].

14.4.10.2 Influenza

Influenza is an acute respiratory infectious disease caused by several types of influenza viruses. According to the World Health Organization, there are 3 to 5 million cases annually of severe illness and about 290,000 to 650,000 respiratory deaths [305]. The severity and mortality of influenza disease are worse for young children, the elderly, individuals with chronic and immunocompromised medical conditions, and pregnant women [179].

Researchers have reported sex differences in influenza severity, mortality, vaccine tolerance, responses, and outcomes [127]. Interestingly, males are more susceptible to infection than females, and females have greater immune responses but experience more adverse reactions to influenza vaccines than males [128, 290]. In addition, females of reproductive age have the worst outcome during pandemic influenza [304]. However, the causes and mechanisms for these discrepancies in susceptibility are not well-known. Research groups have reported that immunity to viruses can vary with changes in hormone concentrations caused by fluctuations over the menstrual cycle, contraception use, pregnancy, and menopause [32].

Most experiments using murine models have shown that young adult females develop greater

respiratory inflammatory responses and have a more severe outcome from influenza infection than males, despite the sexes having similar virus titers [99, 222, 223]. For instance, proinflammatory cytokines (e.g., TNFα, IFNγ, IL6, and IL12) and chemokines (e.g., CCL2, CCL5, and CCL12) are higher in the lungs of influenza-infected females when compared to males [99]. It was also discovered that increased levels of testosterone and amphiregulin, which is an epidermal growth factor that mediates lung tissue repair, improve repair and recovery of lung damage in males [288]. Moreover, infection of female mice of reproductive age with influenza decreases ovarian function and levels of sex hormones suggesting that inhibition of sex hormones may contribute to severe outcomes in female mice [223, 287]. Independent research groups discovered that female mice with influenza that were treated with estrogen showed a decrease in the inflammatory response (e.g., CCL2, IFNγ, TNFα) and an increase in antibody response to influenza vaccine [43, 291]. Importantly, the expression of toll-like receptor-7 is higher in B cells from vaccinated females than males, and its deletion decreased sex differences in vaccine-induced antibody responses and protection [70]. Future research should focus on the molecular mechanisms that regulate how hormones and genes affect immunity to influenza and vaccines in males vs. females.

14.4.10.3 Coronavirus Disease 2019

The coronavirus disease 2019 (COVID-19) is a public health crisis caused by the novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). As of this writing, there have been over 112 million confirmed COVID-19 cases and 2.5 million deaths worldwide. Importantly, demographic and clinical data gathered by multiple health agencies around the globe have demonstrated profound sex differences in COVID-19 outcomes [206]. While the rate of SARS-CoV-2 infection is similar between males and females, male patients infected with the SARS-CoV-2 virus have a significantly higher risk of developing severe COVID-19, being admitted to an intensive care unit (ICU), and dying when compared to female-infected patients [126].

As mentioned earlier, sex-specific immune responses to a diverse array of viral pathogens have been reported [31, 81, 200, 232, 290]. In addition, there are also prominent sex differences in the immune responses mounted by individuals receiving viral vaccines [127, 158]. In the case of infection with coronaviruses, there have been reports of sex differences during prior outbreaks, including the 2003 severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) epidemics, which had a higher case fatality rate and number of deaths in males than females [5, 121, 140].

While not all countries provide sex-disaggregated data, the Sex, Gender and COVID-19 Project [84] has combined efforts from agencies located in several continents to increase reporting of data by sex for confirmed cases, testing, hospitalizations, ICU admissions, confirmed cases among healthcare workers, and deaths. In almost all countries, a significant male predominance in COVID-19 morbidity and mortality has been reported, suggesting a biological mechanism involved [234]. In the United States, most of the states have made public sex-disaggregated data on COVID-19 morbidity and mortality. In an article published in June of 2020, Klein et al. reported that in states providing sex-disaggregated information, data shows that men are twice as likely to die from COVID-19 than women [126]. Moreover, sex differences in the immune response to SARS-CoV-2 have also been reported, where males with mild disease had higher plasma levels of pro-inflammatory cytokines and chemokines than females, but females had higher CD4 and CD8 T-cell activation than males [265]. A study comparing responses to convalescent plasma also showed higher microneutralization and IgG responses to SARS-CoV-2 in males than to females, which correlated with worse COVID-19 outcomes [125].

Some of these sex effects have been attributed to chromosomal differences, since the X chromo-

some has been shown to express a large number of immune-related genes, including some involved in cytokine and toll-like receptor (TLR) signaling, NF-kB signaling, and MAPK signaling [251]. In addition, the gene encoding the human angiotensin-converting enzyme 2 (ACE2), which serves as the receptor for the spike (S) protein of SARS-CoV-2 [46] is also expressed in the X chromosome and can escape X inactivation and be expressed from both the active and inactive X chromosome [39]. This has been shown to lead to sex differences in ACE2 gene expression [80, 142, 279], which has potential consequences for the vulnerability to SARS-CoV-2.

As with other inflammatory lung diseases and infectious processes, a role of sex hormones has been postulated in mediating sex differences in COVID-19 [250, 259, 266]. Estrogen can regulate the expression of SARS-CoV-2 viral entry receptors, including ACE2 and the transmembrane protease, serine 2 (TMPRSS2) [100, 153]. In this context, a recent report showed that postpubertal females have lower levels of serum ACE2 when compared to age-matched males [262]. Furthermore, the serum activity of ACE2 is higher in postmenopausal women when compared to younger women, suggesting a regulation by sex hormones like estrogen [79]. Interestingly, Stelzig et al. recently showed that estrogen can downregulate the expression of ACE2 in normal human bronchial epithelial (NHBE) cells but had no effect on TMPRSS2 [256]. This correlates with prior work conducted in the four core genotypes model indicating that sex differences in enzymatic activity of ACE2 in mice are estrogen-dependent and sex chromosome-independent [146].

Regarding male sex hormones, it is unclear whether androgen levels contribute to SARS-CoV-2 or COVID-19 outcomes [178]. A recent report showed that in males with SARS-CoV-2 pneumonia, low testosterone levels were associated with higher rates of ICU admission and death [215]. This correlates with prior studies showing that testosterone can upregulate IL-1 and downregulate IL-1β, IL-6, and TNF-α leading to a suppression of inflammation [173, 205]. Future studies investigating the effects of androgen levels on COVID-19 should consider the timing of the androgen measurement in the course of the SARS-CoV-2 infection [259]. Testosterone can also regulate the expression of TMPRSS2 [82, 257], thus contributing to viral infection and disease outcomes. Interestingly, TMPRSS2 is also highly expressed in urogenital organs, such as the prostate [44].

Finally, it has been hypothesized that gender factors, i.e., smoking habits, handwashing, caregiver gender roles, etc., can influence the outcome of SARS-CoV-2 infections [34, 79, 283, 300]. There are also significant sex and gender differences in comorbidities that have been associated with COVID-19 progression and outcomes [241]. In general, these comorbidities tend to be more prevalent in men than women [306]. Thus, several structural gender health disparities will need to be addressed in order to effectively mitigate the negative effects of the COVID-19 pandemic [250].

14.5 Conclusion

Gender and sex differences in the prevalence, severity, and susceptibility to a variety of lung diseases have been reported across the life span (Fig. 14.1). While the causes of these disparities have not been fully elucidated, a lot has been accomplished in the past few decades. These investigations have revealed associations of biological factors (sex) such as airway anatomy and physiology, chromosomal contributions, genetics and epigenetics, and sex hormones with lung disease onset and outcomes in men and women. Others have shown that sociocultural and environmental factors (gender) can also influence differential outcomes in lung disease. Understanding the contributions of sex and gender, as well as their complex interplay in the context of respiratory health, represents a fundamental step toward precision medicine and the future development of more effective options to prevent and treat lung disease.

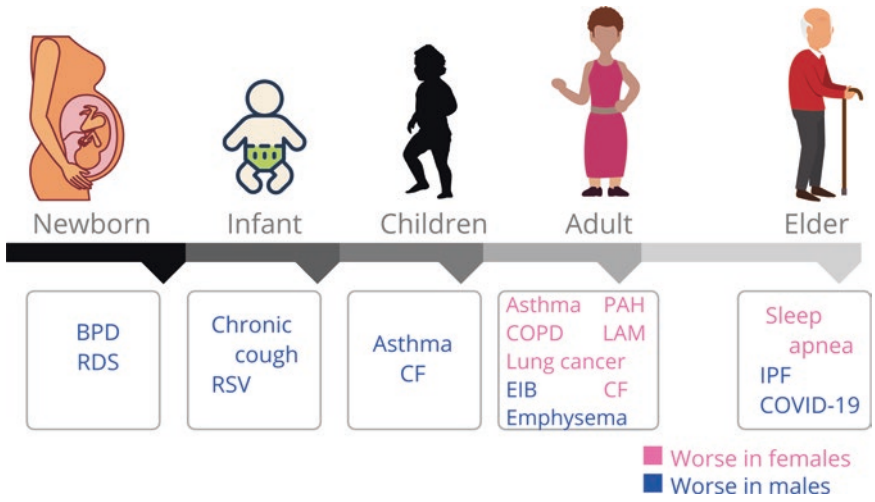

Fig. 14.1 Sex differences in lung disease progression across life span. There are sex differences in the prevalence of several lung diseases across the life span. In pink are lung diseases that are more prevalent in females than males (blue). (Abbreviations: BPD Bronchopulmonary dysplasia, RDS Respiratory distress syndrome, RSV Respiratory syncytial virus, CF Cystic fibrosis, PAH Pulmonary arterial hypertension, COPD Chronic obstructive pulmonary disease, LAM Lymphangioleiomyomatosis, EIB Exercise-induced bronchoconstriction, IPF Idiopathic pulmonary fibrosis, COVID-19 Coronavirus disease 2019)

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Sex Hormones and Lung Inflammation

15

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Abstract

Inflammation is a characteristic marker in numerous lung disorders. Several immune cells, such as macrophages, dendritic cells, eosinophils, as well as T and B lymphocytes, synthetize and release cytokines involved in the inflammatory process. Gender differences in the incidence and severity of inflammatory lung ailments including asthma, chronic obstructive pulmonary disease (COPD), pulmonary fibrosis (PF), lung cancer (LC), and infectious related illnesses have been reported. Moreover, the effects of sex hormones on both androgens and estrogens, such as testosterone (TES) and 17β-estradiol (E2), driving characteristic inflammatory patterns in those lung inflammatory diseases have been investigated. In general, androgens seem to display anti-inflammatory actions, whereas estrogens produce pro-inflammatory effects. For instance, androgens regulate negatively inflammation in asthma by targeting type 2 innate lymphoid cells (ILC2s) and T-helper (Th)-2 cells to attenuate interleukin (IL)-17A-mediated responses and leukotriene (LT) biosynthesis pathway. Estrogens may promote neutrophilic inflammation in subjects with asthma and COPD. Moreover, the activation of estrogen receptors might induce tumorigenesis. In this chapter, we summarize the most recent advances in the functional roles and associated signaling pathways of inflammatory cellular responses in asthma, COPD, PF, LC, and newly occurring COVID-19 disease. We also meticulously deliberate the influence of sex steroids on the development and progress of these common and severe lung diseases.

Keywords

Testosterone · 17β-Estradiol · Inflammation · Asthma · COPD · Lung cancer · Pulmonary fibrosis

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Abbreviations

AA	Arachidonic acid
AC	Adenylate cyclase
AECs	Airway epithelial cells
AHR	Airway hyperresponsiveness
AP-1	Activator protein 1
AR	Androgen receptor
ASM	Airway smooth muscle
ASMCs	Airway smooth muscle cells
BALF	Bronchoalveolar lavage fluid
cAMP	Cyclic adenosine monophosphate
CCL C-C	chemokine ligand
CCR C-C	chemokine receptor
CD	Cluster of differentiation
cGMP	Cyclic guanosine monophosphate
COPD	Chronic obstructive pulmonary disease
CYP11A1	P450 side chain cleavage enzyme
CYP17A1	P450 17α-hydroxylase
DAMPs	Danger-associated molecular patterns
DCs	Dendritic cells
DHEA	Dehydroepiandrosterone
E2	17β-Estradiol
ECM	Extracellular matrix
EGF	Epidermal growth factor
EMT	Epithelial-mesenchymal transition
eNOS	Endothelial nitric oxide synthase
ERK	Extracellular signal-regulated kinase
ERα	Estrogen receptor alpha
ERβ	Estrogen receptor beta
ET	Endothelin
FEV1	Forced expiratory volume in 1 second
FVC	Forced vital capacity
G-CSF	Granulocyte colony-stimulating factor
GM-CSF	Granulocyte-macrophage colony-stimulating factor
HDM	House dust mite
IFN-γ	Interferon gamma
Ig	Immunoglobulin
IL	Interleukin
ILC2	Type 2innate lymphoid cell
IPF	Idiopathic pulmonary fibrosis
JNK	Jun N-terminal kinase
LC	Lung cancer
LTs	Leukotrienes
MAPK	Mitogen-activated protein kinase
MCP-1	Monocyte chemoattractant protein-1
MMP	Matrix metalloproteinase
NF-κB	Nuclear factor kappa B
NO	Nitric oxide
OC	Oral contraceptives
OVA	Ovalbumin
P4	Progesterone
PAMPs	Pathogen-associated molecular patterns
PBMCs	Peripheral blood mononuclear cells
PEFR	Peak expiratory flow rate
PF	Pulmonary fibrosis
PI3K	Phosphoinositide 3-kinase
PMA	Perimenstrual asthma
PR	Progesterone receptor
PRRs	Pattern recognition receptors
ROS	Reactive oxygen species
STAR	Steroidogenic acute regulatory protein
TAM	Tumor-associated macrophages
TES	Testosterone
TGF-β1	Transforming growth factor beta 1
Th	T-helper cell
TLR	Toll-like receptor
TNF-α	Tumor necrosis factor alpha
TSPO	Translocator protein

15.1 Introduction

15.1.1 Lung Inflammation

Inflammation is a complex biological response to harmful stimuli (i.e., bacterial and viral infections, irritants or environmental pollutants, and damaged cells), which is orchestrated by the immune system [1–4]. Two phases of inflammation can be distinguished: acute and chronic inflammation. In the acute phase (hours to days), host cells recognize danger-associated molecular patterns (DAMPs) or pathogen-associated molecular patterns (PAMPs) through the action of pattern recognition receptors (PRRs), expressed predominantly in monocytes, macrophages, neutrophils, and dendritic cells [1, 2, 5, 6]. These cells migrate to the injured site along a

chemotactic gradient mediated by specific cytokines. Cellular stimulation leads to the inflammatory process through the activation of transcription factors like nuclear factor kappa B (NF-κB) and the release of pro-inflammatory cytokines such as tumor necrosis factor alpha (TNF-α), interleukin (IL)-1, IL-6, IL-8, IL-12, IL-17 and interferon (IFN)-I and IFN-II [3, 7–11]. IL-8 acts as a neutrophil chemotactic agent, and TNF-α augments the expression of adhesion molecules in the endothelial cells of lung capillaries. Then, antigen-presenting cells (APCs) present the T lymphocytes with the foreign antigen (virial/bacterial or damaged cell components) and evoke either a type 1 T helper (Th)1 lymphocyte- or Th2 lymphocyte-mediated response [10–13]. The persistence of inflammation due to a long-time exposure to inflammatory stimuli, and a failed or incomplete acute response resolution leads to the chronic phase of inflammation that may last for weeks or months and in some circumstances for years. In this phase, the inflammatory response is amplified, and tissue damage may occur. In most cases of chronic lung inflammation, profibrotic and immunoregulatory Th2 cytokines govern [1, 2, 10]. Acute and chronic inflammation are typical markers in numerous lung disorders, including infectious [14, 15], immunological [16, 17], genetic [18, 19], neoplastic [20, 21], and environmental [22, 23] ailment-related.

Commonly, cellular mechanisms of lung inflammation include the expression of adhesion molecules, the release of systemic inflammatory mediators, and the recruitment of distinct leukocytes into the lung vasculature [10, 13, 24]. Neutrophils are the first type of immune cells to be recruited, followed by the resident macrophages, including both alveolar and interstitial and, in some cases, pulmonary intravascular macrophages. The displayed profile of immune cells and cytokines will depend on the developed type of lung disease or injury [10, 16].

15.1.2 Sex Differences in Lung Inflammatory Diseases

Lung disease is a major health issue. According to the Centers for Disease Control and Prevention and to the National Center for Health Statistics in the USA, the number of deaths from chronic lower respiratory diseases reaches ~154,000 every year. Furthermore, it is estimated that this kind of illnesses affects more than 500 million people across the world [25]. It is well known that sex hormones play diverse regulatory effects on the human lung development and physiology [26–30]. Moreover, sex differences are essential predictors in a lot of common diseases, used in diagnosis, prognosis, and treatment recommendations [31, 32].

The influence of sex hormones in the incidence and severity of the inflammatory response in lung disease has been widely studied and recognized for years. For instance, one of the most prevalent lung inflammatory illnesses, chronic obstructive pulmonary disease (COPD), affects both men and women; nevertheless, recent studies point out that females are at a higher risk of developing COPD with lower exposures to tobacco smoke [31, 33–37]. During childhood, asthma symptoms seem to be more prevalent in boys than in girls, and this trend reverts during puberty; however, the incidence in asthma symptoms increases in older men when testosterone (TES) levels decrease, suggesting a potential protective role of the androgens in this ailment [25, 28, 31, 38–42]. Contrariwise, female sex hormones have been related to negative outcomes in asthma [25, 42–44]. Pulmonary fibrosis (PF), an interstitial lung illness, affects more men than women with a higher mortality rate in males [45–47]. Moreover, murine models of bleomycin-induced PF have shown the influence of sex hormones (both males and females) in the decrease of lung function [31, 48, 49]. In cystic fibrosis (CF), a genetic disease, women have been described to display more severe consequences than men, especially in response to bacterial respiratory infections [31, 50, 51]. Pulmonary arterial hypertension (PAH) is another pulmonary disease influenced by gender showing a female predominance [52–55] that has been related to the estrogen receptor alpha (ERα) [56, 57]. Lung cancer (LC) is also an ailment in which the evidence suggests that its incidence and progression are affected by sex hormones differences, particularly by the action of estrogens and their receptors [58, 59]. Furthermore, gender dif-

ferences have been described as well in lung illnesses caused or enhanced by infectious agents [52, 60, 61].

In spite of the marked gender differences in several lung ailments and the great amount of studies related to them, the role of sex hormones in the mechanisms associated with these illnesses has not been fully elucidated. This chapter summarizes the advances in basic and clinical studies of sex hormones (mainly testosterone and estradiol) as modulators of the inflammatory response in lung disease with particular emphasis on asthma and COPD. The information obtained from sex-specific research on lung physiology and pathology would potentially help in the development of sex-specific therapeutics for inflammatory lung diseases regarding the hormonal status of the patient.

15.2 Sex Hormone Steroidogenesis

15.2.1 Classification of Sex Hormones

Sex hormones are involved in processes such as growth, development, reproduction, and systemic homeostasis [62, 63]. This group of hormones possesses a common structure of cyclopentaneperhydro-phenanthrene, a complex of 17-carbon atoms forming a 4-ring system. According to the number of carbon atoms, sex steroids can be divided into three major groups: progestins (21-carbon atoms), androgens (19-carbon atoms), and estrogens (18-carbon atoms) [64]. The same synthesis pathway of steroid hormone production is carried out by different organs in men and women, i.e., testis, adrenal cortex, ovary, brain, placenta, etc.; however, the amount and the main type of synthetized hormone molecule rely on the expression and activity specific to each tissue [64–66].

Cholesterol is the precursor of sex hormones, both male and female, which are synthetized in specialized cells [62, 65, 67]. This precursor is an indispensable element of the cellular plasma membrane contributing to the fluidity, permeability, and regulation of transmembrane signaling pathways [68]. 3-Hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA or HMGCR) is the enzyme responsible for the metabolic pathway that produces cholesterol from acetyl-CoA [69–71]. Additionally, cholesterol can be taken from low-density lipoprotein (LDL, through the LDL receptor pathway) and high-density lipoprotein (HDL), via the scavenger receptor class B type (SR-BI) pathway or lipid droplets [72–74].

15.2.2 Androgen Biosynthetic Pathway in Leydig Cells

In men, the synthesis of TES (the main androgen) is carried out in a major proportion (95%) by Leydig cells from the adult testis through the action of cytochrome P450 enzymes. The synthesis and secretion of this androgen are tightly regulated by luteinizing hormone (LH) [67]. In addition, smaller amounts of TES are produced in the adrenal cortex [65]. Gonadotropin-releasing hormone (GnRH) is secreted from the hypothalamus and stimulates gonadotropic cells in the anterior pituitary gland to release LH. This hormone stimulates its Gs protein-coupled receptor, resulting in the activation of adenylyl cyclase (AC). AC induces the formation of cyclic adenosine monophosphate (cAMP), which stimulates the mobilization of cholesterol to the mitochondria by activating protein kinase A (PKA) signaling [75]. The importation of cholesterol into mitochondria is carried out by the transduceosome, a protein complex conformed mainly by the steroidogenic acute regulatory protein (STAR) and the translocator protein (TSPO) [73, 74]. After the synthesis of cholesterol, this precursor is converted into pregnenolone by the P450 side chain cleavage enzyme (P450scc/CYP11A1) located in the mitochondrial membrane [63, 65, 74, 76]. Pregnenolone can either be converted to progesterone via 3β-hydroxysteroid dehydrogenase type 2 (3β-HSD2) or be hydroxylated to 17α-hydroxypregnenolone and then transformed to dehydroepiandrosterone (DHEA, an andro-

gen) by cytochrome P450 17α-hydroxylase (P450c17/CYP17A1/C17-C20 lyase, an enzyme with hydroxylase and lyase activity) [63, 65, 77, 78]. DHEA is further reduced to androstenediol via 17β-hydroxysteroid dehydrogenase type 3 (17β-HSD3) [79, 80] or converted to androstenedione by 3β-HSD2 [78, 81]. Androstenediol and androstenedione are finally biotransformed to TES by 3β-HSD2 and 17β-HSD3, respectively [65, 78–81]. Furthermore, TES is reduced to 5α-dihydrotestosterone (5α-DHT) by 5α-reductase and to 5β-dihydrotestosterone (5β-DHT) by 5β-reductase [76, 82, 83]. In addition, TES can be converted to 17β-estradiol (E2, an estrogen) through the P450 aromatase (P450aro/CYP19A1 aromatase) action [63] (Fig. 15.1).

Although TES is necessary for estrogen production, men have much higher plasmatic levels of TES than women. The synthesis of TES by Leydig cells in men is seven to eight times greater than that produced in women ovaries. In men, TES plasma concentration reaches values between 6 and 50 nM depending on the person's age. On the other hand, women display stable TES values between 0.6 and 2.4 nM that are maintained along the different life stages, except during pregnancy when TES concentrations increment (3.5–5 nM) [31].

15.2.3 Estrogen Biosynthetic Pathway in Theca and Granulosa Cells

E2 and progesterone (P4) are considered the main female sex hormones. The former is a type of estrogen and the latter is a type of progestogen, both essentially produced in ovaries [36, 64, 84]. In addition to E2, two more estrogen molecules naturally occur in women: estrone (E1) and estriol (E3). Estriol is the predominant estrogen during pregnancy, while estradiol is the prevalent form in non-pregnant premenopausal females. In menopause, estrone is the predominant type of estrogen [62, 85]. Ovaries are the vastest source of estrogens before menopause. Nevertheless, in postmenopausal women and in men, these female hormones are locally produced from circulating testosterone and adrenal cortex steroids in non-reproductive and reproductive tissues [86–88]. Ovarian steroids are synthetized through the interaction between theca (TCs) and granulosa cells (GCs), a process regulated by LH and follicle-stimulating hormone (FSH) [36, 62, 84, 85, 89, 90]. GnRH secreted from the hypothalamus stimulates LH and FSH. LH acts on both TCs and GCs, and FSH exerts its effects mainly on GCs. These hormones stimulate AC activity and cAMP formation. This cyclic nucleotide triggers PKA activation and the further expression of steroidogenic enzymes [91–93] (Fig. 15.2).

P4 is predominantly produced in luteal cells through a system of three cholesterol-modifying enzymes: STAR, P450scc, and 3β-HSD. STAR catalyzes cholesterol transfer within the mitochondria, which is considered the rate-limit step in the production of all steroids [84]. This regulatory protein is mostly expressed in luteal cells; however, STAR can be found in theca and granulosa cells during follicle development or during luteinizing phase, respectively, conferring to these cells the ability to synthetize progesterone [84, 85]. The first step in female steroidogenesis is the initial conversion of cholesterol into pregnenolone by the action of STAR and P450scc [36, 90, 94]. Subsequently, pregnenolone is converted to progesterone by 3β-HSD2 in both theca and granulosa cells [90, 94]. In theca cells, P450c17 hydroxylates pregnenolone to produce 17α-hydroxypregnenolone and subsequently removes the acetyl group in order to form DHEA. This last product can be either converted into androstenedione via 3β-HSD2 or metabolized into androstenediol by 17β-HSD1 [85, 94, 95]. These androgens are further biotransformed to TES via 17β-HSD5 and 3β-HSD2, respectively. TES and androstenedione diffuse across the follicle membrane into the follicular fluid, where they are taken up by granulosa cells [36, 85, 90, 95]. The endoplasmic reticulum of granulosa cells expresses P450aro, which converts TES to E2 and androstenedione to E1 by the addition of an aromatic A ring. Additionally, in granulosa cells, 17β-HSDs regulate the interconversion between E1 and E2. 17β-HSD1 catalyzes the formation of E2 from E1, and

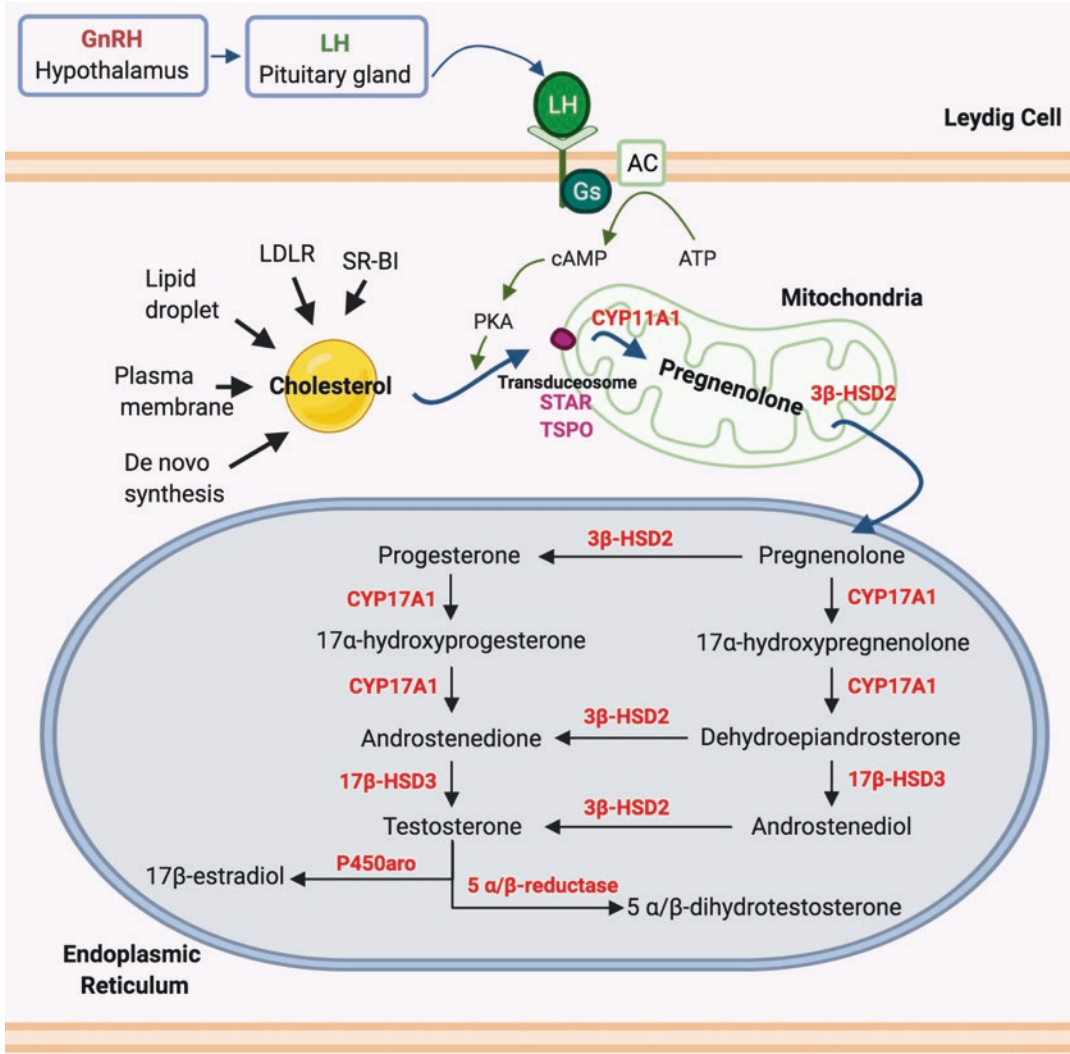

Fig. 15.1 Synthesis of androgens from cholesterol in Leydig cells. Gonadotropin-releasing hormone (GnRH) is secreted from the hypothalamus and stimulates gonadotropic cells in the anterior pituitary gland to release luteinizing hormone (LH), which tightly regulates the synthesis and secretion of androgens in Leydig cells. LH binds to its Gs protein-coupled receptor, resulting in the activation of adenylyl cyclase (AC) and increased intracellular cyclic adenosine monophosphate (cAMP) formation. cAMP stimulates the mobilization of cholesterol to the mitochondria by activating protein kinase A (PKA) signaling. Cholesterol is the precursor of all sex steroids. This lipid precursor can be produced de novo or taken from low-density lipoprotein (LDL) and high-density lipoprotein (HDL) via the scavenger receptor class B type (SR-BI) pathway, plasma membrane, or lipid droplets. Once synthetized, cholesterol is imported into mitochondria through the transduceosome (a protein complex), composed of the steroidogenic acute regulatory protein (STAR), the translocator protein (TSPO), and other proteins. The first step is the conversion of cholesterol to pregnenolone by the C27 cholesterol side chain cleavage cytochrome P450 enzyme (CYP11A1) located on the matrix side of the inner mitochondrial membrane. Then, pregnenolone is converted into testosterone by 3β-hydroxysteroid dehydrogenase (3β-HSD2, located at the mitochondria), 17α-hydroxylase/17,20 lyase (CYP17A1), and type 3 17β-hydroxysteroid dehydrogenase (17b-HSD3) in the endoplasmic reticulum. Furthermore, testosterone can be reduced to 5α- or 5β-dihydrotestosterone by 5α-/β-reductase. Finally, P450 aromatase (P450aro) can convert testosterone to 17β-estradiol in Leydig cells of the adult testis

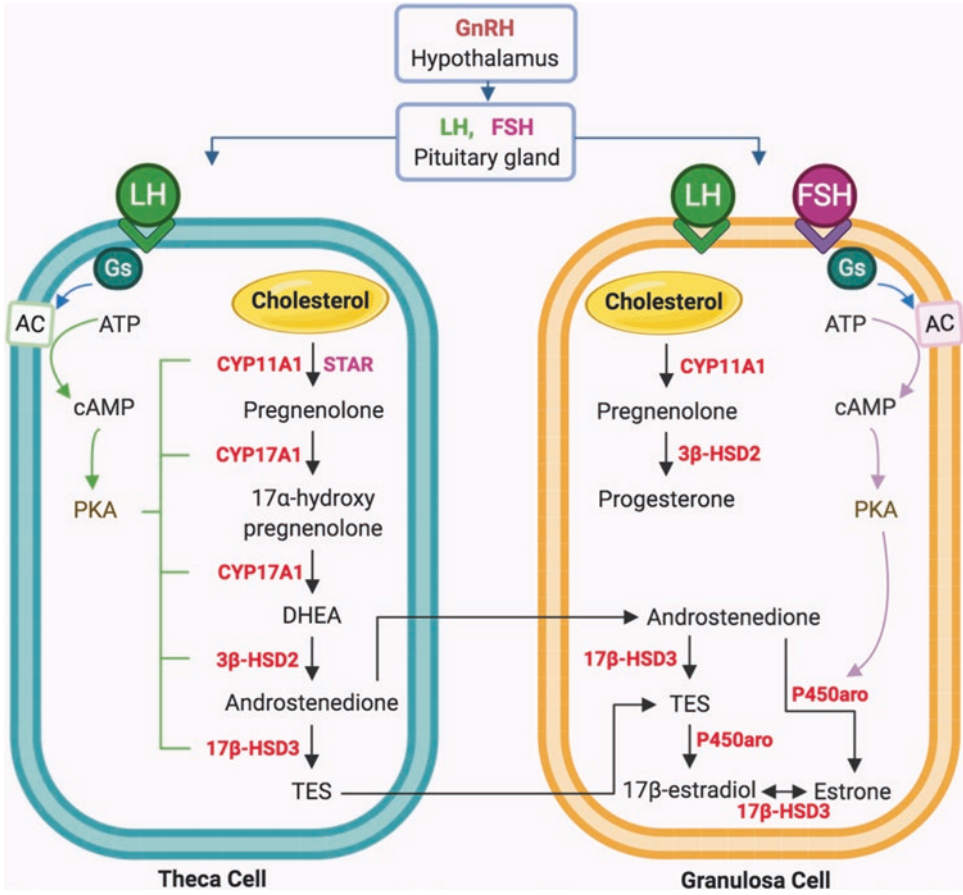

Fig. 15.2 Steroid hormone biosynthesis pathways in the ovary by theca and granulosa cells. Ovarian steroids are synthetized through the interaction between theca and granulosa cells, a process regulated by gonadotropin-releasing hormone (GnRH) secreted from the hypothalamus. GnRH stimulates luteinizing hormone (LH) and follicle-stimulating hormone (FSH). LH acts on both theca and granulosa cells; FSH acts only on granulosa cells. These hormones stimulate adenylyl cyclase (AC) via Gs protein-coupled receptors. The cyclic adenosine monophosphate (cAMP) generated from adenosine triphosphate (ATP) activates protein kinase A (PKA) to stimulate the expression of steroidogenic enzymes in theca and granulosa cells. The first step in female steroidogenesis is the initial conversion of cholesterol to pregnenolone by the action of steroidogenic acute regulatory protein (STAR) and C27 cholesterol side chain cleavage cytochrome P450 enzyme (CYP11A1). Later, pregnenolone is converted to progesterone by 3β-hydroxysteroid dehydrogenase (3β-HSD2). In theca cells, 17α-hydroxylase/17,20 lyase (CYP17A1) hydroxylates pregnenolone to produce 17α-hydroxypregnenolone and subsequently removes the acetyl group in order to form dehydroepiandrosterone (DHEA). This last product can be converted into androstenedione via 3β-HSD2 and further biotransformed into testosterone (TES) via 17β-hydroxysteroid dehydrogenase (17β-HSD3). TES and androstenedione diffuse across the follicle membrane into the follicular fluid where they are taken up by granulosa cells. The endoplasmic reticulum of granulosa cells expresses P450 aromatase (P450aro) that converts TES to 17β-estradiol and androstenedione to estrone. Additionally, in granulosa cells, 17β-HSD3 catalyzes the formation of 17β-estradiol from estrone

17β-HSD2 catalyzes the oxidation of E2 to E1 [89, 90, 94] (Fig. 15.2). Moreover, estrogens can be produced in the Leydig cells, Sertoli cells, and mature spermatocytes from the male gonads [96].

Variation of estrogens levels during life is based on different factors such as age, menstrual cycle phase, and pregnancy. Interestingly, androgen levels in women are higher than estrogen levels most of the time. An exception occurs during

the preovulatory and midluteal phases of the menstrual cycle [31, 85, 97]. In non-pregnant women, E2 serum levels fluctuate between 80 and 800 pM. These levels may increase up to 150 nM during pregnancy and highly decrease, oscillating between 40 and 120 pM in menopausal period. Progesterone plasmatic levels also vary between 1 and 60 nM in non-pregnant women and reach values of 1000 nM during pregnancy [31].

15.3 Sex Hormone Receptors

15.3.1 Sex Hormone Binding Globulin

The distribution of sex hormones to different tissues, including the lung, is regulated by sex hormone binding globulin (SHBG), a key steroid hormone binding protein in human plasma. Plasma SHBG is a homodimeric protein largely produced in hepatocytes [36, 98, 99]. Each monomer possesses a steroid binding pocket and a Ca^{2+}-binding site [99, 100]. This globulin binds steroids such as TES, 5α-DHT, and E2 with nanomolar affinities [36, 99–102]. Normally, in humans, between 40% and 65% of circulating TES and between 20% and 40% of circulating E2 are bound to SHBG [101, 103]. Literature suggests that sex hormones bound to SHBG do not display biological activity. Moreover, sex steroid dissociation from this globulin in the circulatory system allow them to bind and activate male or female sex hormone receptors, triggering gene transcription and protein synthesis [103, 104]. Interestingly, SHBG binds TES with a higher affinity than it does for E2, acting as an estrogen amplifier [36, 98, 103, 104].

Sex steroids exert their physiological effects mostly through the binding to their own receptors, e.g., the androgen receptor (AR), estrogen receptors (ERs), and progesterone receptors (PRs) [25, 31, 76, 105–107]. Sex steroid actions comprise genomic and non-genomic effects. Genomic effects occur from hours to days and involve a direct modulation of gene transcription and protein synthesis via the binding and activation of nuclear hormone receptor complexes. Non-genomic effects are mediated by plasma membrane receptors or ion channels that trigger intracellular signaling pathways that mayresult in transcriptional regulation [25, 31, 36, 76, 106, 108].

15.3.2 Androgen Receptor

The AR modulates the activity and effects of male sex hormones and their influence on lung development. Testes from fetuses produce TES after sex differentiation, and this androgen retards the production of surfactant during gestation [109]. Also, it has been suggested that branching morphogenesis of the human lung is regulated by androgens' effects [110]. The AR is found in several lung tissues and immune cells, including airway smooth muscle (ASM) [111], lung parenchyma, bronchial epithelium [112, 113], dendritic cells (DCs) [114], macrophages, neutrophils, and T and B lymphocytes [115–118]. The AR, also known as NR3C4, is a cytoplasmatic/nuclear receptor that is activated by binding to TES or to its more active reduced metabolite, 5α-DHT, in the cytosol. Male sex steroids binding to the AR promote their dissociation from its chaperon proteins, forming a complex that is translocated into the nucleus. The formed complex acts as a DNA-binding transcription factor that modulates gene transcription and protein synthesis [25, 76, 95, 119, 120]. 5β-DHT, the other reduced metabolite of TES, possesses less androgenic activity than TES and 5α-DHT, because it has a lower binding affinity for the AR [121]. In addition, TES is capable of activating plasma membrane receptors such as ZIP9, a zinc transporter from the ZIP family [122–125], and GPRC6A (class C, group 6, subtype A, G protein-coupled receptor family member) [124, 125]. The binding of TES to ZIP9 or GPRC6A triggers signaling pathways that implicate the activation of G proteins, including Gs, Gi, and Gq11, and the stimulation of extracellular signal-regulated kinases 1 and 2 (ERK1/2) [122–128].

15.3.3 Estrogen Receptors

Estrogen and progesterone receptors contribute to sexual and lung development [30, 37, 95]. Two classes of ERs have been described: nuclear ERs, ERα (ESR1) and ERβ (ESR2), and the plasma membrane ER (mER), G protein-coupled receptor 30 (GPER/GPR30) [25, 129–132]. Estrogen receptors exert their physiological actions through either genomic pathways leading to gene transcription or non-genomic signaling pathways (rapid effects that involve phosphorylation processes) [133–137]. ERα and ERβ function as transcription factors. The stimulation of ERs in the cytoplasm causes dimerization, nuclear translocation, and binding to estrogen response elements (EREs) in the promoter region of target genes. Moreover, ERs are able to indirectly modulate gene transcription by forming complexes with proteins such as c-fos and c-jun, essential components of activator protein 1 (AP-1) [136, 137]. Also, the activation of ERs induces rapid effects mediated by protein members of the mitogen-activated protein kinase (MAPK) family, e.g., ERK1/2, p38 MAPK, and the c-Jun N-terminal kinase (JNK) [138–140]. ERα and ERβ occur in numerous lung cells and tissues, e.g., ASM, bronchial epithelial cells, macrophages, DCs, and T and B lymphocytes [25, 141–146]. Some studies have demonstrated the critical role of both ERα and ERβ in fetal lung development. The expression level of these receptors is significantly elevated in fetal lungs compared to postnatal and adult lungs from mice [147]. Furthermore, ERα and ERβ participate in alveolar formation [148, 149].

In addition, two shorter or truncated splice variants of the human ERα (hERα-66/ER66 due to its molecular weight) have been identified as mERs: 46 kDa ER (hERα-46/ER46) and 36 kDa ER (hERα-36/ER36) [150, 151]. It has been demonstrated that ER66 can translocate to the plasma membrane via the interaction with the scaffolding protein of caveolae (caveolin-1), a process dependent on palmitoylation [152–155]. ER66-induced transcription is mediated by two activation domains: the ligand-independent activation function (AF)-1, which is located in the N-terminal domain, and the ligand-dependent AF-2, situated in the C-terminal domain [156, 157]. The truncated ER46 isoform lacks the AF-1 domain; however, this splice variant maintains the corresponding domains for caveolin-1 association and palmitoylation [150, 152]. The absence of the AF-1 domain in the ER46 supposes null influence in its ability to evoke non-genomic actions. In this context, it has been shown that ER46 variant stimulates the phosphorylation of the endothelial nitric oxide synthase (eNOS) in a higher degree than ER66 [158]. ER36, the other truncated isoform of ER66, lacks the AF-1 and AF-2 domains [151]. Non-genomic actions mediated by ER36 have been described. The activation of ER36 by E2 elicits the mobilization of intracellular Ca^{2+} in different breast cancer cell lines. Also, ER36 triggers MAPK pathways leading to cell growth and proliferation in HEK293 cells [159]. In HEK293 cells as well, saturation binding assays show that the equilibrium dissociation constant (K_d) for the binding of E2 to ER66 and ER46 corresponds with the serum levels of this estrogen found in women (68.8 pM and 60.7 pM, respectively), while ER36 exhibits no saturable specific binding [160]. Furthermore, the evidence about the molecular characterization of ERβ splice variants is still unclear. The presence of membranal estrogen receptor insinuates an additional regulation mechanism for estrogens' actions; however, little is known regarding the function of ER-truncated isoforms in the lung [133, 161].

GPR30 was identified as a functional membrane receptor, different from the ERα-truncated splice variants, involved in rapid E2 signaling pathways [131, 132, 162, 163]. GPR30 binds E2 with high affinity (K_d = 6 nM) [164, 165] and triggers numerous intracellular signal transduction pathways such as cyclic adenosine monophosphate (cAMP) production, Ca^{2+} mobilization, and the activation of phosphatidylinositol 3-kinase (PI3K) and ERK1/2 [129, 131, 132]. Moreover, the stimulation of GPR30 has been involved in the activation of the epidermal growth factor receptor (EGFR)-mediated signaling in breast and lung cancer [132, 162, 165, 166]. The expression and function of GPR30 in the lung have not been fully elucidated yet. In this context, Townsend et al. did not find a significant expression of this receptor in human ASM [167].

15.3.4 Progesterone Receptors

Progesterone (P4) plays a crucial role in the maintenance of pregnancy. This hormone modulates the transition of the endometrium from a proliferative stage to a secretory phase and promotes the implantation of the blastocyst [64]. The lipophilic nature of P4 allows it to cross the cell membrane and binding to the two types of progesterone receptors (PRs) identified in mammals: PR-A and PR-B. Once PRs are activated, enter the nucleus, and promote DNA modulation, gene transcription and protein synthesis [64, 168–171]. Both progesterone receptors are encoded by the same gene but display different patterns on progesterone response elements, i.e., distinct transcriptional activity [172, 173]. PR-B is considered a strong promoter of gene transcription, whereas PR-A is associated with repressor responses [172]. The stimulation of the PRs triggers the activation of transcriptional regulatory proteins known as steroid receptor coactivators 1, 2, and 3 (SRC-1, SRC-2, and SRC-3). SRCs contribute to the regulation of DNA transcription by assisting nuclear receptors [174, 175]. Moreover, PR-B activation allows the association with the N-terminal domain of the ER. The association of the PR-B with the ER causes the proto-oncogene tyrosine-protein kinase (Src)/p21-Ras/ERK pathway [176]. Progesterone receptors have been identified in ASM [111], cilia from the airway epithelium [177], and endothelial cells from vascular beds [178, 179]. The expression of PRs in immune cells is still under debate; however, some reports have suggested the occurrence of this receptors in DCs [179, 180].

Non-genomic effects of P4 are mediated by membrane receptors. The existence of non-classical membrane PRs (mPRs) has been pointed out and reviewed in mammalian tissues, including reproductive and non-reproductive systems [181, 182]. The non-classical PRs were first identified in fish where they modulate gamete physiology [183]. mPRs are classified into the progesterone and adipoQ receptor (PAQR) family, which belongs to the superfamily of GPCRs. Until now five different subtypes of mPRs have been characterized: mPRα (PAQR7), mPRβ (PAQR8), mPRγ (PAQR5), mPRδ (PAQR6), and mPRε (PAQR9) [181, 182, 184, 185]. These receptors have been described in immune cells, such as peripheral blood mononuclear cells (PBMCs) and T cells [181, 182, 186–190]. The stimulation of mPRs evokes intracellular signal pathways implicating Ca^{2+} mobilization, the increase in cAMP levels, and the activation of p38MAPK and JNK [181, 182, 190].

15.4 Immune Cells

15.4.1 Neutrophils

Neutrophils are essential granulocytes of the innate immune system. These cells are the most abundant circulating leukocytes, comprising around 70% of all white blood cells in healthy humans [191]. Neutrophils are commonly the first cells responding to damage and migrating to the injured tissues, including the lung. The activation of neutrophils and the release of chemokines induce the recruitment of monocytes into the inflamed tissues [10, 191, 192]. The evidence of sex steroid actions on the development and physiology of neutrophils is present. A study shows that the genetic ablation of the AR in mice drastically diminishes (90%) the proliferative activity of neutrophil precursors and retards neutrophil maturation. Also, neutropenia is exhibited in mice with testicular feminization (Tfm). The same study points out that androgens induce the production of neutrophils via the modulation of granulocyte colony-stimulating factor (G-CSF) [193]. Additionally, TES suppresses the production of superoxide and the anti-microbial capacity of human neutrophils [194]. Furthermore, in an ozone-induced lung inflammation mice model, the expression of neutrophil-attracting chemokines (*Ccl20*, *Cxcl5*, and *Cxcl2*) and the number of neutrophils are significantly higher in females compared with males [195].

15.4.2 Macrophages

In humans, the respiratory tract harbors mononuclear phagocytic cells to provide one of the first lines of defense against inhaled allergens, pathogens, particles, and gases. Most of these phagocytic cells are macrophages distributed along the lung, airways, and alveoli [196, 197]. Besides the resident macrophages, two more distinct populations are found in the lung: alveolar and interstitial macrophages [198, 199]. Alveolar macrophages are considered the main leukocyte subtype in the lung. Cell counting analysis of bronchoalveolar lavage fluid (BALF) from healthy adults reveals 72–96% of macrophages, 2–26% of lymphocytes, 0–4% of neutrophils, and 0–1% of eosinophils, basophils, and mast cells [200]. After an injury or damage is produced, monocytes derived from the bone marrow are recruited to the lung and differentiated into alveolar macrophages. The differentiation process and the following nesting into the alveoli are dependent on the production of granulocyte-macrophage colony-stimulating factor (GM-CSF) by alveolar type 2 cells. Signals triggered by alveolar type 1 and 2 cells, such as exposure to surfactant-rich fluid and elevated oxygen tension, may modulate different functional phenotypes of alveolar macrophages [196, 201]. In this context, classically activated macrophages (CAM/M1) and alternatively activated macrophages (AAM/M2) have been described. Macrophages may undergo M1 polarization in response to cytokines produced by Th1 lymphocytes, e.g., interferon gamma (IFN-γ), and by Toll-like receptor (TLR) ligands found in bacterial and viral products. The activation of M2 macrophages is provoked by Th2 cytokines such as IL-4 and IL-13 [202].

Regarding sex hormones' influence in these immune cells, it has been shown that TES decreases the expression of the TLR4 in macrophages from mice [203]. Also, TES reduces the production of IL-1β, IL-6, and TNF-α in human macrophages and human monocytes and increases the expression of IL-10 in macrophages from humans, as well as in a murine macrophage cell line [204, 205]. Moreover, TES is capable of diminishing nitric oxide (NO) production induced by the stimulus of lipopolysaccharide (LPS) [205]. Female sex hormones also exert a regulation in the activity of macrophages. Ovalbumin (OVA)-induced asthmatic mice display increased numbers of M2 macrophages in the lung compared with male mice [206]. Estrogens facilitate the resolution phase of inflammation toward a M2 phenotype dependent on IL-10, contributing to tissue remodeling and shortening the pro-inflammatory state [207]. Progesterone inhibits NO production and the release of microparticles (MPs) with pro-inflammatory and prothrombotic properties. MPs are discharged by macrophages stimulated by ligands of TLRs in a NO-dependent process [208].

15.4.3 Eosinophils

Eosinophils are key modulators in allergic inflammation as occurring in asthma [209]. They are developed from granulocytic precursor populations in the bone marrow and are activated through the action of the IL-5 secreted by Th2 cells. The maturation of eosinophils is also mediated by GM-CSF. Degranulation of activated eosinophils releases pro-inflammatory cytokines, leukotrienes (LTs), platelet-activating factor (PAF), reactive oxygen species (ROS), and the cationic proteins, e.g., basic protein and eosinophil cationic protein [209, 210]. LTs contribute to bronchospasm in asthma [211]. While the expression of sex steroid receptors in eosinophils is unclear, the impact of sex hormones on these immune cells has been investigated. In gonadectomized male mice, the peripheral and bone marrow eosinophils are augmented, and TES abolishes peripheral and bone marrow eosinophil responses at the early phase of infection by *Brugia pahangi* in females [212]. Moreover, TES decreases human eosinophil viability and adhesion properties in vitro [213]. Conversely, female mice display more severe eosinophilia than males, a phenomenon that is reversed after gonadectomy [214], and progesterone treatment enhances the recruitment of eosinophils and induces airway hyperresponsiveness (AHR) in a murine model of allergic asthma [215].

15.4.4 Mast Cells and Dendritic Cells

Mast cell development occurs in the bone marrow, and their maturation is mediated by the interaction between the stem cell factor (SCF) with its own receptor c-kit and by the influence of IL-3, IL-4, IL-9, and IL-10. Activated mast cells participate in the acute and chronic phases of inflammation. For instance, these cells contribute to the infiltration of leukocytes, tissue remodeling, and fibrosis [216, 217]. The expression of the AR has been reported in skin mast cells; nevertheless, the numbers and distribution of these cells seem not to be affected by androgens [218, 219]. Instead, TES interferes with the production of IL-6 [220] and induces the expression of IL-33 [221] by mast cells. IL-33 is known to regulate the formation of innate lymphoid cells (ILCs) and the production of Th2 cytokines [222]. Regarding female sex hormone action on mast cells, serum levels of immunoglobulin E (IgE, an antibody that induces the degranulation of mast cells) seem to fluctuate depending on the menstrual cycle phase [223]. Moreover, estrogen enhances IgE-induced mast cell degranulation and the release of histamine [224–226]. Meanwhile, progesterone diminishes the migration of mast cells and histamine secretion [227, 228].

Dendritic cells are originated from a CD34+ hematopoietic precursor that gives rise to myeloid (MP) and lymphoid (LP) progenitors [229]. The maturation of these cells is associated with the recognition of PAMPs and/or DAMPs. The process of maturation also implicates metabolic changes and gene transcription that lead to the migration of dendritic cells from peripheral tissues to secondary lymphoid organs. Mature dendritic cells express large amounts of C-C chemokine receptor type 7 (CCR7) and secrete IL-12 and IL-23, which promotes T-cell differentiation [230–232]. The effect of sex steroids on dendritic cells and their influence on lung disease have not been well explored. The acute exposure of bone marrow-derived dendritic cells (BMDCs) to 5α-DHT during antigen priming decreases the stimulation of T-cell cytokine production (IL-4, IL-10, and IL-13) in vitro [233]. On the other hand, estrogen promotes the differentiation of DCs from bone marrow precursors [234] and enhances their T-cell stimulatory capacity [233, 235]. Progesterone treatment decreases the production of the pro-inflammatory cytokines TNF-α and IL-1β by BMDCs [114].

15.4.5 T and B Lymphocytes

T and B lymphocytes or T and B cells are critical elements in the adaptive immune response. B cells carry out the antibody response, whereas T cells play a critical role in the cell-mediated response. In the antibody response, B cells secrete specialized proteins called immunoglobulins (Igs) that circulate across the bloodstream where they bind to and inactivate foreign antigens. Cell-mediated response employs T cells that react directly against foreign antigens, which are presented to them and further neutralize the cells that have been infected with distinct pathogens (bacteria or virus) [236–238]. The development of T cells occurs through phenotypic changes that involve the expression of essential membrane markers such as CD3, CD4, and CD8 [239]. Th1, Th2, Th17, and regulatory T (reg) cells conform the different lineages of CD4+ effector T cells [240].

T- and B-cell development is negatively regulated by androgen actions. For instance, castrated male mice show increased numbers of double positive CD4+ CD8+ T cells in the thymus and B cells in the spleen [241]. Furthermore, castration not only increases the number of B cells in the spleen but in the bone marrow, and this phenomenon is not altered by preceding thymectomy [242]. The negative regulation of B cells exerted by androgens has shown to be dependent on the AR activity. A murine model of general AR knockout (ARKO), and B-cell-specific ARKO, displays enhanced B-cell lymphopoiesis defined by increased numbers of B cells in the blood and bone marrow. Interestingly, the B-cell-specific ARKO group shows a lesser effect on B-cell lymphopoiesis compared with the general ARKO group, pointing out that the negative effect of androgens comprises a regulation of B cells and

the stroma [243]. Contrariwise, estrogens restrain the B-cell lymphopoiesis by reducing the precursors, pro-B cell, pre-B cell, and mature B cells of the bone marrow [244]. Also, estrogens enhance the activity and antibody production of mature B cells [245].

Likewise, androgens negatively modulate T lymphocytes and monocytes in the blood. In this context, Yao et al. demonstrate in Sprague-Dawley rats that TES reduces the numbers of monocytes. However, the lymphocyte subpopulations show an increase in CD8+ T cells, while the numbers of CD3+, CD4+, and double positive CD4+ CD8+ T cells remain unaffected after TES treatment. Therefore, the immunosuppressive role of TES may be due to a decline in the number of monocytes, the change in CD4+/CD8+ ratio, and the increase of CD8+ T cells [246]. Moreover, TES causes a shift in the balance of Th1/Th2 cytokines through a reduction in TNF-α secretion in T-cell lines [247] and stimulates the production of IL-10 (an anti-inflammatory cytokine) in CD4+ T cells TES [248]. In addition, in a model of androgen deficiency, rats show decreased levels of IL-2, IL-6, IL-10, IL-12, and IL-13, whereas TES supplementation restores those levels [249].

Furthermore, it has been reported that estrogens modulate the differentiation and function of distinct T-cell phenotypes. In this context, E2 signaling through the ERα impedes the differentiation of Th1 and Th17 cells, conferring a protective mechanism against inflammation in experimental encephalomyelitis [250]. Besides, physiological concentrations of E2 promote the proliferation of T lymphocytes and the production of IFN-γ in vitro [251]. In Th2 cells, the stimulation of the ERα by E2 increases the expression of IL-4 [252].

The role of sex hormones on the function of immune cells in lung ailments has been established (Fig. 15.3). For instance, TES negatively regulates type 2 immune response seen in asthma evoked by Th2 cells [253]. E2 enhances the severity of pneumonia in adult mice with cystic fibrosis by improving the inflammation mediated by Th17 cells [254]. The involvement of immune cells, e.g., neutrophils, macrophages, eosinophils, and T and B lymphocytes, in the pathogenesis of lung diseases, such as asthma and COPD, and the influence of sex hormones on these cells and their mediators are discussed in the next sections.

15.5 Sex Hormones in Inflammatory Lung Pathologies

15.5.1 Asthma and Chronic Obstructive Pulmonary Disease

Although asthma and COPD differ regarding pathogenesis, progression, prognosis, and treatment options, both ailments exhibit similar symptoms and inflammatory mechanisms [255–258]. Asthma is a chronic airway inflammatory disease that affects around 339 million people worldwide, as informed by the Global Asthma Report 2018. This airway disease is characterized by episodes of variable airflow obstruction (limitation of expiratory airflow), hyperresponsiveness, inflammation, and mucus production [41]. The etiology of this ailment has been related to heritability, environmental exposures, and sensitization to inhalant allergens [259–261]. Airflow obstruction is defined by spirometry parameters indicating a reduced forced vital capacity (FVC) and a reduced forced expiratory volume in 1 second (FEV1, less than 80%). Moreover, FEV1/FVC ratio is found minor than 0.7 in asthmatic patients [262]. Inhaled bronchodilators and corticosteroids are the main treatment in order to reduce inflammation and mitigate the symptoms of this illness [263]. Gender differences in the incidence and the severity of the asthma symptoms have been described and associated with hormonal changes through different life stages. During childhood, boys are more susceptible than girls to develop this ailment; however, in puberty, this trend reverses, and women display more severe symptoms [31, 264–266]. Fluctuations in progesterone and estrogens levels, such as those occurring during the menstrual cycle, have been correlated with the aggravation

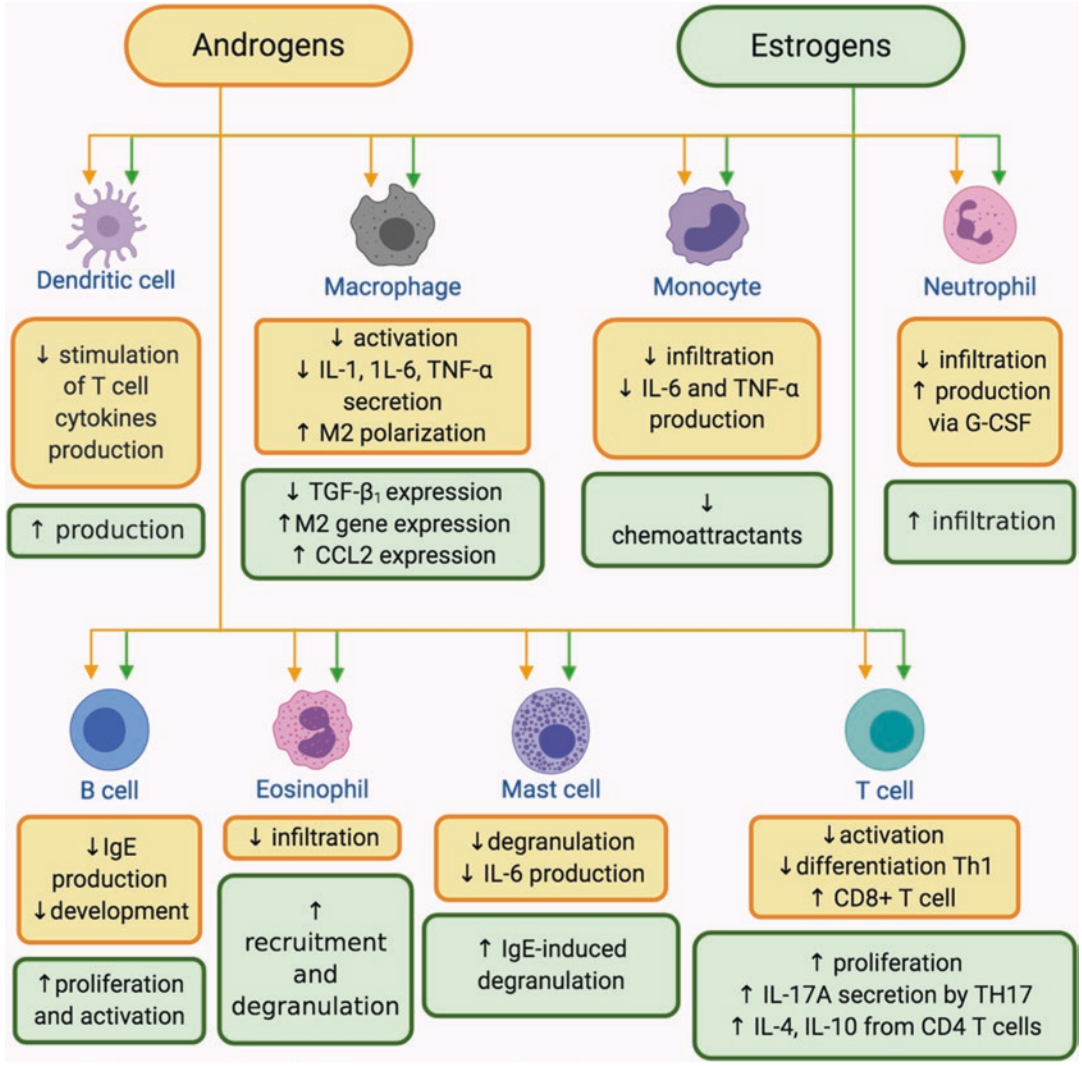

Fig. 15.3 Summary of androgen and estrogen effects on individual inflammatory cell types. Lung disease encompasses a substantial inflammatory component by the action of immune cells playing an essential role in the initial response such as dendritic cells, macrophages, monocytes, and T and B lymphocytes involved in the adaptive immune response. This figure summarizes current knowledge of androgen and estrogen actions on specific types of immune cells that are particularly important in lung ailments. Symbols' meaning and abbreviatures: ↓, inhibits; ↑, enhances. Tumor necrosis factor alpha (TNF-α); interleukin (IL)-1, 4, 6, 10, 17-A; monocyte chemoattractant protein, MCP-1 (CCL2); transforming growth factor beta1 (TGF-β_1); granulocyte colony-stimulating factor (G-CSF); immunoglobulin E (IgE). For details, see the *Immune Cells* section

of this disease [25, 41, 267, 268]. Several studies have shown that 20–40% of premenopausal women experience pre-menstrual or perimenstrual asthma (PMA) [269–276], suffering from an exacerbation of the symptoms with increased bronchial inflammation in the week preceding menstruation [273, 276]. PMA is defined as a cyclical worsening of asthma during the luteal phase and/or during the first days of menstruation [274, 277]. PMA has also been associated with less atopy and poor lung function [273]. Furthermore, the use of oral contraceptives (OC) alleviates perimenstrual exacerbations in women with mild to moderate asthma [278, 279]. In

addition, between 7% and 10% of all pregnant and childbearing-aged women have been reported to present asthma [280–282], and the use of OC does not improve the symptoms in women diagnosed with severe disease [283]. In women from 50 years of age, menopause may correspond with the beginning of asthma or be associated with exacerbations of a preexisting asthma condition, conforming a new phenotype described as menopausal-onset asthma [284, 285]. Around 18% of the total female asthma population suffers from menopausal-onset asthma, which is distinguished by the absence of atopy, aspirin sensitivity, persistent sinusitis, and frequent rate of hospitalizations [285]. In postmenopausal women with asthma, symptoms are commonly severe, and E2 levels have been found higher compared to those in non-asthmatic women [285–287]. Moreover, menopausal hormone therapy (MHT), and particularly the use of estrogen, increases the risk of developing asthma [288, 289]. In addition, progesterone in plasma reaches a peak about 24-fold higher than follicular phases. Interestingly, circulating progesterone is positively correlated with the peak expiratory flow rate (PEFR) during the luteal phase of the menstrual cycle [25].

On the other hand, androgens seem to reduce asthma exacerbations [76]. Higher plasma levels of TES in men, compared with those found in women, are thought to be useful favoring a bigger airway caliber and lung capacity [31, 290, 291]. It has been shown that, following the age of 11 years, the provocative concentration of methacholine necessary to produce a 20% decrement in FEV1 (PC20) increases in teenage boys but not in girls, pointing out an androgen-related improvement in airway responsiveness during puberty [292]. In this regard, non-genomic and genomic effects of androgens on airway smooth muscle [76, 293–297] and the inflammatory response in the asthmatic condition have been extensively explored [38, 42, 253, 298, 299]. Interestingly, the protective role of androgens against asthma in male patients declines after the fifth decade of life, and the symptoms of this ailment appear again. This could be explained by the decrease in plasmatic TES levels during this life stage [31, 300, 301]. Moreover, Mileva and Maleeva [302] reported that male patients with moderate to severe asthma have lower levels of TES compared with those with mild symptoms. In addition, it has been noticed that asthmatic women carrying female fetuses are more susceptible to present symptoms of this illness compared to those with male fetuses [303]. The effects of androgens and estrogens (mainly E2) on the pathogenesis of asthma are discussed below with a special focus in inflammatory cells and their mediators.

COPD is a lung disease characterized by the presence of obstruction ventilator trouble (OVT), i.e., a persistent limitation of airflow that is not fully reversible [304]. This illness is usually caused by exposure to harmful particles or gases that induces emphysematous lung destruction and airway narrowing [305, 306]. Clinical symptoms include cough, sputum production, and progressive dyspnea that is unresponsive to steroids and bronchodilator therapy [307]. Similar to asthma, the diagnosis of COPD relies on clinical evidence and spirometry data, including FEV, FVC, and the ratio FEV1/FVC. A FEV1/FVC ratio less than 0.7, and the lack of full reversibility after the administration of salbutamol (400μg), indicate OVT [304]. It has been estimated that more than 12% of the world population suffers from this illness [308, 309]. The prevalence of COPD is more common in men than in women [308, 310]. This could be explained by the fact that men present higher occupational risks and/or higher rates of smokers [311, 312]. However, data suggests that women have a greater predisposition to this disease. The number of tobacco smoker women with a diagnosis of COPD has notably increased in the last years [33, 313]. The rate of lung function declines faster in female tobacco users than in male smokers. Also, the majority of COPD cases involving non-smokers or never smokers are women [314–317]. Typically, men with COPD have more emphysematous deterioration of the lung, while women tend to have more reactive airways and more pronounced airway narrowing [318, 319]. The apparent increased female susceptibility points out a sex hormone modulation of this illness [37, 320].

Asthma and COPD are characterized to produce chronic inflammation of the airways. Cells and mediators of inflammation implicated in these ailments are even targets for medical treatment [321, 322]. The inflammatory response in both lung diseases involves innate and adaptive immunity. Most asthmatic patients' course with eosinophilic inflammation that is driven by Th2 lymphocytes. This type of inflammation occurs due to exposure to allergens such as pollen, house dust mite (HDM), viruses, cockroach antigens, etc. [323–325]. Dendritic cells present allergenic peptides to uncommitted T lymphocytes and stimulate the production of allergen-specific T cells [326]. Then, epithelial alarmins IL-25, IL-33, and thymic stromal lymphopoietin (TSLP) recruit $CD4^+$ Th2 cells and group 2 innate lymphoid cells (ILC2s) that secrete IL-5 and other interleukins [327]. This interleukin regulates the generation of eosinophils in the bone marrow [325]. Eosinophil migration and recruitment into the lung is regulated by IL-5 as well and by the epithelial-secreted chemokines and C-C motif chemokines (CCL) 11 and 5 [328]. Moreover, type 2 inflammation is also associated with the production of other cytokines, including IL-4 and IL-13, which promote the synthesis of IgE by B lymphocytes [324, 329]. IgE regulates mast cell activity and degranulation. Significantly, mast cell infiltration in the airways has been associated with airway hyperresponsiveness (AHR) [330, 331] mediated by the release of bronchoconstrictor substances such as histamine, LTs, and prostaglandin (PG)-D_2. Mast cells and Th2 cells, additionally secrete IL-4, IL-5, IL-9, IL-13, and TNF-α [332, 333]. TNF-α, a well-known pro-inflammatory cytokine, is elevated in patients with asthma and is involved in the induction of AHR [334]. Experimental evidence has shown that TNF-α potentiates the agonist-induced increase in intracellular Ca^{2+} concentration ($[Ca^{2+}]_i$) [335] and contractile responses [334–339]. In addition to be involved in switching the isotype of B cells, IL-4 plays a key role in the differentiation of Th2 cells from uncommitted Th0 cells and in the initial sensitization to allergens [333]. IL-5 is deeply associated with the differentiation of eosinophils from their precursor cells in the bone marrow as well as in eosinophil survival [340]. The use of glucocorticoids in asthma treatment decreases airway eosinophilia by inducing eosinophil apoptosis and inhibiting the response to IL-5 [341, 342]. IL-9 participates in mast cell proliferation and activation [343, 344]. IL-13 is another representative Th2 cytokine that not only participates in mucus production, airway inflammation, and remodeling but has been suggested to modulate steroid insensitivity [345–347]. In this regard, it has been shown that the administration of the anti-IL-13 antibody improves airflow obstruction in asthma patients when inhaled corticosteroid treatment seems not to work [348].

Nevertheless, not all asthmatic patients show this inflammatory pattern but develop an IL-17-mediated neutrophil inflammatory response that is mostly described in subjects with the most severe symptoms [42, 105]. Th17 cells are recognized as a distinct population of CD4+ T cells secreting IL-17A, IL-17F, and IL-22 [349]. The differentiation of this group of cells occurs after the stimulation of naive T cells by IL-1β, IL-6, IL-21, IL-22, IL-23, and transforming growth factor beta1 (TGF-β1) produced by macrophages and epithelial and dendritic cells [38, 42, 350, 351]. IL17-A is a key inductor of neutrophilic inflammation by evoking granulopoiesis and neutrophil chemotaxis [352, 353]. Furthermore, the inflammatory response mediated by Th17 cells is known to be highly associated with the resistance to corticosteroid treatment [42, 354].

COPD patients suffer from an accelerated decrease of lung function related to progressive airway obstruction caused by mucus hypersecretion and ciliary dysfunction [355, 356]. The inflammation developed in COPD subjects, located predominantly in the peripheral airways and lung parenchyma [357], is characterized by the presence of alveolar macrophages, neutrophils, T lymphocytes, dendritic cells, and B lymphocytes [358]. Most severe cases of COPD are commonly associated with higher numbers of B lymphocytes and neutrophils [304, 358]. T lymphocytes implicated in this disease are mostly CD8+ T-cytotoxic cells (Tc), but CD4+ Th1 cells are also increased [359]. In the blood of COPD

patients, the proportions of IFN-γ- and TNF-α-producing CD8+ T cells are augmented compared with healthy ones [360]. Moreover, increased numbers of Th17 cells have been reported in COPD patients. IL-17A and IL-22 secreted by these cells modulate the recruitment of neutrophils and cause inflammation [361, 362]. Also, the number of macrophages is increased in the lungs from patients with COPD, and this increment corresponds to the severity of the disease [363]. Several inflammatory mediators are involved in the development of this ailment; for instance, alveolar macrophages and epithelial cells from COPD patients release more chemical mediators than in normal subjects [364, 365], including IL-1β, IL-6, TNF-α, CXCL1, CXCL8 (IL8), CCL2 (monocyte chemoattractant protein, MCP-1), reactive oxygen species (ROS), and LTB_4. Notably, some of the former cytokines act as chemotactic factors that promote neutrophil migration [366]. Cigarette smoke stimulates granulocyte production through granulocyte-macrophage colony-stimulating factor (GM-CSF), granulocyte colony-stimulating factor (G-CSF), and TGF-β1 released from airway epithelial cells and lung macrophages. TGF-β1 participates in the activation of myofibroblasts and airway smooth muscle cells, causing proliferation and fibrosis [358, 367]. Furthermore, granulocyte production leads to persistent neutrophilic inflammation present in most COPD patients [367]. Additionally, epithelial cells and alveolar macrophages release chemokines such as CXCL9 (induced by IFN-γ), CXCL10 (IFN-inducible protein 10), and CXCL11 (IFN-inducible T-cell alpha chemoattractant) [358]. The upregulation of CXCL10 and its receptor (CXCR3) contributes to the accumulation of CD4+ and CD8+ T cells in patients with this obstructive disease [368]. CD8+ T cells are cytotoxic entities that release perforins, granzyme B, and TNF-α, contributing to alveolar cell apoptosis in emphysema [369]. Matrix metalloproteinases (MMPs), e.g., MMP-9 and MMP-12, similarly contribute to proteolytic attack on the alveolar wall matrix [364, 370]. Furthermore, airway eosinophilia may occur when COPD exacerbations are mediated by viral infections [371]. IL-33 produced by epithelial cells has been suggested to be the key regulators in Th2- and ILC2-mediated eosinophilia in this illness [372]. Moreover, oral corticosteroid therapy has been shown to be effective in reducing eosinophilic inflammation in patients with COPD [373].

15.5.2 Androgens' Effects on Inflammation in Asthma and COPD

Airway smooth muscle (ASM) is one of the major structural elements of the airways. This smooth muscle layer controls airway caliber and tone [95, 295, 374]. Hyperresponsiveness to physical or chemical stimuli is a characteristic feature of asthma. AHR is described as an exaggerated airway narrowing [375] that is usually reversed with the use of bronchodilators [376]. Given the gender differences in the incidence and the outcomes of this illness, sex steroids' (e.g., androgen) non-genomic and genomic effects on the airways have been widely studied. Primordial evidence of non-genomic actions of androgens on ASM was found in 2006 by Kouloumenta et al. They observed that TES is capable of relaxing rabbit tracheal preparations pre-contracted with cholinergic agonists [377]. Further studies showed that TES and their metabolites 5α-DHT and 5β-DHT induce the relaxation of bovine and guinea pig ASM by blocking L-type voltage-dependent Ca^{2+} channels (L-VDCCs) [378]. In this context, published data from Dr. Montaño's research group confirmed that TES, 5α-DHT, 5β-DHT [379], and DHEA [294] relax the KCl and carbachol pre-contracted guinea pig tracheal tissues. Additional studies from the same research group pointed out that TES not only blocks L-VDCCs but interferes with store-operated Ca^{2+} channels (SOCCs) and inositol 1,4,5-trisphosphate (IP_3) receptor (ITPR), and induces the production of PGE_2 [296, 297]. Most recent published data shows that the chronic exposure to a physiological TES concentration increases the expression of β_2-adrenoceptor (β_2-AR) and upregulates delayed rectifier voltage-dependent K^+ channels (K_V) and high conductance

Ca^{2+}-activated K^+ channels (BK_{Ca}), enhancing the relaxing responses to salbutamol in guinea pig ASM [380].

Androgen effects on immune cells and their inflammatory mediators in healthy subjects and asthmatic patients have also gained relevance. For instance, a study on human peripheral blood mononuclear cells (PBMCs) showed that the number of cells secreting IFN-γ is correlated with the serum levels of DHEA-3-sulfate (DHEA-S, a metabolite of DHEA mainly produced in the suprarenal cortex that possesses weak androgen activity) in premenopausal women and men [381]. Moreover, it has been observed that patients with an asthmatic condition have reduced serum DHEA and DHEA-S concentrations compared with healthy subjects [382–384]. Also, DHEA significantly diminishes both Th1 and Th2 responses in cultured PMBCs from patients with asthma [385], and DHEA-S attenuates chemotaxis and migration of peripheral human neutrophils and inhibits chemokinesis of human ASM [386]. These observations point out that these androgens interfere with cell migration and inflammation in airways, maybe leading to the decrease of asthma symptoms. In this regard, the administration of nebulized DHEA-S to patients with poorly controlled moderate to severe asthma diminished the symptoms and improved the control of this disease [387]. Furthermore, asthmatic women with low serum levels of DHEA-S who received a supplementation with DHEA showed an upgraded lung function in asthma outcomes [388]. In allergic asthma, ILC2s seem to play a pivotal role in initiating and mounting the typical Th2 inflammatory response [343], which induces eosinophilic inflammation, AHR, and remodeling of the airways [42, 389]. In fact, ILC2s are known for producing higher quantities of IL-5 and IL-13 compared with Th2 cells [390–392]. Several reports have shown increased numbers and activation status of ILC2s in blood and sputum samples from adult and pediatric asthma patients [390, 393–397]. Likewise, genetic polymorphisms related to asthma susceptibility have also been shown localized to gene regulatory elements in ILC2s [398]. Animal models have served to prove that androgens exert a downregulation on ILC2s and Th2 inflammatory patterns [106, 253, 299, 399]. Two of these studies illustrate that DHEA reduces house dust mite-induced allergic inflammation by decreasing blood eosinophilia, IL-4, IL-5, and IFN-γ levels [399] and suppresses eosinophil infiltration and AHR through the modulation of Th2 cytokines in ovalbumin (OVA)-sensitized mice [400]. Male mice have low numbers of eosinophils and lymphocytes in bronchoalveolar fluid and lower IL-4 mRNA expression levels in splenic cells than castrated males and females [401]. Moreover, male mice show reduced numbers of ILC2 progenitors (ILC2Ps) and less severe IL-33-driven lung allergic inflammation. Furthermore, IL-5 and IL-13 levels, after IL-33-induced activation of ILC2s, are diminished in male mice compared to females [392]. Likewise, ILC2s from male mice display higher expression levels of killer cell lectin-like receptor subfamily G member 1 (KLRG1) and IL-33 receptor (ST2) [299]. Importantly, 5α-DHT through AR signaling limits the differentiation of ILC2Ps into mature ILC2s in the bone marrow [106, 299] (Fig. 15.4). These insights suggest marked differences between ILC2 development from male and female mice. Additionally, TES decreases house dust mite-induced airway eosinophilic and neutrophilic inflammation, IgE production, and AHR in castrated mice [253]. It is well known that mast cells infiltrate the bronchial epithelium and release bronchoconstrictor mediators in allergic asthma. In this regard, the systemic administration of 5α-DHT inhibits mast cell activation and degranulation. Also, this androgen reduces airway hyperplasia and mucus production in a murine model of OVA-sensitized females [402]. Mast cell degranulation leads to the release of leukotrienes, highly potent lipidic mediators also involved in the allergic response, specifically inducing ILC2 activation and lung inflammation [403]. Macrophages, eosinophils, and basophils are capable of releasing these lipidic molecules as well [404, 405]. Two classes of LTs have been described to modulate different targets. While LTB_4 acts as a potent leukocyte chemoattractant and enhances the macrophages' bacterial killing capability, the cysteinyl leukotrienes (Cys-LTs,

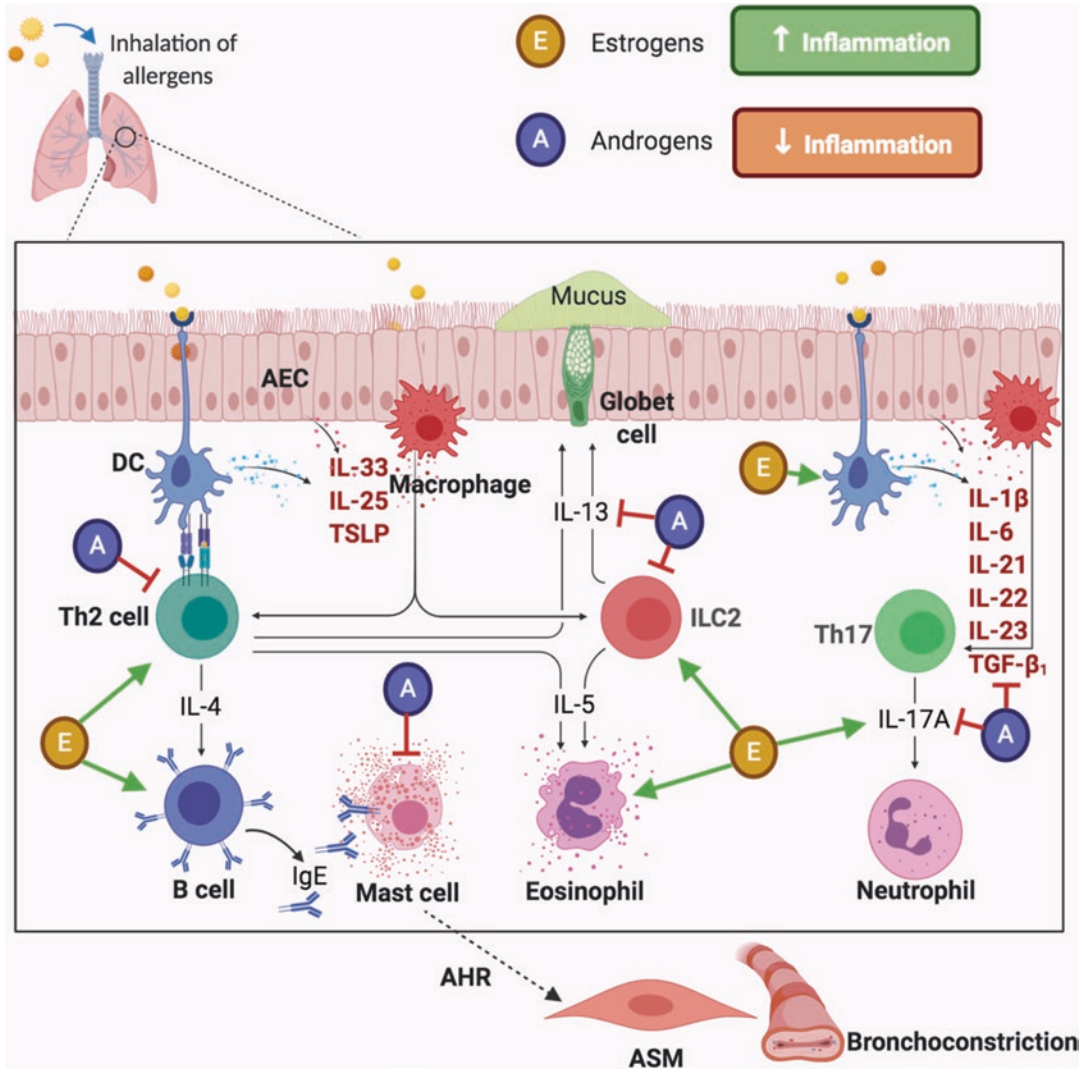

Fig. 15.4 Androgen and estrogen effects on the inflammation in asthma. Asthmatic disease involves an inflammatory-driven response of the airway by the exposure to allergens (pollen, house dust mite, cockroach, fungal antigens, etc.). Dendritic cells (DCs) present allergenic peptides to uncommitted T lymphocytes and stimulate the production of allergen-specific T cell. DCs, airway epithelial cells (AECs), and macrophages secrete epithelial alarmins IL-25, IL-33, and thymic stromal lymphopoietin (TSLP), which recruit Th2 cells and group 2 innate lymphoid cells (ILC2s) that secrete IL-4, IL-5, and other cytokines. Eosinophil migration is induced by IL-5, whereas IL-4 and IL-13 mainly favor immunoglobulin E (IgE) production by B cells with the consequent activation of mast cells. The infiltration of mast cells in the airways has been associated with airway hyperresponsiveness (AHR) mediated by the release of bronchoconstrictor substances such as histamine, leukotrienes, and prostaglandin D_2. These mediators activate their own receptors in the airway smooth muscle (ASM) provoking bronchoconstriction. Moreover, exposure to allergens also initiates an immune response through IL-1β, IL-6, IL-21, IL-22, IL-23, and TGF-β1 produced by DCs, AECs, and macrophages favoring naive Th differentiation to Th17. Th17 cells synthesize IL-17A, a key inductor of neutrophilic inflammation by evoking granulopoiesis and neutrophil chemotaxis. The effects of estrogens (E) or androgens (A) on the illustrated immune cells can differ depending on the hormone concentration and the timing and duration of the stimulus. Androgens diminish Th2 and ILC2 cell population, consequently limiting eosinophilic inflammation and IgE production. They also decrease IL-17A synthesis by Th17, lowering neutrophilic inflammation. Estrogens increase Th2 and ILC2 cell differentiation and induce IL-17A production from Th17 cells. Furthermore, estrogens augment total serum IgE, IL-5 production, and eosinophilia. In conclusion, estrogens may display detrimental effects on airway function by enhancing inflammation, and androgens exert opposite effects

LTC_4, LTD_4, and LTE_4) evoke bronchoconstriction and increase vascular permeability [406, 407]. For LT biosynthesis, arachidonic acid (AA) is excised from phospholipids in the plasma membrane by the action of phospholipase A_2 (PLA_2). Once AA is released, the nuclear membrane-bound 5-LOX-activating protein (FLAP) delivers it to 5-lipoxygenase (5-LOX) that converts AA into the different types of LTs [406, 408, 409]. In this regard, 5α-DHT and TES diminish the biosynthesis of LTs by interfering with 5-LOX localization via activation of type 2 extracellular signal-regulated kinase 2 (ERK 2) [407, 410] and by blocking the assembly of 5-LOX/FLAP [411]. The regulation of ERK2 and 5-LO trafficking exerted by androgens may explain the gender differences observed in the anti-leukotriene therapy, where young girls show better outcomes than boys [412]. Moreover, increase in $[Ca^{2+}]_i$ in ASM cells (ASMCs) is a primordial mechanism that triggers the exacerbated bronchoconstriction seen in asthma. In this context, a study in primary human ASMCs made by Kalidhindi et al. indicates that basal expression of AR is greater in males compared to females but increases with asthma or with an inflammatory condition in both genders. More interestingly, ASMCs from asthmatic females display a greater AR expression than males; however, androgen receptor may take minor functionality in females. In addition, TNF-α and IL-13 enhance histamine-induced increase in $[Ca^{2+}]_i$ in ASMCs; nevertheless, TES and 5α-DHT decrease the enhancement through AR signaling. AR effects on $[Ca^{2+}]_i$ increments are explained by the downregulation of stromal interaction molecule 1 (STIM1) and Orai1, key machineries in store-operated Ca^{2+} entry (SOCCE), and the increasing of SARAF (formerly known as TMEM66, a negative regulator of SOCCE) [413].

Not all patients with asthma course with type 2 inflammation but display an IL-17A-mediated neutrophil inflammatory pattern that is resistant to corticosteroid treatment. IL-17A is secreted by CD4+ Th17 cells and is associated with more severe asthma phenotypes [42, 105]. Moreover, macrophages and DCs express receptors for IL-17A and favor the synthesis of IL-6 and TNF-α [414]. Interestingly, the stimulation of the AR by TES decreases IL-17A protein expression and IL-23 receptor (IL-23R) mRNA expression from Th17 cells, reducing neutrophilic airway inflammation [253]. Also, IL-17A induces glucocorticoid receptor β (GR-β) expression and favors corticosteroid therapy resistance in patients with severe asthma [415]. α and β subtypes have been described as the two known glucocorticoid receptors. GR-β acts as an inhibitor of GR-α, and this latter isoform decreases the expression of inflammatory mediator genes [416, 417]. These findings point out that TES (by downregulating IL-17A) may decrease the expression of GR-β, promoting the anti-inflammatory effect of corticosteroids.

Persistent asthma (as seen in a IL-17A-mediated inflammatory response) is characterized by airway remodeling that involves epithelial-mesenchymal transition (EMT), cell mucus hypertrophy, subepithelial fibrosis, deposition of extracellular matrix proteins, and smooth muscle hypertrophy and hyperplasia [418, 419]. These cell modifications lead to pronounced airflow obstruction and epithelial damage that predispose to AHR. TGF-β1 induces EMT, and its increased expression levels correlate with severe asthma phenotypes [420, 421]. In this context, Xu et al. demonstrated that DHEA (via a genomic effect) inhibits the bronchial TGF-β1-induced EMT and preserves the epithelial morphology [422].

The influence of androgens on COPD patients and the inflammatory response in animal models have not been broadly investigated as occurring in asthma. However, since circulating TES levels have been positively correlated with cardiorespiratory function and muscle growth and strength [423, 424], low levels of this androgen may be associated with worse outcomes in patients with COPD [425]. In this context, numerous studies show that men with COPD have medical relevantly lower levels of TES and DHEA-S compared with healthy men [425–431]. Moreover, a recent research suggests that testosterone replacement therapy (TRT) decreases the rate of COPD patient hospitalizations and slows the progression of the disease [432]. COPD patients' usually

display neutrophil-mediated inflammation, mainly located in the lung parenchyma, influenced by the action of IL-17A [433]. Macrophage activity also plays a crucial role in the lung of smokers and is even higher in COPD patients. Macrophages expressing IL-17A receptors have been observed in mice with myocarditis, and the genetic suppression of these receptors interferes with macrophage recruitment [434]. Similar to neutrophils, macrophages contribute to lung damage by synthetizing and releasing pro-inflammatory mediators, e.g., cytokines, chemokines, and ROS [363]. Moreover, cigarette smoke stimulates the activation and recruitment of macrophages, causing emphysema, involving the action of MMP-9, MMP-12, and CCL2 [197, 363, 435, 436]. In COPD, the role of the two distinct described phenotypes of macrophages (M1 and M2) is unclear, showing no sign of predominance for a determined subtype [197, 363]. The classical activation of macrophages (M1) is associated with Th1 immune response producing pro-inflammatory cytokines such as TNF-α, IL-1β, IL-6, and IL-12 [197, 202]. However, Th2 cytokines (IL-4 and IL-13) can alternatively activate macrophages as occurring in allergic asthma [437]. M2 macrophages commonly produce anti-inflammatory cytokines, including TGF-β, IL-10, CCL18, and CCL22 [197, 437]. Interestingly, evidence suggests that alveolar macrophages may be involved in the pathogenesis of COPD in a non-inflammatory manner; i.e., smoking induces a polarization pattern toward the down-regulation of M1-related inflammatory genes (CXCL9, CXCL10, CXCL11, and CCL5) and the induction of genes associated with the M2 polarization mechanisms (MMP-2, MMP-7, and the adenosine A3 receptor) [438]. Nevertheless, M2 alveolar macrophages contain inflammatory mediators that may cause an increase in cell recruitment, mucus secretion, and airway remodeling if they are immoderately discharged, as occurs in humans and mice asthmatic lungs [439, 440]. In this context and contrary to the anti-inflammatory androgen effects, it was revealed that, although 5-αDHT reduces lung inflammation, the same androgen enhances IL-4-stimulated M2 macrophage polarization in OVA-induced allergic mice. Also, the genetic ablation of AR diminishes eosinophil recruitment and lung inflammation due to the compromised M2 polarization [440]. Therefore, further research is required in order to elucidate the role of androgens on alveolar M2 macrophages and in the inflammatory outcomes of diseases such as asthma and COPD.

The evidence indicates that male sex steroids have beneficial anti-inflammatory properties in asthma patients by attenuating innate lymphoid cells Type 2, Th2 cells, IL-17A-mediated response, and the leukotriene biosynthesis pathway, through different mechanisms (Fig. 15.4). Also, androgens might reduce the neutrophilic inflammation in COPD, but additional studies are required. Moreover, even though the use of androgens in order to increase muscle mass and improve cardiorespiratory functions is promising, the effect of these hormones in men with COPD seems to be modest, and more research is indispensable to resolve whether TRT could be an option in COPD treatment. Regarding the use of androgens as an anti-inflammatory treatment in asthma and COPD, it should be considered the metabolic pathway of DHEA and TES, leading to the production of estrogens. Furthermore, 5α-DHT, a reduced metabolite of TES with important androgenic actions, has been associated with prostate cancer [441]. In this context, 5β-DHT, the other reduced metabolite of TES with minor androgenic activity and without estrogenic effects, might be taken into account as a potential therapeutic choice [76], although clinical studies are imperative to support this notion.

15.5.3 Estrogens' Effects on Inflammation in Asthma and COPD

It has been established that the incidence of asthma is more common in young boys and adult women, and that the severity of the symptoms may increase during pregnancy [26, 31, 105]. The transition from childhood to adulthood is distinguished by a higher probability of persistence of wheezing in females [300, 442].

Therefore, the influence of female hormones (mainly estradiol) on the airway biology has been widely explored [95, 141, 142, 145, 443–446]. Interestingly, a contradicting role of estrogen suggests either the induction of AHR and inflammation [214, 447–449] or an improvement of asthma symptoms by downregulating inflammation and favoring ASM relaxation [214, 450–453]. In this regard, several bronchodilator mechanisms have been shown to be affected through the rapid actions of female sex steroids. In 1983, a group of researchers reported that E2 in supraphysiological concentrations enhances the bronchodilator response to adrenaline and noradrenaline in pig bronchus and the increment in the potency of catecholamine-induced bronchodilation may be mediated by an inhibition of catecholamine metabolism or uptake [454]. Later on, it was exhibited that E2 causes relaxation of isolated trachea muscle strips (pre-contracted with acetylcholine or KCl), independently of the adrenergic system, but possibly involving prostaglandin synthesis and cyclic guanosine monophosphate (cGMP) modulation [455]. It is well known that prostaglandins modulate cyclic adenosine monophosphate (cAMP) and cGMP formation. Cyclic nucleotides stimulate protein kinases that influence the inhibition of Ca^{2+} influx channels, which favors bronchodilation. In this context, E2-induced increase in cAMP has been observed in porcine coronary arteries [456]. Also, physiological concentrations of E2 potentiate the relaxation evoked by isoproterenol via cAMP production in human and guinea pig ASM. The cAMP pathway triggered by E2 in a non-genomic way promotes the blockade of Ca^{2+} influx (mainly through L-VDCCs) and the further decrease in $[Ca^{2+}]_i$ [453]. In addition, as demonstrated by Dimitropoulou et al. [457], the increase in cyclic nucleotides leads to the phosphorylation and the opening of K^+ channels. They observed that a physiological E2 concentration inhibits AHR in asthmatic mice via an ER signaling pathway that implicates the activation of protein kinase G (PKG) and the opening of BK_{Ca} channels. Nevertheless, a recent study demonstrates that 17β-estradiol has a little effect on the formation of cAMP in primary cultured human ASMCs. Interestingly, the same study shows that progesterone is capable of promoting the formation of cAMP after 3 minutes of stimulation [458]. In the last years, some studies have further demonstrated that estrogens diminish Ca^{2+} levels in ASMCs from different species via rapid (non-genomic) effects through ERs or by directly blocking membranal Ca^{2+} channels. Supraphysiological concentrations of E2 lower ASM basal tone through the obstruction of L-VDCCs in guinea pig ASM [295]. Moreover, the acute exposure of physiological concentrations of E2 decreases histamine-evoked Ca^{2+} influx via the inhibition of L-VDCCs and SOCCE in ASMCs from women [167]. It has been shown that asthmatic airways are less responsive to nitric oxide (NO) donors; however, E2 through ERβ reverses this phenomenon favoring ASM relaxation [451]. Also, E2 (in a physiological range) rapidly increases NO production in human bronchial epithelium from women and produces relaxation of bronchial rings pre-contracted with acetylcholine (Ach) [459]. In addition, a study has demonstrated that P4 and 5β-pregnanolone prevent histamine- or carbachol-induced contraction in guinea pig ASM [460].

Chronic effects of estrogens, or the lack of them, on Ca^{2+} handling and AHR have also been investigated. For instance, the genetic ablation of ERα induces AHR among other lung function anomalies and interferes with airway smooth muscle and nerve physiology, probably involving the dysregulation of M2 muscarinic receptors [461]. Matsubara et al. reported that endogenous estrogens downregulate AHR in OVA-induced asthmatic female mice. Correspondingly, 17β-estradiol suppresses AHR in male mice challenged for 10 days with OVA [462]. Dimitropoulou et al. observed that estrogen replacement therapy prevents the development of AHR and inflammation (important markers in asthma) in ovariectomized asthmatic mice. Also, they found a reduction in TGF-β1 levels from bronchoalveolar lavage fluid (BALF) of estrogen-treated mice [463]. Recently, Bhallamudi et al. [464] found in non-asthmatic and asthmatic human ASMCs that long-term exposure (24 h) to propylpyrazoletriol (an ERα agonist) enhances the Ca^{2+} response to

histamine. Differently, ERβ stimulation with the agonist WAY-200070 (WAY) evokes a decrease in histamine-induced $[Ca^{2+}]_i$ increase. Besides, TNF-α and IL-13 improve $Ca^{2+}]_i$ responses evoked by histamine, Ach, and bradykinin; and ERβ activation abolishes this phenomenon. Interestingly, E2, a non-selective ER agonist, does not show significant changes in $[Ca^{2+}]_i$ when ASM cells are stimulated only by histamine. However, E2 induces a decrease in $[Ca^{2+}]_i$ increase elicited by histamine bradykinin and Ach when ASMCs are pre-treated with TNF-α or IL-13. ERβ effects on agonist-induced $[Ca^{2+}]_i$ increases seem to be mediated by an augment on sarco(endo)plasmic reticulum Ca^{2+} ATPase 2 (SERCA2) function and by the inhibition of L-VDCC [464].

Estrogen actions on the inflammatory response and their cellular mechanisms in asthma have been explored as well. Most studies point out that estrogens, mainly through ERα signaling, increase allergic airway inflammation and allergen-induced AHR [141, 142, 145, 461]. Th2 inflammation in asthmatic patients influence B-cell activation that favors increased levels of IgE [465]. Women have been shown to have higher serum IgE levels during puberty, which are associated with more severe asthma symptoms provoked by histamine, IL-4, and IL-13 released from mast cells [442, 465, 466]. Likewise, OVA-induced female asthmatic mice with increased IgE levels (compared with those observed in males) show minor sensitivity to budesonide treatment against IL-5 production and the development of AHR [447]. The exposure to environmental tobacco smoke (ETS) increases Th2 cytokine response after allergic (OVA) sensitization. Female mice exposed to ETS display more IgE-positive cells in the lungs and augmented levels of IL-4, IL-5, IL-10, and IL-13 than males [449]. Additionally, acute exposure of physiological concentrations of E2 elicits the increase in $[Ca^{2+}]_i$ via ERα activation and the subsequent IgE-induced degranulation and LTC_4 production in a rat basophilic leukemia cell line (RBL-2H3M) and in a human mast cell line (HMC-1) [226]. These insights indicate that females are more susceptible to develop a more damaging inflammatory response after the exposure to tobacco smoke as occurring in COPD. Furthermore, it has been proposed that female sex steroids are responsible for inducing eosinophilia in allergic asthma. A study performed by Riffo-Vázquez et al. shows that gonadectomy decreases total serum IgE, IL-5 production, and pulmonary eosinophilia in female mice sensitized to OVA [214]. In addition, it has been demonstrated in a murine model of allergic asthma that progesterone promotes airway eosinophilia and provokes AHR [215].

Dendritic cells and macrophages are also modulated by estrogen actions. These cells present allergenic peptides to uncommitted T lymphocytes and favor type 2-mediated airway inflammation [51]. In this context, it has been observed that E2 triggers the expression of DC-derived cytokines, such as IL-6, IL-8, and MCP-1 [467], and enhances the production of human DC population, promoting the proliferation and differentiation of Th cells into Th2 cells [468]. Asthmatic patients present significantly increased numbers of M2 macrophages in BALFs compared to normal subjects [469, 470]. OVA-sensitized female mice also have more M2 alveolar macrophages compared to males [471, 472]. In addition, alveolar macrophages from female mice exhibit greater expression of M2 genes, IL-4 receptor (IL-4R)-α, and ERα after OVA challenge. Furthermore, IL-4 induces M2 gene expression in female mice macrophages, and exogenous E2 potentiates this polarization [473].

Female sex hormones have also been associated with the IL-17-mediated inflammatory pattern displayed in some patients with asthma. This phenotype is distinguished by manifesting neutrophilic inflammation as occurring in COPD [42, 304]. In this context, Newcomb et al. found that women with severe asthma have increased numbers of Th2 cells and greater production of IL-17A compared with asthmatic men [474]. Given these insights, the authors claimed that female sex steroids are responsible for increasing Th17 cell differentiation and IL-17A production from these cells. However, they did not observe a correlation between E2 and P4 plasma levels (at the time of obtaining blood samples) with IL-17A

protein expression in Th17 cells from women and further suggested that the increase in the production of IL-17A in women compared to men is due to the exposure of T cells to female sex hormones during the development of Th17 cells in the body. To further determine the mechanism by which sex steroids modulate the production of IL-17A, they performed an experiment where it was observed that the administration of E2 and P4 augments the expression of IL-17A and IL-23 receptor (IL-23R) in Th17 cells from ovariectomized mice [474]. In this regard, it has been established that IL-17A requires IL-23R signaling to maintain and stabilize the Th17 cell phenotype [475, 476]. Moreover, the same authors found an increased expression of IL-23R in Th17 cells from women compared to men [474]. Another study shows that E2 chronic stimulation enhances the expression of IL-6 and IL-17 in peripheral blood mononuclear cells from asthmatic patients, both females and males [477]. Interestingly, it has been demonstrated that the estrogen deficiency occurring in postmenopausal women is associated with increased serum levels of IL-17A [478]. Anti-inflammatory effects of estrogen in asthma have been reported as well. E2 inhibits cell recruitment into the lungs during the allergic inflammatory process, preventing the cell adhesion through the downregulation of E-selectin. Finally, estradiol treatment of ovariectomized OVA-induced allergic rats diminishes the release of LTB_4, IL-10, and TNF-α [267].

More severe asthma symptoms reported in women appear to be associated with hormonal changes occurring during the different life stages, i.e., menstruation, pregnancy, and menopause [38, 276]. During pregnancy, asthma can change its manifestations, and women with severe disease may present worsening of symptoms that do not improve with the use of OC [283]. It has been described that in the third trimester of pregnancy, one third of women with asthma show an improvement, one third show no change, and another third get worse [479, 480]. In this regard, highest estrogen levels during the third trimester of pregnancy may explain the different manifestations of the disease [265]. Cytokines with an anti-inflammatory role such as IL-10 and IL-4 have been shown augmented after the stimulation with E2 (in concentrations occurring during pregnancy) in CD4 T cells from humans and mice [252, 481, 482]. Furthermore, higher physiological concentrations of estrogen reduce the T-cell production of TNF-α [483]. In the menopausal period, asthmatic patients tend to experience more pronounced respiratory complications [484]. It has been proposed that E2 serum levels may function as an appropriate biomarker for asthma severity in postmenopausal women [285]. Height reduction of the thoracic spine due to osteoporosis related to estrogen deficit in menopausal women might be implicated in the decrease of lung function [485]. Menopause hormone therapy based on estrogen administration is used to alleviate climacteric symptoms, including osteoporosis; vasomotor disorders; skin, urogenital, and weight changes; etc. [486]. Nonetheless, risks as developing thromboembolic venous diseases via alterations in blood coagulation must be taken into account when high doses of MHT are used [486–488]. Aminoestrol, butolame, and pentolame, types of 17β-aminoestrogens, have been suggested as an alternative of MHT, considering their weak estrogenic and antithrombotic activity [489–491]. In this regard, Flores-Soto et al. observed that butolame and pentolame but not aminoestrol, cause hyperresponsiveness to carbachol, histamine, and KCl in guinea pig ASM through the activation of L-VDCCs [492]. This finding points out that aminoestrol is a good alternative for MHT, but further studies are required to critically asses the role of aminoestrogens in postmenopausal asthma exacerbations, particularly in the inflammatory response.

Several recent works have shown a differential expression and activation of both ERα and ERβ in non-asthmatic and asthmatic ASMCs that may explain the distinct outcomes regarding airway inflammation, remodeling, and responsiveness in females [141, 142, 145, 161, 443]. Aravamudan et al. quantified the expression of ERα and ERβ in ASMCs from asthmatic and non-asthmatic subjects. They observed that ERβ expression is greater in asthmatic ASMCs and in ASMCs exposed to TNF-α or IL-13 as well. The expression of the ER isoforms is regulated by inflam-

matory signaling pathways such as p42/pp44 mitogen-activated protein kinase (p42/44MAPK), phosphatidylinositol 3-kinase (PI3K), and NF-κB, proteins implicated in airway remodeling and asthma development [161]. Furthermore, the dual effects of 17β-estradiol on smooth muscle have been reported. Some works demonstrate that this estrogen promotes a mitogenic effect in female and male rabbit ASM [493] and induces rat vascular smooth muscle proliferation via ERs and MAPK signaling cascade [494], while other studies show that E2 inhibits the proliferation and migration of vascular smooth muscle cells [495, 496]. Recent studies by Ambhore et al. suggest that ERβ plays a protective role against airway remodeling and hyperresponsiveness. One of these studies confirmed that ERβ but not ERα activation inhibits platelet-derived growth factor (PDGF)-induced proliferation in ASMCs from asthmatic and non-asthmatic males and females by interfering with cell cycle mechanisms and suppressing proliferative proteins [443]. Also, the administration of a selective ERβ agonist (WAY) decreases airway remodeling and AHR in a murine model of allergen-induced asthma; specifically, ERβ activation abolishes the increase in vimentin, fibronectin, and collagen I caused by allergic sensitization [141]. Fibronectin and collagen are molecules highly involved in extracellular matrix (ECM) deposition that leads to airway remodeling and hyperresponsiveness [497–499]. In this regard, another study shows that ERβ activation diminishes TNF-α-induced increased protein expression of ECM proteins such as collagen I, collagen III, and fibronectin in human ASMCs from asthmatic and non-asthmatic subjects. Also, ERβ signaling reduces the activity of MMP-2 and the expression of MMP-2 and MMP-9 in both asthmatic and non-asthmatic ASMCs [142]. These proteolytic enzymes are key regulators in the ECM degradation and the progression of asthmatic airway remodeling [500–502]. Interestingly, the inhibitory effect of ERβ on MMP expression and activity seems to be mediated by the NF-kB signaling pathway [142]. The most recent study about the protective role was performed by Kalidhindi et al., using an allergen-induced asthma model in ERα and ERβ knockout (KO) mice [145]. Initially, they observed that female mice exposed to the allergen show a more pronounced decay in lung function (in terms of airway resistance and compliance) compared to male mice. Correspondingly, KO animals display a deteriorate lung function compared to ERα KO and WT KO animals. In addition, the genetic ablation of ERβ results in a more prominent airway remodeling and responsiveness and increased expression of fibronectin, vimentin, and alpha smooth muscle actin (α-SMA), consistent with the observations made by Ambhore et al. [141, 142]. These explorations help to clarify the role of estrogen receptors both α and β, pointing out a protective role for the latter one, and contribute to explain the gender differences observed in asthma prevalence after puberty, when women present more severe symptoms.

Otherwise, the influence of estrogens in COPD has been poorly explored. Data suggest that women are more likely to have COPD and present a faster decline of lung function than men. Also, epidemiological studies have shown that hormone replacement therapy (HRT) containing estrogens exacerbates COPD [503]. Unlike the reported for asthma, the expression of the ERs seems not to play an essential role in the development of COPD, since the three major subtypes, ERα, ERβ, and GPR30, are expressed in the same grade in lung tissues from COPD patients and normal subjects, including both men and women. However, the intracellular pathways that lead to the production of female sex steroids are upregulated. Aromatase and 17β-HSD1, two of the main enzymes responsible for the generation of estrogens, are increased in alveolar macrophages of COPD patients compared with controls [504]. Moreover, once smoke cigarette is inhaled, chemicals are metabolized in two separate phases. Cytochrome P450 enzymes accomplish the phase I. These enzymes are a large family of proteins with the critical function of metabolizing cigarette smoke and other environmental irritants, turning them into intermediate compounds. Phase II enzymes conjugate and secrete the metabolites produced in the former clearance steps. A downregulation in either

expression or function of phase II enzymes might suppose the accumulation of metabolites produced by CYP in the lung, causing oxidant injuries to the tissue [36, 505]. Interestingly, it has been suggested that E2 upregulates CYP enzymes. For instance, female mice show a more pronounced sensitivity to naphthalene (an important component of cigarette smoke) toxicity and a more prominent pattern of airway epithelial injury than male mice [506]. Also, female mice have more significant expression of CYP enzymes and augmented accumulation of naphthalene metabolites [507]. Furthermore, the stimulation of the ERα by E2 increases the basal and the smoke-induced expression of CYP1A1 and CYP1B1 (two members of CYP family) in human bronchial epithelial cells [508]. Moreover, a CYP1A1 differential metabolic activity and distinct outcomes of the produced metabolites have been claimed. It has been demonstrated that CYP1A1 shows high metabolic activity for E2 2-hydroxylation, followed by 15α-, 6α-, 4-, and 7α-hydroxylation [509]. 4- and 16α-hydroxylated estrogens may contribute to cancer development [510, 511], while 2-hydroxylated estrogens are thought to have anti-cancerogenic activity and a higher rate of excretion the in premenopausal female smokers [512–514]. The augment in the expression of CYP is associated with increased levels of estradiol and oxidants, mediated by the enhancement in the metabolism of cigarette smoke [36, 514]. These insights point out that COPD female patients may have increased production of E2 and a higher production of cigarette smoke metabolites leading to more severe lung damage.

These basic and clinical reports indicate contradictory outcomes regarding anti-inflammatory and pro-inflammatory properties of estrogen. Although several studies show that E2 is capable of relaxing ASM and reducing AHR, this sex steroid may lead to disadvantageous results in asthma patients by enhancing allergic and IL-17A-mediated inflammation (Fig. 15.5). Also, dual hormonal effects exerted by E2 and the differential expression and activation of estrogen receptors may limit the use of female hormones in asthma treatment. Moreover, the findings suggest that women under menopause hormone therapy and experiencing PMA might consider the risk of worsening the lung function. Furthermore, estrogen may promote neutrophilic inflammation in subjects with COPD, but further studies are necessary in order to corroborate this appreciation. Additionally, the use of aromatase inhibitors in a pulmonary illness such as lung cancer has been validated in preclinical assays [515, 516]. In this regard, the possibility of 17β-HSD1 and aromatase serve as potential therapeutic targets in COPD patients should be explored.

15.5.3.1 Pulmonary Fibrosis

Pulmonary fibrosis (PF) is a chronic interstitial lung disease characterized by progressive remodeling of the lung parenchyma with extracellular matrix deposition that leads to an abnormal tissue repair (lung scarring) [517, 518]. This disease affects approximately three million persons worldwide and is more common in men than in women [519–521]. The etiology of this disease has been related to infections [522–524], environmental and occupational pollutants [525, 526], cigarette smoke [527, 528], obstructive sleep apnea, and others [529, 530]. However, it can also manifest without any associated pathology, known as idiopathic pulmonary fibrosis (IPF). The PF symptoms, such as dyspnea and dry cough, progressively worsen, resulting in a median survival time of 3 to 5 years after diagnosis [518, 531]. Spirometry reveals a restrictive respiratory pattern, attributed to the accumulation of parenchymal scar tissue and the subsequent alteration of normal lung architecture [532, 533].

Fibrogenesis in the lung involves the fibroblast hyperproliferation at alveolar injuries and the excessive deposition of extracellular matrix (ECM) components, along with signaling pathways that degrade the ECM [534–536]. The alveolar endothelial injury caused by infections, tobacco smoke, gastroesophageal reflux contents, and environmental pollutants favors an impaired epithelial regrowth above an irregular matrix. During PF development, epithelial-mesenchymal transition (EMT) occurs. In this process, profibrotic cytokines, including TGF-β1, confer to

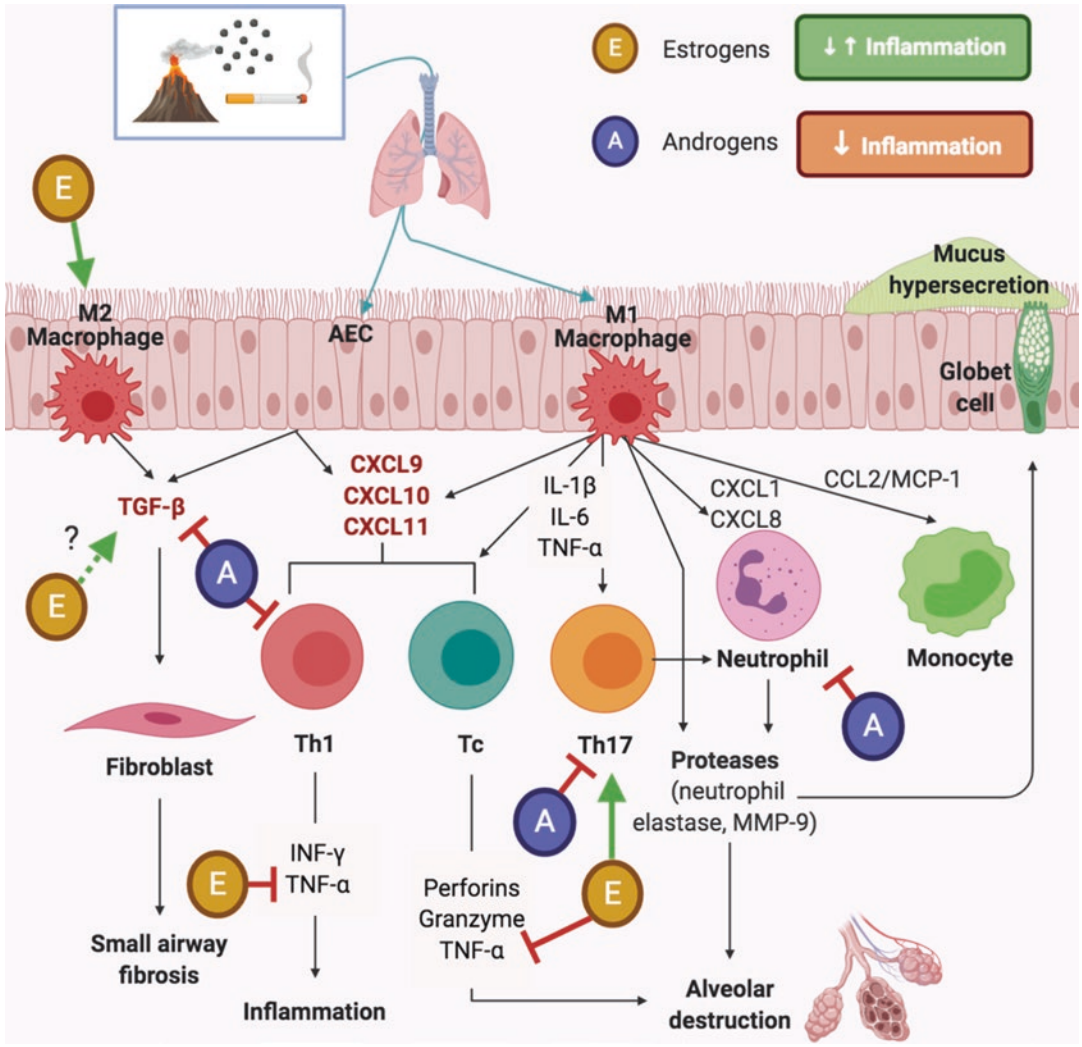

Fig. 15.5 Androgen and estrogen actions on inflammation in chronic obstructive pulmonary disease (COPD). Inhaled cigarette smoke and environmental and occupational exposures activate airway epithelial cells (AECs) and macrophages to release several chemotactic factors that attract T helper 1 (Th1) cells and Th1 CD8+ T cells (Tc) to the lungs, including CXC-chemokine ligand 9 (CXCL9), CXCL10, and CXCL11. Th1 cells release cytokines that induce inflammation, and Tc release perforins, granzyme B, and tumor necrosis factor α (TNF-α), contributing to alveolar cell apoptosis. Cytokines (IL-1β, IL-6, TNF-α) released from M1 macrophages (pro-inflammatory cells) activate Th17 cells, which modulate the neutrophilic inflammation. The attraction of neutrophils and monocytes is mediated by CXCL1, CXCL8, and CC-chemokine ligand 2 (CCL2), respectively. Inflammatory cells secrete matrix metalloproteinase 9 (MMP-9), which causes elastin degradation and emphysema. Neutrophil elastase evokes mucus hypersecretion. AECs and M2 macrophages (anti-inflammatory cells) release transforming growth factor β1 (TGF-β1), which stimulates fibroblast proliferation, provoking fibrosis of the small airways. The effects of estrogens (E) or androgens (A) on these immune cells can change depending on the hormone concentration and the timing and duration of the stimulus. Androgens diminish Th1 responses and inhibit TGF-β1-induced epithelial-to-mesenchymal transition (EMT) and preserve the epithelial morphology. In addition, androgens decrease IL-17A synthesis by Th17 cells, lowering neutrophilic inflammation. On the other hand, estrogens potentiate the M2 polarization of macrophages, favoring an anti-inflammatory condition, and might enhance the secretion of TGF-β1. Moreover, high physiological concentrations of estrogen reduce the T-cell production of TNF-α. Estrogens may present dual effects on airway inflammation in COPD, and androgens may reduce this response

epithelial cells, properties of mesenchymal cells to produce collagen [537–539]. This cytokine also promotes the accumulation of fibronectin in the ECM and the differentiation of fibroblasts into myofibroblasts [540, 541].

Moreover, T cells modulate lung fibrosis development. Th1 cytokines attenuate fibrosis, whereas Th2 cytokines promote fibrogenesis [542, 543]. In this regard, several studies have shown increased IL-13 expression in patients with IPF and in animal models [544–547]. IL-13 is mainly produced by Th2 lymphocytes, epithelial cells, ILC2s, and M2 macrophages [548–550]. This interleukin stimulates the proliferation of fibroblasts and induces pro-fibrotic cytokines, e.g., TGF-β1 and PDGF [551, 552]. In animals, exposure to bleomycin is the standard model of injury-associated PF since it promotes lung damage associated with apoptosis of alveolar epithelium, loss of the epithelial function, and an increased inflammatory response [553–555]. Interestingly, bleomycin also stimulates IL-13 production and myofibroblast differentiation [556]. Additionally, IL-17 has been linked to profibrotic effects through interactions with TGF-β signaling [555, 557, 558]. It has been proved that, by blocking IL-17 production, the progression of PF is delayed in different murine models of lung fibrosis [557, 559, 560].

15.5.3.2 Androgens' Effect on Inflammation in Pulmonary Fibrosis

Gender is an important factor in determining the risk and prognosis for PF. The prevalence of PF is greater in men, who display faster progression and less survival rates compared to women [561, 562]. Moreover, the incidence of this disease increases with age, appearing between the fifth and seventh decades of life [563, 564]. Studies suggest that androgens may contribute to increase lung injury and fibrosis [48, 49]. However, the sex differences in PF have been studied mostly in animal models. In this context, Voltz et al. found in a murine model of bleomycin-induced PF that males show a decreased lung function and an increased fibrosis compared with females. Furthermore, mice castration restores lung function, and 5α-DHT replacement therapy aggravates it [49]. Another research group using the same model observed that aged male mice exhibit augmented collagen deposition and neutrophilic alveolitis, and an elevated mortality, compared to female mice or young mice [565]. Also, young and old mice exposed to bleomycin show exacerbatedlevels of TGF-β, and aged male mice present increments in neutrophil chemoattractants such as IL-17A, chemokine (C-X-C motif) ligand 1 (CXCL1), and CXCL2 [565, 566]. These observations suggest that androgens promote the fibroproliferative response associated with fibrocyte recruitment and favor the susceptibility to present lung fibrosis. In another study, since decreased levels of DHEA have been related to immunosenescence [567], the levels of DHEA and DHEA-S in BALF and plasma from patients with IPF were analyzed. Interestingly, DHEA/DHEA-S ratio is significantly decreased in plasma from males with IPF. Furthermore, the same study shows that DHEA (100μM) reduces human lung fibroblast proliferation and differentiation into myofibroblast induced by TGF-β1 [568]. Recently, Cephus et al. suggested that androgens negatively regulate ILC2 and ILC2-derived IL-13 production. They demonstrated that chronic administration of 5α-DHT to mice reduce IL-13 production from lung ILC2s. Moreover, IL-13+ ILC2s are also significantly decreased in sham-operated male mice compared to gonadectomized male mice and sham-operated female mice [298]. In conclusion, studies show discrepancies, indicating that androgens may play a promoting or protective role in the development of PF, and more information is needed related to androgen effects on the inflammatory response in lung fibrosis.

15.5.3.3 Estrogen Effects on Inflammation in Pulmonary Fibrosis

The development PF has also been thought to be influenced by estrogen actions. Distinct reports indicate a protective role for estrogen; however, animal models have shown mixed results. In this context, Gharaee-Kermani et al. observed that female Fisher rats with bleomycin-induced PF

have higher mortality rates and more severe fibrosis compared to male rats. Furthermore, the authors found that ovariectomized animals presented less fibrosis and estradiol replacement therapy (ERP, 1 and 10 nM) increases procollagen 1, IL-4, and TGF-β1 mRNA expression in fibroblast from bleomycin-treated rats [48]. In contrast, a protective role of estrogen on lung fibrosis has also been proposed. A study conducted in ovariectomized female relaxin gene KO (Rln1−/−) mice revealed an increment in collagen concentration and deposition in the lung. Relaxin is a hormone capable of diminishing fibrosis in several organs [569]. Other research group demonstrated in Sprague-Dawley (SD) rats that ovariectomy exacerbates bleomycin-induced PF and pulmonary hypertension, and 2-methoxyestradiol attenuates this condition [570]. The discrepancy of results in which estrogen may promote or inhibit lung fibrosis can be explained by the difference among the species of rodents used in the former studies since ovariectomized Fisher rats develop a less severe inflammatory response to pneumotoxins and have twice higher plasma levels of E2 than SD rats. Moreover, elevated levels of E2 potentiate the activity of NF-κB, which, along with E2, contribute to a pro-inflammatory state [570–572].

Monocytes and their derivatives participate in the immune response developed in lung fibrosis. Studies confirmed that estrogen might inhibit the expression of monocyte chemoattractants [573–575]. Alveolar macrophages are a vast source of pro-fibrotic molecules such as TGF-β1, PDGF, and MMPs [566, 576]. PDFG is a potent fibrogenic molecule that promotes PF through fibroblast activation [577]. In the lungs of IPF patients, PDGF expression is increased in epithelial cells and macrophages [578, 579]. It has been reported that this growth factor induces Ca^{2+} waves through IP_3 receptors and modulates gene expression of ECM proteins in human pulmonary fibroblasts [580]. In this context, Ambhore et al. postulated that the activation of the ERβ by a selective ERβ agonist suppresses PDGF-elicited proliferation of human ASMCs [443]. Furthermore, estrogen regulation on the main pro-fibrotic cytokine has also been reported. In a rat model of congenital diaphragmatic hernia (CDH) induced by nitrofen, the administration of E2 (0.2 mg/kg) significantly reduces the TGF-β1 expression in lung tissue [581]. Correspondingly, tamoxifen (an anti-estrogen drug used in breast cancer treatment) seems to promote TGF-β1 expression, leading to lung fibrosis [582]. Recently, Smith et al. claimed that E2 might modulate TGF-β1-induced mesenchymal transition in bronchial epithelial cells; however, TGF-β1-induced EMT was not significantly affected by E2 [583]. According to the authors, this fact may be due to the decrease in mRNA expression of ERs (ERα, ERβ, and GPR30) and the reduction in protein expression of ERα elicited by TGF-β1. The authors also found that E2 downregulates the expression of chloride intracellular channel protein 3 (CLIC3) and retinol binding protein 7 (RBP7), proteins associated with pathogenic mechanisms of PF. Recently, Elliot et al. demonstrated that ERα is augmented in lung human tissues and myofibroblasts from IPF patients and in bleomycin-treated mice. Moreover, a decrease in the expression of ERα in human myofibroblasts lessens fibrosis-associated pathways [584]. The evidence so far indicates that E2 mostly downregulates the inflammatory response in PF, conferring a protective status in women. However, the mixed results observed in lung tissues in vitro and in animal models require further exploration.

15.5.3.4 Lung Cancer

Lung cancer (LC) is characterized by morphological cellular transformations and alterations of key pathways in cellular homeostasis. According to the World Health Organization, LC is one of the most frequent causes of cancer-related death in men and women worldwide. Interestingly, about 80–90% of these cases are produced by tobacco smoking; however, only ~15% of smokers develop lung cancer, suggesting a genetic susceptibility [585–587]. The estimated number of new cases and deaths in men continues to exceed those values in women [588]. However, trends suggest that the number of deaths from LC in women will exceed those in men in the future [589, 590]. The augmented incidence in women

is related to an increase in smoking habits. However, non-smokers diagnosed with LC are more likely to be female, pointing out an additional hormonal component [591–593]. Non-smoker women with this pathology diagnosed at early ages have better survival rates than men [594–596].

Lung cancer is categorized in small cell lung carcinoma (SCLC) and non-small cell lung carcinoma (NSCLC, the most predominant type). NSCLS subtypes are squamous cell carcinoma, large cell carcinoma, and adenocarcinoma [597]. In LC, tumor microenvironment, made up of tumor cells, fibroblasts, vascular and lymphatic endothelial cells, growth factors, and others, favors a pro-inflammatory state. Fibroblast exposure to cigarette chemicals or another pro-carcinogenic factor leads to an increased inflammatory response by secreting PGE_2 and IL-8 and promoting the activity of ERK1/2 [598, 599]. Macrophages and neutrophils play a critical role in the inflammatory condition of LC. In this regard, two distinct types of macrophages are involved in the tumoral condition: resident macrophages which play a cytotoxic role against tumor development and tumor-associated macrophages (TAMs) with a pro-tumoral function [600]. TAMs are recruited at the tumor site by monocyte chemoattractant protein-1 (MCP-1/CCL2) [601, 602]. M1 macrophages (activated via IFN-γ) display pro-immunogenic characteristics, and M2 macrophages promote tumor growth, angiogenesis, invasion, and metastasis [603–606]. In addition, neutrophil infiltration into the tumor microenvironment, as described in the adenocarcinoma LC subtype, is associated with lower survival. In this context, neutrophils promote the EMT and potentiate the migration activity of tumor cells, and notably, neutrophil infiltration is associated with hemoptysis (coughing up of blood) [607]. Moreover, these immune cells release pro-inflammatory cytokines, proteases, and ROS, which damage DNA and activate oncogenes [608, 609]. Contrariwise, CD8+ and CD4+ T cells appear to have a protective role in LC, as they improve the survival rate by reducing the progression of the disease [610–612].

Several cytokines that regulate the tumor microenvironment have been studied in LC as well. For instance, TNF-α favors the survival of tumor cells by inducing genes encoding NF-κB-dependent anti-apoptotic molecules and inflammatory cytokines, including IL-1β, TNF-α, TGF-β1, IL-6, and IL-8 [613–615]. TGF-β is overexpressed in LC and displays pleiotropic effects such as cell growth, proliferation, differentiation, and apoptosis [616–619]. IL-10 has been shown to exert dual effects on the tumor microenvironment. In this context, it has been demonstrated that IL-10 possesses immunosuppressive functions by promoting T-cell apoptosis and anti-angiogenic properties [620–622]. Also, higher levels of IL-10 have been shown to be associated with metastasis [623, 624].

15.5.3.5 Androgens' Effects on Inflammation in Lung Cancer

The androgen pathway and its relevance to lung cancer cells have been studied. The AR (a member of the nuclear receptor superfamily) is found in normal and in lung cancer cells [625–627]. The expression of nuclear receptors has been suggested as a prognostic biomarker for survival and relapse of LC patients [628, 629]. In 2012, Jeong et al. proved that the exposure of SCLC and NSCLC cell lines to 5α-DHT (at physiological concentrations) increases the mRNA expression of the AR and stimulates cellular growth [630]. TES is also capable of stimulating the growth of SCLC cell lines expressing the AR [627]. An epidemiological study shows that high concentrations of total serum TES are associated with the presence of LC [631]. Furthermore, the use of 5α reductase inhibitors in patients with LC is associated with long better survival [632]. These insights suggest that the suppression of the androgen pathway may have a direct effect on lung cancer.

The correlation between androgens and inflammation on lung carcinogenesis has been scantly investigated. Regarding the survival of patients, T cells have been related to favorable prognosis in LC [610, 612]. In this context, it has been observed that androgen deprivation posi-

tively regulates the infiltration of T cells in the lung tissue [633]. Furthermore, Wu et al. found that androgen deprivation by castration increases the radiation-induced inflammatory response in mice [634]. They demonstrated that mRNA levels of TNF-α, IL-6, IL-1, and TGF-β are increased after castration. According to the authors, androgens could downregulate the actions of NF-κB and, consequently, inhibit the activation of genes encoding inflammatory cytokines. These data point out that TES might restrict the inflammatory response in LC by limiting the reactivity of T cells and interfering with the NF-κB signaling.

The influence of androgens on macrophages is well known; nonetheless, the relationship between androgens and macrophages in lung cancer has not been explored. In this context, Padgett et al. found that physiological concentrations of DHEA abolish the secretion of TNF-α, IL-1, and IL-6 in murine macrophages [635]. Another study proved that TES at physiological and supraphysiological concentrations suppresses the expression and release of TNF-α from human macrophages [636]. These results point out that androgens possess anti-inflammatory properties that modulate macrophage activity. In LC, IL-10, mainly produced by TAMs, has protumoral qualities and correlates with nonresponse to anti-tumoral therapy [600, 624, 637]. In 2012, Wang et al. proposed that this interleukin promotes tumor malignancy by stimulating T-cell apoptosis and tumor cell survival in the lung [620]. Interestingly, IL-10 transgenic mice injected with Lewis lung (3LL) carcinoma cells develop larger tumors than control mice, pointing out that this interleukin may prevent an adequate response against tumor cells [638]. Moreover, patients with NSCLS show increased IL-10 serum levels (compared to healthy subjects), and this increase is associated with reduced survival [639]. In this regard, the androgen effects on IL-10 have been studied in tissues different from lung cancer cells. It was demonstrated that TES at physiological concentrations acts as an inducer of IL-10 synthesis in mice monocyte macrophages [205]. Furthermore, TES replacement therapy in men with symptomatic androgen deficiency resulted in increased serum concentrations of IL-10 and decreased levels of TNF-α and IL-1 [204]. These studies suggest that probably androgens favor the pro-tumoral IL-10 effects, but specific studies in lung cancer cells are needed to confirm this assumption.

Another target of androgen regulation is the transmembrane prostate androgen-induced protein (TMEPAI). The synthesis of TMEPAI is elicited mainly by androgens, but also by TGF-β1 [640–642]. This oncogenic protein is expressed in lung cancer cell lines. Moreover, TMEPAI plays a vital role in TGF-β1-induced EMT by modulating ROS signaling and causing changes in epithelial cells, including migration, invasion, and proliferation of the tumor [643]. Furthermore, a research group found in lung cancer cells that the ablation of TMEPAI prevents cell proliferation, migration, and invasion. Also, they observed that the expression of TMEPAI in nude mice facilitates tumorigenesis. Finally, they proposed that the activation of TGF-β pathway induces TMEPAI expression and, subsequently, TMEPAI downregulates TGF-β signaling by promoting lysosomal degradation of the TGF-β receptor [644].

In conclusion, the evidence suggests that androgens might positively or negatively regulate lung cancer development. On the one hand, androgens may stimulate the growth of lung cancer cells and might play a role in the EMT by inducing the synthesis of TMEPAI. On the other hand, androgens may interfere with the signaling of NF-κB, leading to the downregulation of inflammatory cytokines.

15.5.3.6 Estrogens' Effects on Inflammation in Lung Cancer

Histological subtypes of lung cancer differ between men and women, being adenocarcinoma and bronchioloalveolar carcinoma, the most common subtypes in women [645, 646]. Estrogens have an essential role in lung carcinogenesis and can be locally synthesized by lung cancer cells [647, 648]. Moreover, ERs are found in lung cancer cells, suggesting that local production of estrogens is a response to a process of car-

cinogenesis [649, 650]. Increasing evidence shows that estrogens are involved in lung cancer proliferation and progression and most human lung tumors express the ERβ subtype and the aromatase enzyme [651–653]. In patients with NSCLC, elevated aromatase and ERβ expression are associated with poorer survival [653, 654]. Furthermore, Stabile et al., using a murine model of lung cancer induced by tobacco carcinogen (NKK, 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone), demonstrated that aromatase is expressed in TAMs, whereas ERβ is found in both macrophages and lung tumor cells. Interestingly, they also observed that the combination of anastrozole (aromatase inhibitor) and fulvestrant (ER antagonist) inhibits tobacco carcinogen-induced lung tumorigenesis [655]. Moreover, the increased ERα expression has been linked to macrophage infiltration into the tumor microenvironment [656]. The infiltration of macrophages is favored by CCL2 and its receptor (CCR2), i.e., the stimulation of ERα by E2, may activate the CCR2 signaling, leading to macrophage infiltration, MMP9 production, tumor progression, growth, and metastasis [656, 657].

During the inflammatory response, IL-6 acts as a regulator of neutrophil trafficking [658]. Some authors have focused on IL-6 and its role as a biomarker of ongoing inflammation. It has been reported that patients with LC have increased serum levels of this interleukin [659, 660]. Another research group observed that ovariectomized mice have decreased total neutrophils and this condition was recovered by E2 replacement therapy [661]. Human NSCLC cell lines and more important human NSCLC samples show tumor expression of IL-6 and its receptor. This interleukin can stimulate and enhance pathways in tumorigenesis, including signal transducer and activator of transcription 3 (STAT3), which regulates cell cycle progression, apoptosis, and tumor angiogenesis [662, 663]. In 2018, Huang et al. confirmed that E2 induces the activation of ERβ and promotes IL-6 expression via the MAPK/ERK and the PI3K/AKT signaling pathways in lung cancer cells. Moreover, they proposed that ERβ/IL6 signaling pathway could be a target for therapeutic intervention [664]. Furthermore, the estrogen-related receptor alpha (ERRα), a protein with a similar structure to ERα, has been implicated in LC. This receptor is expressed in LC cells and can regulate cell proliferation and migration [665, 666]. In 2018, Zhang et al. demonstrated that ERRα was significantly elevated in NSCLC cell lines compared with a normal bronchial epithelial cell line. They also reported that the overexpression and activation of ERRα increase the expression of IL-6 and the inhibition of NF-κB eliminates the ERRα effect in IL-6 synthesis [667]. The role of estrogen action on the inflammatory response in lung cancer is much better understood than the role of androgens. Moreover, it has been proposed that aromatase inhibitors may serve as potential drugs in lung cancer therapy [515, 516]. In this regard, further research on estrogen-targeted therapies that could improve patient survival and reduce tumor invasion is needed.

15.5.3.7 Coronavirus Disease 2019

The coronavirus disease 2019 (COVID-19) is caused by a virus named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). According to the World Health Organization, by September 17, 2020, SARS-CoV-2 had infected more than 30,055,710 people worldwide and killed more than 943,433. This disease is characterized by respiratory symptoms and is transmitted from human to human through respiratory secretions and saliva [668, 669]. Patients with COVID-19 exhibit fever, dry cough, difficulty in breathing, myalgia, headache, diarrhea, and nausea [670–672]. Also, clinical data indicate decreased oxygen saturation, blood gas deviation, and abnormalities observed by chest X-rays, lymphopenia, and an increase of C-reactive protein [673].

Severe COVID-19 cases progress to acute respiratory distress syndrome (ARDS), around 8–9 days after symptom onset, and may lead to respiratory failure [674–676]. Essentially, SARS-CoV-2 binds to host cells such as airway epithelial cells, alveolar cells, vascular endothelial cells, and macrophages in the lung by the angiotensin-converting enzyme 2 (ACE2) host

target receptor [677–680]. After the SARS-CoV-2 infection, a reduction in the ACE2 function that is associated with acute lung injury occurs [681–683]. Furthermore, ACE2 may be cleaved by transmembrane serine protease-2 (TMPRSS2), leading to an enhancement in the entry of the virus [684, 685]. On the other hand, there is an association between the gender of COVID-19 patients and fatality rates. In this context, data from the WHO show that a lower percentage of women (1.7%) infected with the virus will die in comparison with men (2.8%). Other investigations reported that less female patients with the severe form of the disease require intensive care or die compared to male patients [60, 686]. In this context, it has been insinuated that there may be alleles that confer resistance to this disease, since ACE2 gene is located on the X chromosome [687]. Interestingly, it also has been demonstrated that E2 downregulated the expression of ACE2 in differentiated normal human bronchial epithelial (NHBE) cells [688], which might explain the lower fatality rate in females.

The severity of COVID-19 is due to the host response featured by an uncontrolled inflammation associated with high levels of circulating cytokines, lymphopenia, and mononuclear cell infiltration in the lungs [676, 689]. When SARS-CoV-2 infects epithelial cells expressing the surface receptors ACE2 and TMPRSS2 in the airway, it activates a local immune response that in most cases resolves the infection [690]. Alveolar endothelial cells and macrophages detect the released PAMPs such as viral RNA and trigger the generation of pro-inflammatory cytokines and chemokines including IL-6, IFN-γ-induced protein 10 (IP-10/CXCL10), macrophage inflammatory protein 1α (MIP1α), and MIP1β in order to recruit immune cells [674, 676, 691]. The infiltration of monocytes, macrophages, and T cells to the site of infection promotes further inflammation [689, 692, 693] and may explain the lymphopenia seen in patients with this disease [670, 694]. In addition, it has been suggested that high exhaustion and a decreased functional diversity of T cells in peripheral blood may be an indicator of developing severe acute respiratory syndrome in patients with COVID-19 [695].

Moreover, higher levels of cytokines and chemokines have been related to the severity of the disease and eventually death [674, 694, 696]. In a study, a research group measured plasma levels of diverse cytokines in patients with severe COVID-19, founding increased levels of IL-2, IL-7, IL-10, G-CSF, IP-10, MCP-1, MIP1, and TNF [674]. Interestingly, Zhou et al. showed that IL-6 levels were elevated in non-survivors compared with survivors [697]. This cytokine storm, along with the cell infiltration, provokes lung damage by the excessive secretion of proteases and ROS [689, 692]. In addition, neutralizing antibodies produced by B cells can block viral infection, a situation that may occur around 1 week following symptoms onset [698, 699]. However, it has been suggested that some patients may not develop long-lasting antibodies to this virus and is unknown whether they are susceptible to reinfection. In this context, Elizaldi et al. conducted a study focused in CD4 T follicular helper (T_{fh}) cells (entities with high importance in the generation of long-lasting and specific humoral protection against viral infections) and reported that following infection with SARS-CoV-2, adult rhesus macaques exhibited transient accumulation of activated proliferating T_{fh} cells toward a Th1 response. They also proposed that a vaccine promoting Th1-type T_{fh} responses that target the S protein of the virus may lead to protective immunity [700]. Since the disease continues to spread worldwide, several immunosuppressive therapies have been used. Clinical trials have been focused on targeting pro-inflammatory mediators such as IL-6 and GM-CSF (clinical trials: ChiCTR2000029765).

15.5.3.8 Androgens' Effects on Inflammation in Coronavirus Disease 2019

More male patients with COVID-19 have higher mortality and develop the severe form of the disease than women [60, 701]. The difference in the number of cases reported by gender augments progressively in favor of male patients [702]. Studies have proposed that androgens modulate

the immune system response and may predispose men to different clinical course and prognosis of COVID-19. Since men with severe COVID-19 are ≥60 years old, decreased TES levels during aging may be involved in a pro-inflammatory condition [703–705]. Furthermore, it is well established that TES concentration in plasma is reduced by comorbidities like obesity, diabetes, and COPD, which are prevalent in COVID-19 patients [706–711]. In this regard, it has been shown that hypogonadism is highly prevalent (22–69%) in male patients with COPD [712]. Meanwhile, testosterone treatment improved the exercise capacity, muscle strength, and oxygen consumption in men [713].

It has been established that ACE2 mediates the cell entry of SARS-CoV-2, insinuating a protective role of this receptor against the viral infection [702]. Remarkably, this enzyme is selectively expressed by adult Leydig cells [714], pointing out a possible role of testicular secretion of TES in COVID-19 patients [702]. Also, it has been exhibited that patients with SARS-CoV-2 pneumonia, who were transferred to the intensive care unit (ICU) or died in respiratory ICU (RICU), had lower amounts of total TES and calculated free TES, compared to patients who were transferred to the internal medicine unit or were at a stable condition in RICU [715]. Alveolar endothelial cells and macrophages detect the SARS-CoV-2 and trigger the generation of pro-inflammatory cytokines and chemokines. In this regard, it has been demonstrated a correlation between hypogonadism and augmented pro-inflammatory cytokines and that testosterone treatment reduces IL-1β, IL-6, and TNF-α [704]. Furthermore, a study reported that low serum TES concentrations were significantly associated with elevated levels of TNF-α, MIP1α (CCL3), and MIP1β (CCL4) [716]. In the healthy immune response, these and other cytokines promote the infiltration of monocytes, macrophages, and T lymphocytes to the site of infection, leading to a pro-inflammatory feedback loop [691]. Moreover, it was reported that DHEA (at physiological concentrations) eliminates the release of TNF-α, IL-1, and IL-6 in murine macrophages [635]. Another study proved that TES at physiological and supraphysiological concentrations suppresses the expression and secretion of TNF-α from human macrophages [636]. In relation to T cells, Olsen et al. reported that an increase in peripheral T cells was reversed by androgen replacement [717]. Other research group found that castration of post-pubertal male mice increases T-cell numbers in peripheral lymphoid tissues [718]. In peripheral blood cells, TES treatment reduces the relative number of monocytes and increases CD8+ T-cell number [246]. Therefore, it is possible that androgen actions on CD8+ T cells favor the recognition and elimination of infected cells with SARS-CoV-2.

On the other hand, some critically ill patients have been treated with convalescent plasma, and growing evidence indicates positive results [719–721]. In an observational study, male patients with COVID-19 respond with a lower generation of effective SARS-CoV-2 IgG antibodies compared to women, confirming that a reduced antibody response in men is associated with worse prognosis [722]. This finding suggests a sexual hormone influence on B-cell proliferation. In this regard, androgen/AR actions on B lymphocytes have been studied by Altuwaijri et al. They reported that the lack of AR in B cells in different strains of mice results in increased B cells in the blood and bone marrow [243]. This insight supports the hypothesis that androgen-mediated B-cell maturation is AR dependent.

As previously mentioned, TMPRSS2 is a critical protease for the pathogenesis and spread of SARS-CoV-2 [723, 724]. The gene transcription of TMPRSS2 depends on the activity of the AR. It has been suggested that TES may promote higher expression of this protease in the lung of males, which might improve the ability of SARS-CoV-2 to enter cells [725–727]. The regulation of TMPRSS2 by TES has been suggested to influence on the male predominance displayed in COVID-19 infection [726]. Moreover, the hyperandrogenic condition could explain the severe COVID-19 cases in young males [702]. Also, it has been proposed a role for TMPRSS2 variants and their expression levels in the regulating the severity of COVID-19; however, further experimental research and a hypothesis that fosters

validation on large cohorts of patients with different clinical manifestations are required [727]. Given the fact that TRPMSS2 is found in the lung, the use of inhibitors of this protease (currently employed for cancer prostate) against COVID-19 pneumonia seems a promissory therapeutic tool. Additionally, the assessment of potential drugs that interfere with androgen activity, such as androgen receptor inhibitors, steroidogenesis inhibitors, and 5-alpha reductase inhibitors, has been suggested [702].

Finally, it is well established that androgens play inhibitory roles in the inflammatory response, and the evidence indicates that reduced TES levels associated with age or comorbidities may increase the pro-inflammatory response in men, contributing to the development of a severe form of COVID-19. In this context, the quantification of TES levels may be considered when a COVID-19-positive patient is identified. Moreover, if the values are low, the use of testosterone has been remarkably proposed to reduce the associated pulmonary syndrome, thus preventing the progression to severe COVID-19 disease [702].

15.5.3.9 Estrogens' Effects on Inflammation in Coronavirus Disease 2019

Emerging studies have suggested that women are less susceptible to COVID-19 and exhibit lower mortality than men [670, 671], which may be explained by a potential protective role of estrogens. X chromosome encoding the greatest density of genes related to immune response [728] supposes the immunological advantage of women over males. Interestingly, Channappanavar et al. examined the gender-dependent difference outcomes of the infection by SARS-CoV. They demonstrated that the estrogen depletion by ovariectomy or the use of an ER antagonist increases the morbidity and mortality in SARS-CoV-infected female mice [729]. In addition, they suggested that infected female mice have a sex-specific protection during their reproductive period. These findings strengthen the crucial hypothesis about the protective role of estrogen and the ER signaling against the respiratory virus. Another research group observed that, in an age group of 40–60 years, the transcriptomic profile of female lung tissue has more similarities to that evoked upon SARS-CoV-2 infection compared to male tissue [730]. In this regard, characterizing the most activated intracellular pathways during the viral infection may provide a molecular explanation of the lower incidence of COVID-19 in females.

The estrogen/ER signaling regulates the development of immune cells and the pathways of innate and adaptive immune system [731–733]. It appears that the development and severity of COVID-19 depend on individual propensities for the massive release of pro-inflammatory mediators [674, 676]. Data have pointed out that high doses of E2 may inhibit the production of inflammatory cytokines (IL1, IL6, and TNF-α), whereas stimulation with low doses of E2 enhances the production [734–736]. It was proved that, in the early phase of antiviral immune response against SARS-CoV infection, pro-inflammatory mediators (IL-6, CCL2, and CXCL1) display similar increased levels in both sexes and 72 h post-infection these cytokines are upregulated in the lung of male mice compared with females [729]. To understand this finding, it has been suggested that monocyte-macrophage recruitment is suppressed by estrogens, which favor the downregulation of CCL2/MCP-1 expression and inhibit NF-κB activation in macrophages [737, 738]. Similarly, reduced TNF-α and CCL2 levels are observed in gonadectomized mice treated with estrogen, which protect them from influenza virus infection [739, 740]. Furthermore, in SARS-CoV-infected mice, the predominant sources of these pro-inflammatory mediators are the inflammatory monocyte macrophages (IMMs) [741]. In male mice, these cells are increased in numbers and also produced more mediators compared with female mice [729]. Additionally, increased numbers of IMMs in ovariectomized mice compared with intact female mice suggest that estrogen signaling in females abolishes the accumulation and function of IMMs in the lung [729]. Moreover, it has been reported that the downregulation of IL-6 gene expression by E2

is induced via the interaction of the estrogen receptor with NF-κB [742].

Zheng et al. showed in an observational study that, the humoral response in seriously ill male patients exposes a delayed peak of antibody response with a lower generation of effective IgG compared to women [722]. Females exhibit a predominant Th2 cytokine profile, which could be involved in immune responses characterized principally by the secretion of antibodies [743]. Estrogen significantly enhances the generation of a Th2 response [233, 744], corresponding to the findings that this hormone increases the frequency of antibody secreting B cells in the follicular phase (when the levels of estrogen are high) of the menstrual cycle in rhesus macaques. Furthermore, the stimulation of a CD8 + -enriched cell population induced the expression of IFN-γ and IL-12 [745]. These findings are actually attributable to estrogen influence on B-cell proliferation, activation, and maturation by upregulating the expression of CD22, Src homology region 2 domain-containing phosphatase-1 (SHP-1), and B-cell lymphoma 2 (Bcl-2) [733, 746]. Finally, it has been hypothesized that estrogens could protect women from the most serious complications of COVID-19, especially women before the menopause due to high serum estrogen levels [747].

15.6 Conclusions

Inflammation is a complex biological process that involves multiple immune mechanisms. The literature confirms the influence of sex hormones on the incidence and severity of the inflammatory response in lung diseases. The effects of sex steroids have been observed in pathophysiological conditions of the lung related to diseases such as asthma, COPD, lung fibrosis, lung cancer, and COVID-19. This chapter highlights the importance of sex-specific research taking into account the hormonal status of the patients. Moreover, sex steroid actions depend on very particular circumstances such as the hormone concentration, duration of the stimulus, genomic or non-genomic pathway, and interaction between male and female sex hormones. The evidence indicates that sex hormone actions on the inflammatory response can be beneficial or detrimental. Generally, male sex steroids have beneficial anti-inflammatory properties in asthma, COPD, and other lung diseases. On the other hand, E2 displays anti-inflammatory and pro-inflammatory properties on lung diseases. It is crucial to consider that the effects of sex hormones on the inflammatory responses in lung diseases need to be further explored in order to find novel therapeutic approaches and pursue an individualized medicine in the future.

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Declaration of Interest Figures in this book chapter were created with BioRender.com. The authors declare that they do not have a conflict of interest or financial relationship that may have influenced the work.

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Synopsis of Clinical Acute Respiratory Distress Syndrome (ARDS)

16

Archana Mane and Naldine Isaac

Abstract

The entity of acute respiratory distress syndrome (ARDS) is an acute inflammatory lung condition associated with lung damage and increased vascular permeability. In the ICU, ARDS was reported to be the cause of 10.4% of admissions. The syndrome is associated with conditions such as sepsis, burns, trauma, and many others. The Berlin Definition which is the most up-to-date definition defines ARDS as an early onset of severe and refractory hypoxemia, PaO2/FiO2 ratio less than 300 mmHg, bilateral infiltrates on chest x-ray, and alveolar edema not explained by a cardiogenic cause or fluid overload.

The entity of ARDS and its treatment have been studied for many years to better understand it and help find therapies. However, the mainstay of medical management is supportive with specific strategies for mechanical ventilation. No specific drug therapy is available at present.

In this chapter, the history, clinical picture, and therapeutic approaches to ARDS will be discussed. We include lung-protective ventilation, prone positioning, use of neuromuscular blockade, corticosteroids, as well as discussion of studies done on this important clinical and morbid condition. We emphasize that there are ongoing trials and research being done to better identify patients earlier in their clinical course so that supportive care with lung-protective ventilation and a conservative fluid approach can be implemented. We also mention promising therapies such as cell-based therapies which would help in decreasing lung inflammation.

Keywords

Acute respiratory distress syndrome (ARDS) · Definition · Diagnostic criteria · Inciting events · Ventilator strategies · Future therapies

16.1 Introduction

Acute respiratory distress syndrome (ARDS) is a severe respiratory response to damage of the lungs leading to acute respiratory failure and often multi-organ failure. Medical management of this common and clinically morbid condition is constantly evolving. With multiple therapies under evaluation and ongoing research, this field of lung injury remains challenging and imperative, as it carries a high rate of mortality [1].

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Part of the challenge in identifying effective therapeutic modalities can be attributed to the complex pathogenesis of this syndrome along with the insensitive and nonspecific diagnostic criteria used to diagnose ARDS. (These may also contribute to the under-detection of ARDS by clinicians.) The definition of ARDS has been reported to have a relatively low specificity of 51% [2].

Up until the 1990s, the mortality rate for ARDS was reported to be as high as 40–70%. A better understanding of the disease etiology, recognition of its management by specific mechanical ventilation protocols, and early treatment has contributed to the decline in mortality [3]. More recently, mortality has been correlated with increases in disease severity. According to Bellani et al., unadjusted ICU and hospital mortality rates were reported to be 35% among those with mild ARDS, 40% for moderate disease, and 46% for severe ARDS. The cause of early mortality is most commonly due to the underlying source of the disease. In contrast, nosocomial pneumonia and sepsis are the most common causes of death among patients who die later in their clinical course. It is less common for patients to die from the respiratory failure alone [4].

16.2 The Evolving Definition of ARDS

The historical identification and description of the syndrome of ARDS are interesting, dating back to the work of Laennec in 1821. He first documented pulmonary infiltrates in the lungs of trauma patients which he called "idiopathic pulmonary edema" or "shock lung" [5]. In 1964, Ashbaugh and his colleagues made some noteworthy observations in 12 civilian patients who were victims of trauma and other conditions such as hemorrhagic pancreatitis. Over a period of 24 hours, these patients developed respiratory distress with severe hypoxemia, fluffy infiltrates on x-ray, and the need for increased ventilatory pressures [6].

They published their findings in *The Lancet* in 1967 which was read by military surgeons who were able to identify these findings in Southeast Asia during the Vietnam War when previously healthy young servicemen developed respiratory failure after trauma that did not respond to oxygen therapy [7].

More recently in 1994, the American Thoracic Society and the European Society of Intensive Critical Medicine established a task force to address discrepancies in identifying the mechanism, incidence, outcomes, and preventative strategies for ARDS globally. The definition for ARDS included "arterial oxygen tension/fractional inspired oxygen (PaO2/FIO2 ≤200 mmHg) regardless of the level of positive end-expiratory pressure (PEEP), bilateral pulmonary infiltrates, and no evidence of left heart failure as measured by pulmonary wedge pressure" [8, 9].

In 2011, the definition was updated to its current definition due to ongoing concerns over the reliability of the definition. The reliability of the chest radiographic criteria of ARDS by this definition has been demonstrated to be moderate, with substantial interobserver variability. In addition, the hypoxemia criterion (i.e., PaO2/FiO2 <200 mmHg) was in question as it could be markedly affected by the patient's ventilator settings, especially the PEEP level used. Finally, the wedge pressure was considered difficult to interpret, and if a patient with ARDS develops a high wedge pressure, that should not preclude diagnosing that patient as having ARDS [10, 11].

16.3 Today's Definition of ARDS

The Berlin Definition declared a new classification of ARDS in 2011. All four of the following criteria must be met to diagnose the condition:

1. Acute onset: respiratory failure or significant worsening of respiratory status <1 week of a predisposing factor.
2. Imaging: bilateral chest opacities on chest x-ray or CT.

3. Respiratory failure must not be explained by heart failure or fluid overload.
4. Hypoxemia:
   (a) Mild: PaO2/FiO2 ratio ≤300 and >200
   (b) Moderate: PaO2/FiO2 ratio 100–200
   (c) Severe: PaO2/FiO2 ratio <100 [12]

Of note, a lesser form of respiratory failure is known as acute lung injury (ALI). While ARDS defines hypoxemia as a PaO2/FiO2 < 200 mmHg, ALI is defined as a PaO2/FiO2 < 300 mmHg [13].

16.4 Etiology

There are a multitude of factors that can lead to the development of ARDS. These possibilities can be divided into two categories: pulmonary ARDS or extrapulmonary ARDS [14] (Table 16.1, Fig. 16.1).

Table 16.1 Pulmonary ARDS vs extrapulmonary ARDS

	Pulmonary ARDS	Extrapulmonary ARDS
Etiology	Direct insult to the lung (trauma, contusion, pneumonia, aspiration)	Sepsis, smoke inhalation, intra-abdominal infections, pancreatitis
Site of damage	Alveolar epithelium	Vascular endothelium
Ventilator duration	~28 days	~28 days
Chest x-ray	Alveolar consolidation, intra-alveolar damage	Ground-glass appearance from interstitial edema
Treatment with PEEP, lung recruitment, prone positioning	Not as effective	Effective
CT	Extensive consolidation with equal amounts of normal lung and ground-glass opacification (Fig. 16.1)	Predominantly ground-glass opacification (Fig. 16.1)

16.5 Pathophysiology of ARDS

In pulmonary ARDS, injury originates at the thin alveolar membrane which is largely composed of Type 1 pneumocytes responsible for gas exchange. In extrapulmonary ARDS, the site of injury is at the vascular endothelium [1]. Both result in damage that occurs in three stages.

1. Exudative Stage: Cellular damage results in the release of pro-inflammatory cytokines such as tumor necrosis factor (TNF), IL-1, and IL-6. Neutrophils are activated and release additional toxic mediators. This leads to the movement of fluid from the vasculature that contains plasma proteins, red blood cells, and leukocytes. The fluid enters the alveoli resulting in pulmonary edema, preventing the adequate exchange of oxygen across the membrane. Additionally, damage to the surfactant-producing alveolar Type 2 cells causes alveolar collapse.
2. Proliferative Stage: In response to injury, alveolar Type 2 cells proliferate to regenerate the endothelium, and remodeling occurs. This leads to decreased lung compliance.
3. Fibrotic Stage: Some patients progress to an irreversible fibrotic stage. The inflammatory exudates result in the scarring of the lung tissue leading to fibrosis, cysts, and permanent changes to the architecture of the lung [15].

16.6 Risk Factors for ARDS

16.6.1 Age

With increasing age, the incidence of ARDS rises. After the age of 74, the incidence has been reported to be as high as 73.9 cases per 100,000 individuals [5].

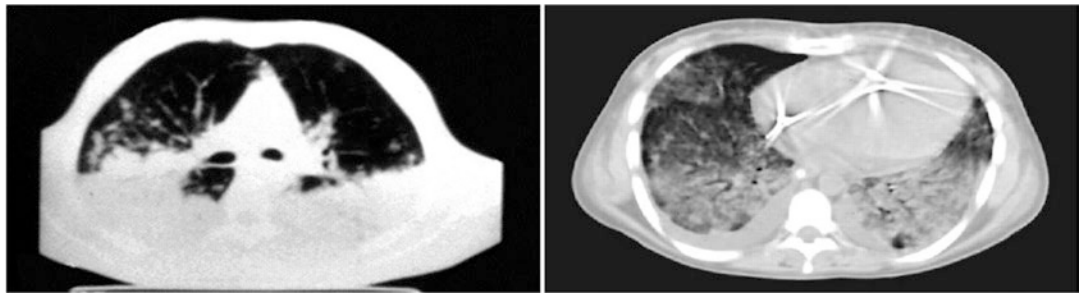

Fig. 16.1 The computed tomography of the lungs showing ground-glass opacities (especially in the posterior gravity-dependent portions) with some normal lung tissue (*left*) and more diffusely dispersed bilateral ground-glass opacities (*right*). (The images were taken from a previous publication by Pelosi et al. [14])

16.6.2 Burns

Incidence of ARDS in burn patients depends on the severity and ranges between 22% and 56%, making it one of the leading causes of death among burn patients [16]. Inhalation burns and full-thickness burns covering over 20% of the total body surface area were determined as risk factors for the development of ARDS [17].

16.6.3 The Obesity Paradox

Obesity carries an increased likelihood of developing ARDS due to increased inflammatory cytokines and impaired pulmonary vascular homeostasis. Obese patients have altered pulmonary mechanics and increased incidence of atelectasis and pulmonary mismatch. However, the mortality risk is decreased. The reason for this paradox is unclear, but may be related to the increase in metabolic reserve found in adipose tissue [18].

16.6.4 Alcohol

A meta-analysis by Simou et al. reported that there was an increased incidence of ARDS arising from sepsis in those who abused alcohol. Although the mechanism for this is not well understood, the study postulates that the effects of alcohol on the function of macrophages and the depletion of glutathione may play a role [19].

16.6.5 Diabetes

Diabetes is associated with a decreased incidence of ARDS as shown in many but not all studies. This reduced incidence is seen in both Type I and Type II diabetes. Diabetes may reduce development of ARDS through a compromised immune system and attenuation of cytokine release and impairment of neutrophil function [20].

16.7 Clinical Presentation

Generally, the clinical presentation of ARDS develops within 24 hours. Respiratory symptoms such an acute onset of tachypnea, cough and decreased oxygen saturation by pulse oximetry develop. Lung auscultation may be normal, but as the syndrome progresses, rales are often heard. The patient may complain of chest pain and experience tachycardia. As illustrated in Fig. 16.2, the chest radiography shows patchy infiltrates that progress to diffuse opacities [15].

Analysis of arterial blood gases plays a critical role in the evaluation and management of ARDS. More specifically, it allows a provider to assess oxygenation as a marker of the severity of ARDS. Additionally, the alveolar-arterial gradient can detect the degree of hypoxemia [21].

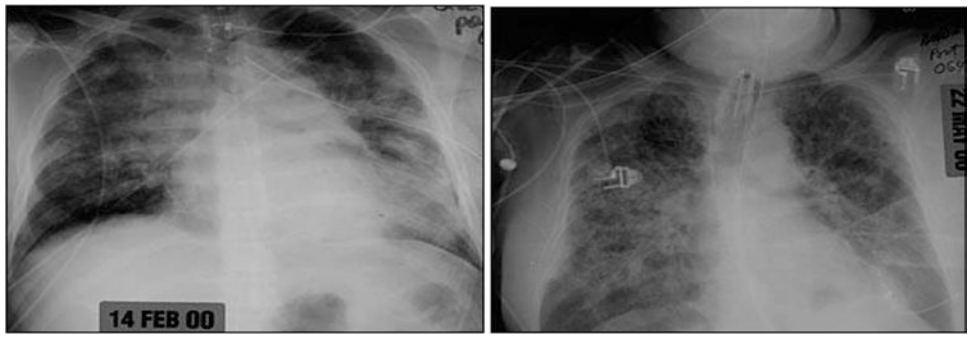

Fig. 16.2 Chest x-ray taken during early ARDS, showing that the opacities are patchy and less dense than those observed in later stages (*left*), and during late ARDS, illustrating the consolidation and bilateral infiltrates that are dispersed throughout the lung tissue (*right*). (The images were adapted from a previous study [15])

16.8 Management of ARDS

The variety of clinical presentations makes it challenging to treat. Additionally, patients can deteriorate rapidly over the span of hours leading to refractory hypoxemia. The mainstay of treatment is mechanical ventilation and supportive care.

Other possible methods include prone positioning, neuromuscular blockade, sedation, fluid management, corticosteroid therapy, and management of stress ulcers.

GRADE (Grading of Recommendations Assessment, Development and Evaluation) Method: The quality of evidence from various studies is analyzed and given a score that determines the reliability of the recommendation for therapy. GRADE 1 demonstrates a high level of validity, while a GRADE 4 signifies lower validity of evidence [22], as shown in Fig. 16.3. GRADE 1 recommendations include maintaining low tidal volume, limiting plateau pressure, placing patients in the prone position for at least 12 hours a day, and avoiding the use of oscillatory ventilation. GRADE 2 recommendations supported the utilization of PEEP in moderate and severe ARDS for the recruitment of the lungs, as well as the use of muscle relaxants and extracorporeal membrane oxygenation (ECMO) [22–24].

16.8.1 Mechanical Ventilation

The utilization of low tidal volumes via endotracheal intubation (~6 ml/kg) has been shown to reduce mortality when compared to higher tidal volume (~12 ml/kg) therapy from 39.8% to 31%. Lower tidal volumes reduce the overdistension of the alveoli that would otherwise lead to volutrauma and barotrauma. PEEP is employed to help prevent lung damage by inhibiting the cyclic opening and closing of alveoli and reducing shear stress [25].

16.8.2 Non-invasive Methods of Ventilation and Oxygenation

Ventilatory modes such as pressure support, bilevel positive airway pressure (BiPAP), and continuous positive airway pressure (CPAP) may be used with devices such as a venturi mask or a high-flow nasal cannula. This method is reserved for patients presenting with mild ARDS who are able to maintain their own airway. It is not sufficient for patients with a PaO2/FiO2 lower than 150 mmHg, as it is associated with higher ICU mortality in this population. However, it is important to note that there is not yet enough research on these methods of ventilation to support their use [26].

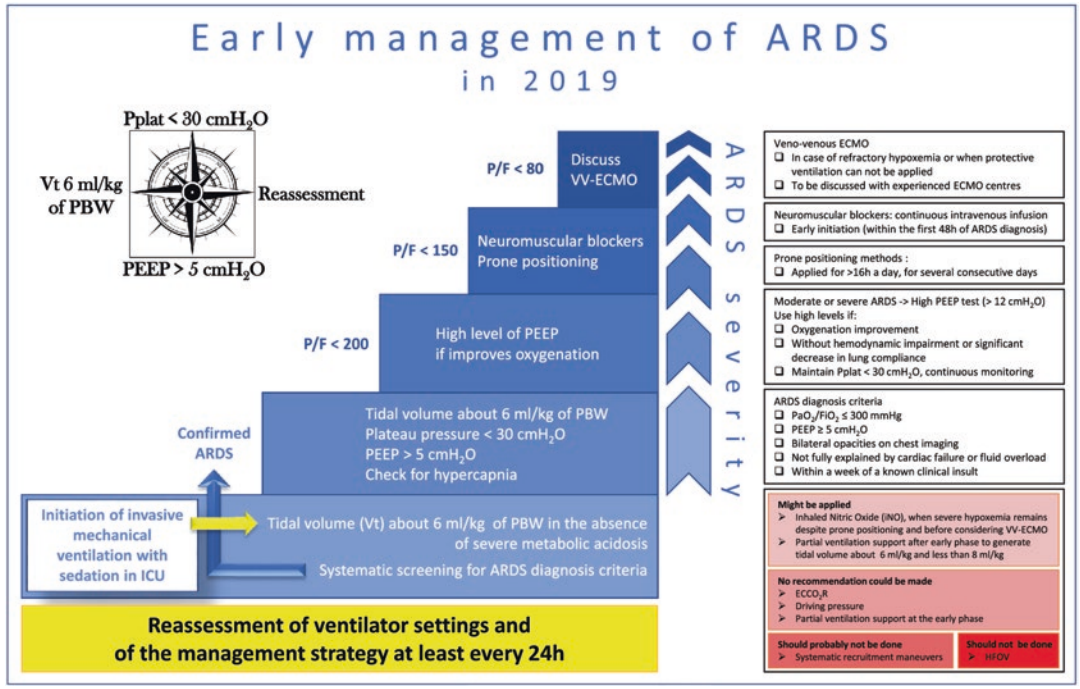

Fig. 16.3 Formal guidelines: management of acute respiratory distress syndrome. (Taken from a previous publication [22])

When all else fails, ECMO may be a possibility, although several studies have not provided enough evidence to support its use. In a study by Combes et al., 60-day mortality was not significantly lower with ECMO when compared to conventional mechanical ventilation that included ECMO as rescue therapy. It still remains an option for severe refractory ARDS [27].

16.8.3 Weaning from Ventilator Therapy

Weaning a patient off of ventilator support depends on the individual's condition. It often takes 24–48 hours, but can be longer.

It involves gradually decreasing FiO2 and PEEP and then shifting to either a spontaneous breathing trial or reduction in the amount of ventilatory support.

16.8.4 Prone Positioning

Prone positioning is a strategy used in order to recruit the dorsal regions of the lungs. This provides better distribution of air throughout the lungs and improves perfusion to the lung tissue. The PROSEVA (Proning Severe ARDS Patients), a large randomized clinical trial, demonstrated a major decrease in mortality rate at 28 and 90 days in patients who were treated with prone positioning within 48 hours of ARDS diagnosis. This treatment involved remaining prone 12 hours a day. At 28 days, prone patients had a mortality rate of 16% compared to 32.8% in supine patients. At 90 days, the mortality rate was 23.6% for prone patients versus 41.0% in the supine group. In addition, prone patients had better outcomes with successful extubation and were weaned from ventilatory support earlier than their supine counterparts [28].

16.8.5 Neuromuscular Blockade Agents (NMDAs) and Sedation in ARDS Management

Invasively ventilated patients are often given neuromuscular blockade requiring sedation to prevent recall. Commonly used sedating agents include dexmedetomidine, propofol, and midazolam as continuous infusions. This combined therapy prevents patient-ventilator asynchrony which is key to reducing the incidence of ventilator-induced lung injury. In severe ARDS, NMBA therapy had a 90-day mortality benefit of up to 9.1% according to ARDS et Curarization Systematique (ACURASYS) trial, an international study. NMBAs assist with lung recruitment which increases oxygenation. Furthermore, NMBAs allow patients to tolerate the endotracheal tube, decrease systemic inflammation, and improve V/Q mismatch [29, 30].

16.8.6 Fluid Management in ARDS

Studies have supported the benefits of negative fluid balance in improving patient outcomes. Limiting the administration of fluids is recommended due to the increased permeability of the pulmonary membranes. Colloid therapy with albumin has been shown to improve oxygenation, although more research is needed. Oftentimes, diuretics are also administered to help with fluid balance [31, 32].

16.8.7 Corticosteroids

Dexamethasone is another potential therapy worth exploring as a means of decreasing the duration of mechanical ventilation and decreasing mortality [33].

16.9 Potential Complications of ARDS

A potential complication of ARDS treatment is ventilator-related injury. Several mechanisms can result in this type of injury:

1. Volutrauma is caused by high tidal volumes and is the most harmful of the VILI.
2. Atelectrauma is caused by repetitive opening and closing of the airway.
3. The interaction of collapsed or fluid-filled alveoli with surrounding alveoli.
4. The endotracheal tube can cause laryngeal edema.
5. A patient may become dependent on the ventilator requiring a tracheostomy.

Other sources of complication include nosocomial infections and antibiotic resistance. Immobility can cause conditions such as DVT and muscle weakness [34, 35].

16.10 Future Directions

Further exploration is being done on pharmacologic therapies such as vitamin C, vitamin D, thiamine, corticosteroids, and many others [36].

Finelli et al. claimed that those being treated with a low tidal volume ventilation of 6 ml/kg may still suffer from VILI. He proposed that an even lower tidal volume ventilation of 4 ml/kg may provide more benefit. A barrier preventing this decrease in ventilation is the potential accumulation of CO2. His group is therefore now studying extracorporeal carbon dioxide removal [37].

Another potential therapy targets the FLT1 gene which encodes vascular endothelial growth factor receptor 1 (VEGFR-1). The goal is to use VEGFR-1 to repair the vascular endothelium [38].

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17

Redox and Inflammatory Signaling, the Unfolded Protein Response, and the Pathogenesis of Pulmonary Hypertension

Adiya Katseff, Raed Alhawaj, and Michael S. Wolin

Abstract

Protein folding overload and oxidative stress disrupt endoplasmic reticulum (ER) homeostasis, generating reactive oxygen species (ROS) and activating the unfolded protein response (UPR). The altered ER redox state induces further ROS production through UPR signaling that balances the cell fates of survival and apoptosis, contributing to pulmonary microvascular inflammation and dysfunction and driving the development of pulmonary hypertension (PH). UPR-induced ROS production through ER calcium release along with NADPH oxidase activity results in endothelial injury and smooth muscle cell (SMC) proliferation. ROS and calcium signaling also promote endothelial nitric oxide (NO) synthase (eNOS) uncoupling, decreasing NO production and increasing vascular resistance through persistent vasoconstriction and SMC proliferation. C/EBP-homologous protein further inhibits eNOS, interfering with endothelial function. UPR-induced NF-κB activity regulates inflammatory processes in lung tissue and contributes to pulmonary vascular remodeling. Conversely, UPR-activated nuclear factor erythroid 2-related factor 2-mediated antioxidant signaling through heme oxygenase 1 attenuates inflammatory cytokine levels and protects against vascular SMC proliferation. A mutation in the bone morphogenic protein type 2 receptor (BMPR2) gene causes misfolded BMPR2 protein accumulation in the ER, implicating the UPR in familial pulmonary arterial hypertension pathogenesis. Altogether, there is substantial evidence that redox and inflammatory signaling associated with UPR activation is critical in PH pathogenesis.

Keywords

Antioxidant signaling · Cytokines · Endothelial dysfunction · Endothelial injury · NADPH oxidase · Oxidative stress · Protein folding · Pulmonary vascular remodeling · Vasoconstriction

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Abbreviations

Ang II	Angiotensin II
AP-1	Activator protein 1
APx	Ascorbate peroxidase
ARE	Antioxidant response element
ASC	Apoptosis-associated speck-like protein containing a CARD
ASK1	Apoptosis signal-regulating kinase 1
ATF	Activating transcription factor
ATFS-1	Activating transcription factor associated with stress 1
Bach1	BTB and CNC homology 1
BAK	BCL-2 homologous antagonist/killer
BAX	BCL-2-associated X protein
BBF2H7	Box B-binding factor 2 human homolog on chromosome 7
BCL-2	B cell lymphoma 2
BH3	BCL-2 homology 3
BH4	Tetrahydrobiopterin
BIM	BCL-2-interacting mediator of cell death
BiP	Immunoglobulin binding protein
BMPR2	Bone morphogenic protein type 2 receptor
BPA	Bovine pulmonary artery
bZIP	Basic leucine zipper
C/EBP	CCAAT/enhancer-binding protein
CaMKII	Calcium/calmodulin-dependent kinase II
CHOP	C/EBP-homologous protein
CO	Carbon monoxide
COMP	Cartilage oligomeric matrix protein
COPII	Coat protein II
CRE	Cyclic AMP response element
DAMP	Damage-associated molecular pattern
EC	Endothelial cell
ECM	Extracellular matrix
eIF2α	Eukaryotic translation initiation factor 2α
EndMT	Endothelial-mesenchymal transition
eNOS	Endothelial nitric oxide synthase
EPC	Endothelial progenitor cell
ER	Endoplasmic reticulum
ERAD	ER-associated degradation
ERK	Extracellular signal-regulated kinase
ERO1	ER oxidoreductase 1
ERSE	ER stress response element
ET-1	Endothelin-1
FAD	Flavin adenine dinucleotide
FPAH	Familial pulmonary arterial hypertension
GADD34	Growth arrest and DNA damage-inducible 34
GAG	Glycosaminoglycan
GCLC	Glutamate-cysteine ligase catalytic subunit
GCN2	General control nonderepressible 2
GM-CSF	Granulocyte-macrophage colony-stimulating factor
GPx7/8	Glutathione peroxidase 7 and 8
GR	Glutathione reductase
GSH/GSSG	Glutathione (reduced/oxidized)
GSH1	γ-glutamylcysteine synthetase
GST	Glutathione S-transferase
H/R	Hypoxia/ischemia and reoxygenation
H_2O_2	Hydrogen peroxide
HA	Hyaluronan
HDAC4	Histone deacetylase 4
HIFα	Hypoxia-inducible factor α
HIV-PAH	HIV-induced pulmonary arterial hypertension
HO-1	Heme oxygenase 1
HOCl	Hypochlorous acid
HPAEC	Human pulmonary arterial endothelial cell
HPMEC	Human pulmonary microvascular endothelial cell
HRE	Hypoxia response element
HSP47	Heat shock protein 47
IKK	Inhibitor of nuclear factor-κB (IκB) kinase
IL	Interleukin
IP3R	Inositol 1,4,5-triphosphate receptor
IRE1	Inositol-requiring protein 1
ISR	Integrated stress response
IκB	Inhibitor of nuclear factor-κB
JNK	JUN N-terminal kinase
KEAP1	Kelch-like ECH-associated protein 1
LC20	20-kDa regulatory light chain of myosin II
LPS	Lipopolysaccharide

MA	Methamphetamine
Maf	Musculoaponeurotic fibrosarcoma
MAM	Mitochondria-associated membrane
MAPK	Mitogen-activated protein kinase
MCP	Monocyte chemoattractant protein
MCT	Monocrotaline
Mdm2	Mouse double minute 2 homolog
MEF	Myocyte enhancer factor
MIP	Macrophage inflammatory protein
MLCK	Myosin light chain kinase
MMP	Matrix metalloproteinase
NAD	Nicotine adenine dinucleotide
NF-Y	Nuclear transcription factor Y
NF-κB	Nuclear factor kappa-light-chain-enhancer of activated B cells
NIK	NF-κB inducing kinase
NLRP3	Nucleotide-binding oligomerization domain (NOD)-like receptor (NLR) family, leucine-rich repeat (LRR), and pyrin domain (PYD)-containing protein-3
NO	Nitric oxide
NOX	NADPH oxidase
NQO1	NAD(P)H: quinone oxidoreductase 1
NRF2	Nuclear factor erythroid 2-related factor 2
O_2	Oxygen
OASIS	Old astrocyte specifically induced substance
PAEC	Pulmonary arterial endothelial cell
PAH	Pulmonary arterial hypertension
PAMP	Pathogen-associated molecular pattern
PASMC	Pulmonary artery smooth muscle cell
PCNA	Proliferating cell nuclear antigen
PDI	Protein disulfide isomerase
PERK	Protein kinase RNA-like endoplasmic reticulum kinase
PH	Pulmonary hypertension
PHD	Proline hydroxylase
PI3K	Phosphoinositide-3 kinase
PKB	Protein kinase B
PKC	Protein kinase C
PP1C	Protein phosphatase 1C
PRxIV	Peroxiredoxin IV
PTP	Permeability transition pore
PUMA	p53 upregulated modulator of apoptosis
QSOX	Quiescin sulfhydryl oxidase
RHAMM	Receptor for HA-mediated motility
RIDD	Regulated IRE1-dependent decay
ROS	Reactive oxygen species
RVSP	Right ventricle systolic pressure
S1P	Site 1 protease
S2P	Site 2 protease
SFN	Sulforaphane
SMC	Smooth muscle cell
SOD	Superoxide dismutase
SRXN-1	Sulfiredoxin-1
Tat	Trans-activator of transcription
TGFβ	Transforming growth factor β
TIM	Translocase of the inner membrane
TLR	Toll-like receptor
TNF-α	Tumor necrosis factor α
TOM	Translocase of the outer membrane
TRAF	Tumor necrosis factor receptor-associated factor
Treg	Regulatory T cell
TRx	Thioredoxin
TXNIP	TRx interacting protein
UGT	UDP glucuronosyl transferase
UPR	Unfolded protein response
UPR^{am}	UPR activated by protein mistargeting
UPR^{mt}	Mitochondrial UPR
UPS	Ubiquitin-proteasome system
VDCC	Voltage-dependent calcium channel
VHL	Von Hippel-Lindau
VKOR	Vitamin K epoxide reductase
VPO1	Vascular peroxidase 1
XBP1	X-box binding protein 1

17.1 Introduction

17.1.1 Relevance of Redox Modulation of the Unfolded Protein Response to Pulmonary Hypertension

Within a cell, the processes of protein translation and post-translational modification are highly regulated. All secretory proteins, resident proteins of the secretory pathway organelles, and membrane surface proteins are co-translationally

inserted into the endoplasmic reticulum (ER) lumen for processing [204]. The ER handles approximately 30% of proteins that are folded in a typical cell, with an even higher percentage [83] in specialized secretory cells.

Secretory proteins are translated directly into the ER lumen, where they mature to the proper conformation by acquiring post-translational modifications, including the introduction of disulfide bonds between cysteine residues [22]. This folding process involves oxidation and reduction as disulfide bonds are added, removed, and shuffled around within the protein as it acquires its shape [94]. Proper protein folding and maturation requires the integration of multiple signals and feedback mechanisms [83].

Protein overexpression can overload the folding capacity of the ER, during which proteins are translated but cannot be folded and exported fast enough to accommodate for the influx of nascent polypeptides [83]. Misfolded proteins accumulate and oxidative stress increases within the ER lumen to activate the unfolded protein response (UPR), which is conserved in eukaryotes from yeast through humans and controls the fate of the stressed cell [184]. First, there is an adaptive response aimed at restoring homeostasis. If the adaptive phase is insufficient and the stress is prolonged, the UPR promotes apoptosis [255]. The UPR regulates several cellular processes including energy homeostasis, inflammation, and cell differentiation [197]. Importantly, altered redox homeostasis is involved in the activation of the UPR as well as downstream of the UPR, and may lead to the development of several diseases [212].

Pulmonary hypertension (PH) is a rare and incurable life-threatening disease in which mean pulmonary arterial pressure is greater than 25 mm Hg at rest as measured by right heart catheterization [87]. PH is characterized by pulmonary vascular remodeling at the different layers of the vascular wall: proliferation and dysfunction of endothelial cells of the intima as well as the pulmonary artery smooth muscle cells (PASMCs) of the media [34, 219]. The adventitia lacks precise boundaries in the human lung, making it difficult to measure remodeling, but the adventitia does play a role in PH as a hub for signaling interactions between local fibroblasts and arriving macrophages [190, 221]. Nevertheless, pulmonary vascular remodeling in PH results in a thickening of at least two levels of the vascular compartment [236].

Expansion of the extracellular matrix (ECM) is involved in vascular remodeling at all layers [230]. Excess production of secreted ECM proteins may overload the ER of pulmonary vascular cells to trigger UPR signaling and PH progression. Interestingly, PH patients have upregulated UPR genes [129], and several recent studies have shown UPR activation in PH models using rodents and cultured PASMCs [29, 60, 264, 265]. Conditions leading to PH including hypoxia and endothelin-1 (ET-1) production induce elevated pulmonary vascular pressure and exacerbate oxidant formation [35, 141, 250], which may stimulate UPR signaling to further PH pathogenesis in a feed-forward manner. However, little is known about the precise pathways connecting UPR activation with the development of PH.

This chapter will present information indicating that altered ER redox homeostasis serves to activate the UPR as well as signaling downstream of the UPR, potentially leading to PH. First will be a definition of the UPR and a brief discussion of the redox-related aspects of the adaptive and apoptotic phases following activation of each UPR sensor. Next will be a discussion of the role of redox in protein folding at the ER and how these thiol redox mechanisms activate the UPR and may play a role in PH. Finally, other redox mechanisms both upstream and downstream of the UPR will be discussed along with their implications in PH.

17.2 The UPR Is Redox-Regulated and Promotes Redox Signaling

17.2.1 Chronological Order of the Stress Response

The UPR is a response to stress that consists of several complementary adaptive mechanisms, both transcriptional and non-transcriptional. This

has been well-covered in several other reviews [83, 84, 184, 204, 220, 255], but we will include a description here of the events relevant to redox signaling and PH. The collective function of these responses is to reduce the unfolded protein load at the ER and increase its folding capacity. The ER has several sensors that send information about the status of the ER lumen to the nucleus and cytosol where the UPR is carried out.

The most immediate adaptive action after activation of the UPR sensors is the phosphorylation of eukaryotic translation initiation factor 2α (eIF2α), which deactivates it [78]. This significantly slows the translation of new proteins, because eIF2α is necessary for the initiation of translation. At the same time, degradation of misfolded proteins begins through the process of macroautophagy, including ER-phagy, in which portions of the ER including misfolded proteins are degraded in lysosomes [83].

The slower actions of the UPR involve the activation of transcription factors that promote gene expression to relieve ER stress, which takes more time than phosphorylation. These UPR-activated genes are involved in adaptive processes such as expanding the ER membrane [218], ER-associated degradation (ERAD) to eliminate misfolded proteins via the proteasome [234], translating more folding chaperones [244], and increasing quality control by preventing certain proteins from entering the ER [101]. The redox balance of both the cytosol and the ER is affected by antioxidant genes that are upregulated via the UPR-activated protein activating transcription factor 4 (ATF4) and others [83].

Finally, the UPR shifts to become pro-apoptotic if the ER stress or cellular damage is prolonged or severe. Excess reactive oxygen species (ROS) contribute to mitochondrial damage and apoptotic signaling, resulting in cell death [255].

17.2.2 Specific Actions of Each UPR Sensor

Sensors of ER stress that carry out the UPR reside in the ER membrane. They are all activated by ER luminal stress but primarily act on the cytosolic side of the membrane [204]. One sensor, inositol-requiring protein 1 (IRE1), is also sensitive to cytoplasmic stress [91]. Each sensor can be affected by altered redox homeostasis and may also activate downstream mechanisms to either correct or potentiate the redox state, depending on whether UPR activity is adaptive or pro-apoptotic.

17.2.2.1 IRE1

IRE1 is the most evolutionarily conserved sensor of the UPR [197]. Mammalian cells express both IRE1α and IRE1β, transmembrane proteins with kinase and endoribonuclease activity [43, 171, 233]. During non-stress conditions, IRE1α exists as an inactive monomer in the ER membrane, bound to the chaperone immunoglobulin binding protein (BiP; also called GRP78 and HSPA5). During ER stress, BiP dissociates to interact with unfolded proteins [18], allowing the IRE1α monomers to dimerize or oligomerize and then autotransphosphorylate (Fig. 17.1). There is some evidence showing that phosphorylation is not necessary to activate IRE1, but only a conformational change [196]. Kinase activity may instead attenuate IRE1 endoribonuclease activity, inactivating IRE1 by separating it into monomers [196].

Once IRE1 is activated, the adaptive response begins through its endoribonuclease activity, in which it splices X-box binding protein 1 unspliced (XBP1u) mRNA to the spliced form (XBP1s) [267]. Once XBP1s is translated, it acts as a transcription factor, interacting with the general nuclear transcription factor Y (NF-Y) at gene promoters containing an X-box element or the ER stress response element (ERSE) to regulate expression [204, 267]. The newly expressed genes aid in several processes, including protein folding through the expression of chaperones such as BiP [43].

Another process promoted by XBP1s is the ubiquitination and proteasomal degradation of misfolded ER proteins, known as ERAD [234]. The ubiquitin-proteasome system (UPS) is itself redox-controlled [238]. The 20S proteasome specifically degrades oxidized proteins and is upregulated by elevated ROS and mito-

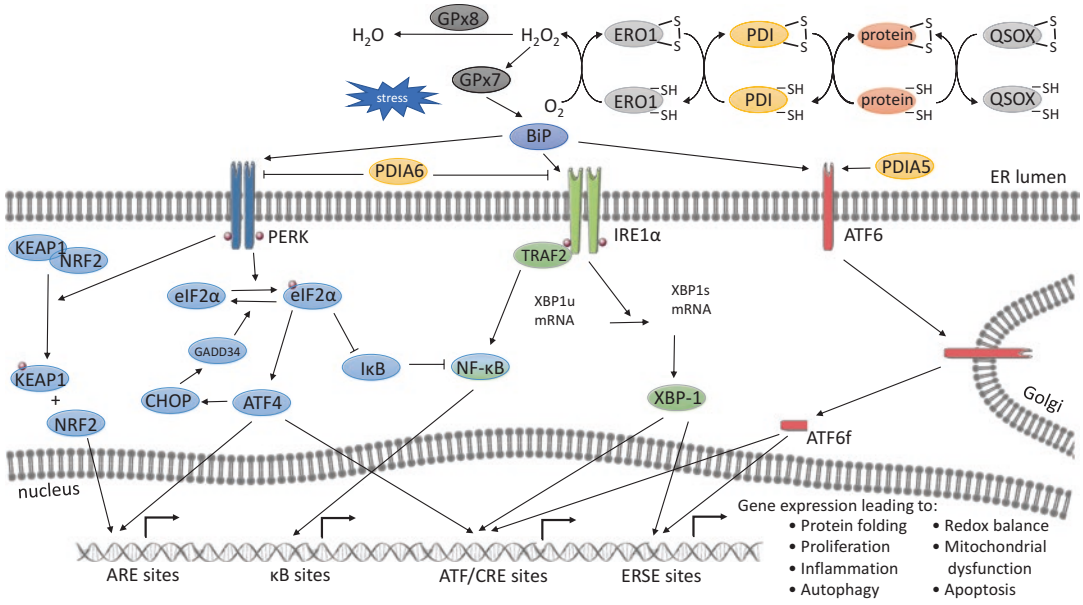

Fig. 17.1 Protein-folding overload activates adaptive and apoptotic UPR signaling to potentially promote PH pathogenesis. Disulfide bond formation in protein substrates occurs though electron relay involving enzymes including protein disulfide isomerases (PDIs), endoplasmic reticulum (ER) oxidoreductase 1 (ERO1), and quiescin sulfhydryl oxidase (QSOX). Excess protein-folding load can overwhelm chaperones, leading to thiol redox-mediated activation of the unfolded protein response (UPR) due to disrupted redox homeostasis. ERO1α has two regulatory disulfide bonds. Disrupting these bonds deregulates the enzyme, resulting in the hyper-oxidation of substrates and production of excess reactive oxygen species (ROS; denoted H_2O_2). Glutathione peroxidase 8 (GPx8) is induced by ER stress and binds to ERO1, converting H_2O_2 to water (H_2O). Some ROS avoids this and oxidizes GPx7, forming a disulfide bond which then oxidizes BiP, allowing BiP to interact more strongly with protein substrates and dissociate from the UPR sensors, promoting UPR activation. If redox homeostasis is restored, UPR signaling ceases. However, if the redox state is not restored, sustained UPR signaling can lead to adaptation or apoptosis. PDIs are active during protein-folding overload, forming and isomerizing disulfide bonds to result in hyperoxidized and misfolded substrates. Specific PDIs activate and inhibit specific UPR sensors to promote and prevent adaptive and apoptotic signaling. The UPR sensors protein kinase RNA-like endoplasmic reticulum kinase (PERK) and inositol-requiring protein 1 (IRE1) are activated by oligomerization associated with disulfide bond formation between monomers after the dissociation of BiP as well as phosphorylation (dark red circles). PERK phosphorylates eIF2α, promoting the transcription of activating transcription factor 4 (ATF4) which regulates transcription in the nucleus at ARE and ATF/cyclic AMP response element (CRE) sites. Activated nuclear factor erythroid 2-related factor 2 (NF-κB) translocates to the nucleus and increases the expression of genes regulating inflammation and autophagy. PERK also phosphorylates the Kelch-like ECH-associated protein 1 (KEAP1)/nuclear factor erythroid 2-related factor 2 (NRF2) complex in the cytosol, allowing the transcription factor NRF2 to dissociate and translocate to the nucleus to upregulate gene expression at ARE sites. IRE1 also acts as an endonuclease to splice mRNA encoding transcription factor X-box binding protein 1 (XBP-1). After translation and nuclear entry, it promotes gene expression at ATF/CRE and ER stress response element (ERSE) sites. ATF6 activity begins at the ER membrane, where disulfide bonds are reduced to produce ATF6 monomers, which travel to the Golgi for processing. The mature ATF6 fragment then acts in the nucleus as a transcription factor at ATF/CRE and ERSE sites. Sustained adaptive and apoptotic signaling from UPR sensors alters gene expression to affect cellular processes in pulmonary artery smooth muscle cells (PASMCs) and endothelial cells (ECs), leading to pulmonary hypertension (PH). TRAF2 tumor necrosis factor receptor-associated factor 2

chondrial dysfunction. It is also redox-activated by glutathionylation during oxidizing conditions. However, this shift to the 20S may decrease 26S proteasome activity, promoting the accumulation of non-oxidized misfolded proteins and possibly a further shift away from homeostasis. There is some evidence that the high ratio of oxidized to reduced nicotine ade-

nine dinucleotide (NAD^+:NADH) in the cytoplasm during oxidizing conditions may open and activate the 26S proteasome [238]. While the UPS is clearly subject to redox control, the precise nature of this control is still under debate.

Other gene products upregulated by XBP1s act to deny ER entry to certain nascent polypeptides based on their signal sequences, preventing their translation within the ER and resulting in protein quality control [101]. Another process promotes phospholipid synthesis at the ER, expanding the ER membrane and increasing the volume of the lumen to make more space for folding proteins [218]. These activities all promote a decrease in ER stress through increasing ER folding capacity or decreasing protein folding load at the ER.

Aside from XBP1s, IRE1 also activates the regulated IRE1-dependent decay (RIDD) pathway to degrade mRNA [89]. RIDD decreases protein folding load at the ER by making mRNA unavailable for translation, thus abrogating the need to fold any resulting proteins.

Tumor necrosis factor receptor-associated factor 2 (TRAF2), an adaptor protein, can bind to activated IRE1, which then activates apoptosis signal-regulating kinase 1 (ASK1) and further targets in a signaling cascade eventually leading to "alarm stress pathways" that activate JUN N-terminal kinase (JNK), which is pro-apoptotic and promotes macroautophagy. Other distinct adaptor proteins interact with IRE1 to activate p38, extracellular signal-regulated kinase (ERK), and the pro-inflammatory transcription factor nuclear factor kappa-light-chain-enhancer of activated B cells (NF-κB) [83, 100, 179, 237]. These "alarm stress" pathways promote the reduction of ER stress through increased protein folding or autophagy of misfolded or damaged proteins and organelles. In addition to these adaptive processes, IRE1 may be involved in the apoptosis phase under some conditions, but the mechanism is unclear [83].

17.2.2.2 Protein Kinase RNA-Like Endoplasmic Reticulum Kinase

Protein kinase RNA-like endoplasmic reticulum kinase (PERK) exists as an inactive monomer in the ER membrane during non-stress conditions. During ER stress, PERK monomers are activated by dimerization and autotransphosphorylation (Fig. 17.1). Once phosphorylated, PERK dimers are active kinases [77]. PERK activity is perhaps most important during the early stages of the UPR.

The adaptive response begins with the phosphorylation of eIF2α, a protein required for the initiation of translation at a ribosome [77]. Phosphorylation of eIF2α inactivates most translation initiation [79]. Importantly, phosphorylated eIF2α represses translation of the NF-κB inhibitor IκB, thus activating NF-κB, a redox-sensitive transcription factor that regulates gene expression at κB sites in the promoters of genes that regulate inflammatory processes [51, 112, 173]. However, phosphorylated eIF2α does allow for the selective translation of ATF4, which is expressed at low levels during unstressed conditions [78]. The ATF4 protein is a transcription factor for genes involved in adaptive processes including autophagy, amino acid metabolism, and the antioxidant response [204].

PERK signaling also activates nuclear factor erythroid 2-related factor 2 (NRF2), a transcription factor that regulates redox and antioxidant metabolism along with ATF4 [178]. NRF2 is kept inactive in the cytoplasm by associating with Kelch-like ECH-associated protein 1 (KEAP1), which targets NRF2 for proteasomal degradation. KEAP1 contains several redox-sensitive cysteine residues that may affect its ability to interact with NRF2 [88]. PERK phosphorylates this complex to dissociate NRF2, allowing its nuclear import and regulation of gene expression [45]. Additionally, oxidation-dependent aggregation of p62 both stimulates autophagy and allows p62 to occupy the NRF2-binding site in KEAP1, further stabilizing NRF2 [30, 114, 238].

If the ER stress fails to resolve, apoptosis signaling begins, regulated by the B cell lymphoma 2 (BCL-2) family of proteins. Pro-apoptotic BCL-2 homology 3 (BH3)-only proteins such as BCL-2-interacting mediator of cell death (BIM) and p53 upregulated modulator of apoptosis (PUMA) are upregulated, which then activate BCL-2-associated X protein (BAX) and/or BCL-2 homologous antagonist/killer (BAK), promoting permeabilization of the outer mitochondrial membrane and further pro-apoptotic signaling [255].

During the apoptosis phase, ATF4 upregulates C/EBP-homologous protein (CHOP, also known as GADD153) [78, 204]. CHOP both upregulates the expression of BIM and downregulates the expression of BCL-2, an anti-apoptotic BH3-containing protein. Additionally, ATF4 directly upregulates BH3-only proteins including PUMA [255]. ATF4 and CHOP also promote growth arrest and DNA damage-inducible 34 (GADD34) expression. GADD34 then upregulates a phosphatase complex including protein phosphatase 1C (PP1C), which dephosphorylates eIF2α and promotes the resumption of translation [180]. This causes further oxidative stress at the ER, generating ROS and ultimately leading to apoptosis.

17.2.2.3 Activating Transcription Factor 6 (ATF6)

ATF6 is different from IRE1α and PERK, which have enzymatic activity and are inactive as monomers. ATF6 represents a group of structurally similar basic leucine zipper (bZIP) transcription factors in the ATF6α/β and old astrocyte specifically induced substance (OASIS) families [266]. They are specialized in their activation, tissue distribution, and response element binding [5]. Interestingly, the OASIS family member box B-binding factor 2 human homolog on chromosome 7 (BBF2H7) is strongly expressed during ER stress in the lungs, as well as the long bones, spleen, gonads, and nervous system [115]. ATF6 is kept inactive in non-stress conditions through glycosylation as well as oligomerization via intra- and inter-peptide disulfide bridges, which trap it at the ER membrane. During ER stress, ATF6 is under-glycosylated, reduced, and monomeric [90, 220]. It is then free to be sent to the Golgi for additional processing and activation. Some OASIS family members lack both sites for BiP interaction and a Golgi-localization sequence, and hence they are activated by an alternate mechanism [5, 175].

The adaptive response to ER stress begins with the transport of monomeric ATF6 from the ER to the Golgi apparatus via coat protein II (COPII)-coated vesicles [36, 203]. Once at the Golgi membrane, site 1 protease (S1P) and site 2 protease (S2P) cut ATF6 at specific sites to release a cytosolic fragment (ATF6f) that can travel to the nucleus [263]. ATF6f interacts with DNA, acting as a transcription factor at the ER stress-response element (ERSE) to upregulate the expression of genes for components of ERAD as well as XBP1 [266]. XBP1 itself, as described earlier, promotes the transcription of genes involved in several adaptive processes, including ERAD, protein folding, and quality control. ATF6f, ATF4, and XBP1s all partially overlap in the target genes whose expression they regulate (Fig. 17.1). Both the type of stress stimulus and the cell type affect the activation of the UPR and the gene products that are ultimately expressed to produce the adaptive response [83].

17.2.3 Activation of the UPR Sensors

The mechanism for activation of the UPR has been studied most extensively in IRE1α, which probably does not directly recognize unfolded proteins in mammals [83]. There is evidence that PERK interacts directly with misfolded proteins, causing its oligomerization and subsequent activation [246]. The individual UPR sensors respond to stress signals; here there will be a focus on the signals caused by misfolded proteins that are related to the redox state of the ER.

During non-stress conditions, the ER chaperone BiP binds to the inactive IRE1α and PERK monomers, suppressing their oligomerization or dimerization. During ER stress, BiP is required

to fold excess unfolded or misfolded proteins. BiP must dissociate from the UPR sensors to interact with these misfolded proteins [18]. This allows the free UPR sensors IRE1α and PERK to dimerize or oligomerize and begin activation through autotransphosphorylation. However, the activation of each of the individual UPR sensors is dependent on slightly different regulatory mechanisms. For example, IRE1α may specifically require heat shock protein 47 (HSP47) to help displace BiP [208]. Also, deleting the BiP-binding site on IRE1 does not alter the induction of ER stress, indicating that other factors govern the activation of the UPR [110].

BiP also binds ATF6 family members during normal conditions, blocking the Golgi-localization signal and retaining them at the ER [209]. In non-stress conditions, ATF6 family members are sufficiently glycosylated, and the lectin-like ER chaperone calreticulin may interact with them to further retain them at the ER. ER stress conditions result in under-glycosylated ATF6, which is unable to interact with calreticulin [90]. The disulfide bridges that oligomerize ATF6 must be also be reduced before ATF6 can travel to the Golgi as monomers.

The UPR is highly regulated by complex feedback mechanisms, which allows for responses that are dynamic and diverse that may be either transient or sustained. The UPR pathways are not linear or parallel. There is overlap among the UPR pathways: for example, ATF6 and XBP1s can form a heterodimer, promoting transcription of the same genes [210]. Redox metabolism and inflammation pathways also interact both upstream and downstream of the UPR sensors, which together play a role in PH.

17.2.4 Mitochondrial UPR Redox Signaling Activates the UPR

The mitochondrial genome encodes 13 essential proteins that are localized in the mitochondria. The remainder of the proteins that reside in the mitochondria are nuclear-encoded and are translated on cytosolic ribosomes [161]. They must be imported through both mitochondrial membranes via the translocase of the outer membrane (TOM) and the translocase of the inner membrane (TIM) [31]. Once inside the mitochondria, these polypeptides must be folded with the help of chaperones to achieve their proper conformations. This echoes the protein folding that takes place in the ER lumen, and oxidative stress at the mitochondria can similarly disturb protein folding [161].

Mitochondrial stress, including increased ROS due to respiratory chain dysfunction, can activate the cytosolic kinase general control nonderepressible 2 (GCN2) as part of the integrated stress response (ISR), which, like PERK, phosphorylates eIF2α to slow general protein synthesis and alleviate oxidative stress [8, 80]. During mitochondrial stress, there is a reduced ability to import nascent polypeptides, resulting in the accumulation of misfolded proteins in the cytosol. The UPR activated by protein mistargeting (UPR^{am}) is one response that promotes decreased protein synthesis and the proteasomal degradation of these potentially toxic proteins [257]. There is also an adaptive mitochondrial UPR (UPR^{mt}) coordinated by the activating transcription factor associated with stress 1 (ATFS-1) that promotes the expression of mitochondrial chaperones, proteases, protein import components, and ROS detoxification enzymes [177].

The exchange of calcium between the ER and the mitochondria at the mitochondria-associated membrane (MAM) ties mitochondrial stress to ER stress [214]. Additionally, ROS produced during mitochondrial metabolic stress enhances UPR activation of XBP1 and CHOP associated with inflammation marked by interleukin (IL)-23 and IL-6 expression [168]. If the UPR is insufficient to resolve oxidative stress, severely damaged mitochondria are degraded via mitophagy as a last resort [6, 161]. A prolonged UPR^{mt} might delay or impair mitophagy. Interestingly, there is evidence of increased mitochondrial fragmentation, indicating inadequate mitophagy, in PASMCs of PH patients [153].

17.3 Thiol Redox Dysregulation During ER Protein Folding Activates the UPR, Leading to PH

17.3.1 Thiol Redox and Protein Folding Overload Cause ER Stress, Leading to UPR Activation

Protein folding at the ER is stabilized by the formation of disulfide bonds [204]. Disulfide bond formation between cysteine residues in a protein is an oxidative process that can help maintain stability, allowing the protein to remain functional in the potentially harsh extracellular environment [22]. This process essentially requires both a source of oxidizing equivalents and an enzyme to catalyze the electron transfer. An understanding of the process of disulfide bond formation during protein folding illustrates the role of dysfunctional thiol redox homeostasis in the activation of the UPR, potentially leading to the development of PH.

17.3.2 The Role of Glutathione in Protein Folding

Glutathione is abundant in animal cells, so it is considered the major cellular redox buffer and was previously considered to be the source of oxidizing equivalents for disulfide bond formation [151]. Glutathione in its reduced form (GSH) is a tripeptide consisting of glutamate with a gamma peptide linkage to glycine, which has a peptide linkage to cysteine. Oxidized glutathione disulfide (GSSG) contains a disulfide bond between the cysteines of two glutathione molecules. Due to its abundance, the redox state of the local cellular environment is indicated by the redox state, or ratio, of the two forms of glutathione [10].

More than half of the glutathione in the ER is in the form of mixed disulfides with proteins [14]. These mixed disulfide bonds are likely to be with both nascent polypeptides that are in the process of folding and exposed free thiols on mature resident ER proteins, both membrane-bound and within the ER lumen. It is not known whether these mixed disulfides are formed with specific proteins or a broad range, but there are a few potential consequences [14]. First, glutathionylation of proteins can affect their function if the active site requires a free thiol group [14]. Additionally, any bound glutathione may contribute even further to the redox buffering capacity of the ER lumen. Importantly, the fact that glutathione forms bonds with ER proteins shows that it plays a role in protein folding, even if it is not required as the major contributor of oxidizing equivalents [14]. The ER environment must be tightly regulated, as a change in the redox state in either direction can affect ER function [10].

The concentration of glutathione in both the cytoplasm and the ER is about 1–10 mM or higher [94, 95]. However, the redox ratio in each compartment differs. In the cytoplasm, the ratio of reduced glutathione to glutathione disulfide ranges from 30:1 to 100:1 but in the secretory pathway, which includes the ER, the ratio is closer to 3:1 [61]. This indicates that the ER is a more oxidizing environment than the cytoplasm. More recent studies using fluorescent probes to report directly from the ER lumen in live cells suggest that the ER may be more reducing than originally thought, perhaps with a GSH:GSSG of 35:1 [94]. However, the ER is still considered to be a more oxidizing environment than the cytoplasm.

One reason for this oxidizing nature is that reduced glutathione, which is synthesized in the cytoplasm, is capable of slow, mediated transport across the ER membrane, but oxidized glutathione disulfide is trapped inside the ER [9, 49]. Furthermore, there is very little glutathione reductase (GR) in the ER lumen, so glutathione remains in its oxidized form [186]. This trapped glutathione may then slowly convert into mixed disulfides with ER proteins.

There has been some debate over whether glutathione acts as an oxidant, a reductant, or that it simply reflects the oxidative ER milieu [49]. Previously, glutathione was thought to provide oxidizing equivalents for protein folding [204]. However, *Saccharomyces cerevisiae* (budding

yeast) mutants lacking the γ-glutamylcysteine synthetase (GSH1) gene, which is required for glutathione biosynthesis, can form disulfide bonds at their normal rate, indicating that GSSG is not required as an oxidant [67].

The most accepted current model suggests that glutathione is not a source of oxidizing equivalents, but that GSH acts as a reductant, or electron donor, for PDI and its protein substrates, allowing disulfide bonds to be isomerized until the protein achieves its final conformation [10, 151]. This is in parallel with another thiol reducing pathway involving thioredoxin (TRx) and thioredoxin reductase [49]. Fortunately, GSH is less likely to reduce native disulfides on proteins due to the oxidizing nature of the ER lumen [22].

17.3.3 Disulfide Bond Formation as an Electron Relay

Protein disulfide formation is catalyzed by an electron relay system independent of glutathione in which oxygen (O_2) is the ultimate electron acceptor (Fig. 17.1). The process is mediated by thiol-oxidoreductase enzymes including ER oxidoreductase 1 (ERO1) and the protein disulfide isomerase (PDI) family as the main ER protein folding chaperones [10]. ERO1 shuttles oxidizing equivalents via its flavin adenine dinucleotide (FAD) cofactor to PDI. There is evidence in vitro showing that ERO1 oxidizes PDI. However, there is conflicting evidence regarding whether ERO1 is required to oxidize glutathione in yeast [46, 235].

17.3.4 Formation of Disulfide Bonds in Protein Substrates Occurs Through a Thiol Redox Mechanism

PDI and other thiol-oxidoreductases help to catalyze thiol-disulfide exchange with protein substrates [33]. Two reduced thiols in the protein substrate are exchanged with an oxidized disulfide in a thiol-oxidoreductase enzyme such as PDI. The thiol-oxidoreductase, now in the reduced thiol form, must subsequently be reoxidized to the disulfide by a thiol oxidase such as ERO1 to regain its oxidative activity. The protein substrate contains a new disulfide bond; disulfide bonds are often formed due to the spatial proximity of cysteine residues, even if the bond is not part of the final conformation of the protein substrate. Disulfide bonds can be rearranged until the substrate achieves the final conformation [118]. Other ER chaperones such as BiP detect exposed hydrophobic regions of the protein, which often indicate an incorrect or unstable conformation [61, 204]. The disulfide bonds are progressively rearranged until the hydrophobic regions are no longer exposed.

PDI catalyzes protein folding in a variety of substrates, acting as both an oxidase to introduce new disulfide bonds and an isomerase to rearrange incorrect disulfide bonds. PDI consists of four TRx-like domains: two A domains and two B domains [275]. The A domains are catalytically active and carry out the oxidase activity. The B domains are redox-inactive, but the full protein is required to perform the isomerase activity. PDI introduces disulfide bonds co-translationally, acting as a placeholder that is removed when the two cysteine thiol groups of the protein substrate are paired [118]. The enzymes in the TRx superfamily that catalyze thiol-disulfide exchange share a structural fold and a highly conserved Cys-X-X-Cys motif in the active site [69, 118].

The reaction mechanism for both oxidase and isomerase activity of PDI involves the formation of a mixed disulfide between the N-terminal cysteine in the PDI active site and a cysteine in the protein substrate [69, 118]. The difference arises in the initial redox state of the PDI active site and the protein substrate. For oxidase activity, the PDI active site cysteines are initially oxidized in the form of a disulfide bond. After the oxidized PDI active site disulfide forms a mixed disulfide with a reduced cysteine in the protein substrate, another reduced cysteine in the substrate attacks the mixed disulfide to release reduced PDI, resulting in a new disulfide bond in the substrate [69, 118]. For isomerase activity, the PDI active site cysteines are initially in the reduced thiol form. The reduced N-terminal PDI active site

cysteine forms a mixed disulfide with an existing disulfide bond in the substrate. The C-terminal cysteine in the PDI active site then reacts with the mixed disulfide to release oxidized PDI and a reduced protein substrate with free cysteine residues [69, 118].

17.3.5 Thiol Oxidases Regenerate Oxidizing Equivalents After Substrate Oxidation by PDI

After a disulfide bond is introduced into the protein substrate through PDI oxidase activity as described above, the PDI active site cysteine thiol groups are reduced and must be re-oxidized to the disulfide form before another substrate can be oxidized. This requires a continuous influx of oxidizing equivalents that are usually provided by ERO1, which directly oxidizes PDI [69]. In a yeast model with a conditional loss-of-function Ero1p mutation, protein substrates that usually contain oxidized disulfide bonds remain reduced [68]. Conversely, overexpression of functional Ero1p confers resistance to the reducing agent DTT by promoting oxidation [187].

Some mammalian thiol oxidases for the PDI family, including ERO1α and β and the quiescin sulfhydryl oxidase family (QSOX), use O_2 as the electron acceptor and generate ROS in the form of hydrogen peroxide (H_2O_2) [227]. Other mammalian thiol oxidases in the ER include peroxiredoxin IV (PRxIV), glutathione peroxidase 7 and 8 (GPx7/8), and ascorbate peroxidase (APx), which are ROS scavengers and consume H_2O_2 as the electron acceptor to generate water [272]. These thiol oxidases become reduced when they oxidize their substrates, so they transfer electrons to O_2 or H_2O_2 to regain their oxidative activity. Altogether, this electron relay system maintains the redox homeostasis that is critical to maintaining the oxidative protein folding environment of the ER. However, the use of O_2 as the primary electron acceptor means that excess protein folding activity results in excess ROS, causing ER stress that can activate the UPR.

ERO1, the primary oxidase of PDI, is tightly associated with its FAD cofactor that assists with electron transfer starting at the cysteine thiols of substrate proteins and continuing through PDI to the ERO1 shuttle disulfides to the ERO1 active site to FAD to O_2 [227]. ERO1 activity, as well as overall protein folding, is highly sensitive to levels of free FAD. FAD is rapidly equilibrated between the cytosol and the ER lumen with a robust transport system. This dependence on FAD links protein folding to the metabolic status of the cell [235]. Additionally, mutations in the FAD-binding site cause ERO1 to lose stability as well as its ability to oxidize PDI [53]. O_2 entry and H_2O_2 exit from the flavin cofactor at the ERO1α active site is regulated by a pair of cysteines, Cys208-Cys241, that block the cofactor and are unlocked by forming a mixed sulfide complex with PDI [194]. ERO1 dysfunction and FAD displacement disrupt protein folding, promoting UPR signaling [21].

Alternatively, the QSOX family is capable of directly oxidizing protein substrates without the involvement of PDI (Fig. 17.1). QSOX can fold proteins efficiently as the sole oxidant in conditions where PDI is reduced and is only capable of isomerase activity [94]. QSOX, like ERO1, uses FAD as a cofactor to aid in electron transfer from thiols to O_2. Also like ERO1, QSOX uses a shuttle disulfide to mediate electron transfer from the protein substrate to the active site [113]. In yeast with a deletion of the ERO1 gene, overexpression of the QSOX family member hQSOX1a restores disulfide bond formation, suppressing lethality [32].

Reduced glutathione can compete as a substrate for any of these enzymes. While the oxidation of glutathione is a by-product of protein folding, it also allows glutathione to act as a buffer preventing the overoxidation of true protein substrates [46, 61]. Glutathione may further protect against hyperoxidizing conditions driven by ERO1 in the ER by consuming excess oxidizing equivalents in the place of PDI or protein substrates, preventing oxidative stress and subsequent UPR activation [46].

17.3.6 Thiol Redox Dysregulation Disrupts Protein Folding and Activates the UPR

The presence of misfolded proteins in the ER induces the expression of folding chaperones including BiP and PDI [55, 120]. Additionally, overexpression of GPX1 and PDI1 in yeast rescues correct protein folding [50]. However, if these enzymes are unable to compensate for the protein load, misfolded proteins can accumulate in the ER lumen, generating ROS through fruitless disulfide bond formation and activating PERK and IRE1 signaling. UPR signaling can be attenuated by antioxidants [147], but if left unchecked, the altered redox state may potentially lead to pathophysiological conditions such as PH.

ERO1α activity converts one molecule of O_2 to one molecule of H_2O_2 for each disulfide bond formed, and increased ERO1 activity promotes ER hyperoxidation and stress. ERO1 contains several cysteine residues that can form regulatory disulfide bonds, which might constrain the flexible loop containing the shuttle disulfide and prevent it from migrating to the active site [227]. ERO1α contains two: Cys94-Cys131 and Cys99-Cys104. Deregulating ERO1α by changing cysteine to alanine (C104A/C131A) is hyperoxidizing, highlighting the importance of ER thiol redox balance for regulating thiol oxidase activity to ultimately regulate ER redox balance [75]. Similarly, ERO1β contains two regulatory cysteine pairs: Cys90-Cys130 and Cys95-Cys100. ERO1β mutants lacking these residues or changing cysteine to alanine (C100A/C130A) also increases ERO1β activity, resulting in the hyperoxidation of substrates, protein misfolding, and UPR activation [76]. Indeed, ERO1β was initially characterized as inducible during treatments to specifically elicit the UPR. Additionally, ERO1α is upregulated later in the UPR downstream of CHOP, potentially contributing to apoptosis signaling [227].

The H_2O_2 produced by ERO1 may be cleared by GPx8, which forms a complex with ERO1 (Fig. 17.1). This peroxidase activity is induced by ER stress to protect against ERO1-mediated hyperoxidation [193]. In contrast, PRxIV is not induced in response to ER stress [228]. ERO1 and PDI may operate at increased levels in a futile attempt to fold misfolded protein substrates during high ER load, resulting in excess ROS production [199]. Unresolved ROS production and ER stress due to ERO1α activity is a factor contributing to UPR signaling, including increased expression of BiP [75].

GPx7 (also called NPGPx) acts as a ROS sensor, transmitting oxidative stress signals through thiol redox. ROS promote the oxidized form of GPx7, which has a disulfide bond between Cys57 and Cys86 [192, 249]. Cys86 then binds to Cys41 or Cys420 of BiP, promoting the disulfide bond formation between Cys41 and Cys420. This bond enhances the interaction of BiP with misfolded proteins. Cells lacking GPx7 have impaired BiP activity and are sensitive to oxidative stress [249].

Thiol redox alterations at the specific UPR sensors can affect their activity, altering downstream events. For example, sulfenylation of IRE1 by ROS at Cys715, which is in the kinase activation loop, attenuates canonical UPR signaling by impairing IRE1 kinase activity but promotes the antioxidant response [91].

Members of the PDI family have been shown to directly interact with the ER luminal domains of specific UPR sensors (Fig. 17.1), affecting their activity level and duration of signaling [57]. The PDI family member PDIA6 interacts with Cys148 of IRE1α, preventing Cys148 from forming an interchain disulfide bond during IRE1α oligomerization. This limits IRE1α activation and helps return it to the inactive monomeric form [58]. The depletion of PDIA6 prolongs and increases the amplitude of both IRE1 and PERK signaling in mammalian cells [57, 58]. Additionally, PDIA5 activates ATF6α, reducing the intermolecular disulfide bonds that retain it at the ER and allowing it to be transported to the Golgi for activation after dissociation from BiP [85]. Upregulation of PDIA5 and PDIA6 promotes cell survival, possibly though this redox regulation that both promotes adaptive signaling through ATF6 and inhibits sustained apoptotic signaling of IRE1 and PERK [58]. Additionally, oxidized PDIA1 activates PERK signaling during ER stress in colon carcinoma cells [121].

17.3.7 Alternative Pathways in the ER for Thiol Oxidation Leading to UPR Activation

There are also alternative minor redox pathways involving molecules that may re-oxidize the protein-folding ER enzymes by assisting in the transfer of electrons from reduced thiols to O_2. Dehydroascorbate, the oxidized form of ascorbate (vitamin C), is transported into the ER via facilitated diffusion in species that are unable to synthesize it [176]. It can accept electrons from PDI and other protein thiols, supporting non-enzymatic oxidative disulfide bond formation while itself reducing to ascorbate [10, 94, 176, 252]. Ascorbate can then act at the ER membrane to regenerate tocopherol (vitamin E) from its radical form, allowing it to scavenge radicals and other ROS to prevent lipid peroxidation and ROS accumulation [44]. Also, vitamin K-dependent proteins in the ER require reduced vitamin K as a cofactor during γ-carboxylation. After its oxidation during this process to vitamin K epoxide, reduced vitamin K can be regenerated by accepting electrons from PDI via vitamin K epoxide reductase (VKOR) [94, 243].

Dysregulation of these alternative pathways can lead to UPR signaling. Elevated levels of dehydroascorbate upregulate UPR signaling through BiP, CHOP, and XBP1s in neuroblastoma cells [231]. Treatment of liver cancer cells with menadione, a vitamin K precursor and oxidizing agent, when combined with NADPH depletion, can trigger UPR pro-apoptotic signaling through induction of CHOP and activation of ATF6 and procaspase-4. Interestingly, this signaling does not induce apoptosis via the activation of the effector caspases but instead promotes autophagy [225].

17.3.8 Altered ER Redox Homeostasis and Subsequent UPR Activation Lead to PH

ER protein folding is easily disrupted because of the complexity of the process, which involves a careful balance of folding chaperones, calcium ions, and redox signaling molecules including ROS, glutathione, and FAD; they work together to help fold protein substrates into their final conformations and introduce post-translational modifications such as N-linked glycosylations and the disulfide bonds discussed above [204]. Disulfide bond formation demonstrates how altered thiol redox states of protein-folding chaperones and their substrates can activate specific signaling pathways of the UPR or alter the length or strength of signaling, ultimately affecting cell function and fate. Thiol redox dysfunction within the ER, along with additional redox and antioxidant mechanisms generating ROS and inflammation both upstream and downstream of the UPR sensors, shifts the cell toward either adaptive, potentially dysfunctional, survival; or apoptosis, both of which may contribute to the development or attenuation of PH. For example, ROS including superoxide and H_2O_2 stimulate the proliferation of fetal PASMCs, but antioxidants such as ascorbate slow cell proliferation and even promote PASMC apoptosis [248].

17.4 Hypoxia-Generated ROS Modulates UPR Signaling and PH Development

17.4.1 ROS-Induced UPR Activation Induces Gene Expression to Modulate ROS

The loss of redox homeostasis in the cell promotes oxidative stress, which contributes to the pathogenesis of a vast number of diseases [251]. ROS are generated at very low levels as a by-product of normal oxidative protein folding in the ER, catalyzed by PDI and ERO1α [270]. Increased protein-folding load may cause an accumulation of ROS, which may, in turn, disrupt disulfide bond formation in the ER and interfere with proper protein folding, causing a buildup in misfolded and unfolded proteins in the ER lumen leading to ER stress and UPR activation [188, 204]. ROS-induced ER stress activates the PERK-eIF2α-ATF4 axis, which suppresses global cellular translation and, among other

functions, promotes the expression of several antioxidant genes that modulate ROS [17, 45, 80]. The IRE1α axis is also activated in response to ROS-induced ER stress to splice XBP1 mRNA, allowing the translated XBP1 protein to increase the expression of proteins involved in disulfide bond formation, which attenuates excess ROS generation [58, 198, 267]. The ATF6 axis is also activated in response to ROS-induced ER stress, but it does not appear to be directly involved in modulating ROS.

17.4.2 Hypoxia-Inducible Factor Plays a Key Role in the Cellular Response to Hypoxia

Mammals express three isoforms of the transcription factor subunit hypoxia-inducible factor α (HIFα): HIF1α, HIF2α, and HIF3α. HIF1α is ubiquitously expressed in all cells, while HIF2α and HIF3α are expressed in certain cell types such as vascular endothelial cells, renal interstitial cells, liver parenchymal cells, and type II pneumocytes [20, 146].

Under normoxic conditions, the HIF1α subunit is produced by the cell and marked for degradation by O_2-sensitive proline hydroxylases (PHD). This post-translational regulation is achieved through the hydroxylation of proline residues at the O_2-dependent domain of HIFα [19, 146]. PHD-modified HIFα is then recognized by Von Hippel-Lindau (VHL) E3 ubiquitin ligase, resulting in HIFα ubiquitination and subsequent 26S proteasomal degradation to minimize HIFα half-life in the cell [19, 98].

During hypoxia, decreased O_2 levels inhibit PHD, preventing PHD modification of HIFα and allowing HIFα to escape degradation and accumulate in the cell. HIFα then forms a heterodimer with the constitutively produced HIFβ subunit, yielding the functionally active HIFα/β transcription factor [13, 98]. HIF binds to hypoxia response elements (HREs) in the promoters of key genes, modulating their transcription and translation to result in a cell-wide adaptive response to hypoxia.

17.4.2.1 HIF1α Promotes Redox Homeostasis Through a Metabolic Shift from Oxidative Phosphorylation to Non-oxidative Glycolysis

HIF1α reprograms cellular metabolism by shifting the flow of carbon atoms away from oxidative phosphorylation and toward non-oxidative glycolysis. This metabolic shift lessens O_2 dependence during ATP generation, allowing for minimal ROS production [72]. This shift is achieved through HIF1α-mediated upregulation of glucose transporters and glycolytic enzymes [72]. HIF1α also upregulates pyruvate dehydrogenase kinase 1, which represses the conversion of pyruvate to acetyl-CoA, attenuating the citric acid cycle and by extension oxidative phosphorylation [109]. Moreover, HIF1α upregulates lactate dehydrogenase A, which converts pyruvate to lactate and concomitantly converts NADH to NAD^+, which is required to sustain glycolysis [72].

17.4.2.2 HIF2α Promotes Redox Homeostasis Through the Upregulation of Key Antioxidant Genes

HIF2α contributes to redox homeostasis under hypoxic conditions through the targeted upregulation of key enzymes such as pyruvate dehydrogenase kinase 4, which inhibits mitochondrial utilization of glucose-derived carbon to attenuate oxidative phosphorylation [92]. HIF2α upregulates the expression of mitochondrial superoxide dismutase 2 (SOD2) and the antioxidant heme oxygenase 1 (HO-1) [20, 72]. HIF1α and HIF2α promote increased electron transfer efficiency from cytochrome *c* oxidase to O_2, and by extension increase the efficiency of the electron transport chain under hypoxia [72].

17.4.3 Hypoxia-Induced UPR Activation

Despite the mitigating role played by HIF, hypoxia can result in the deregulation of many mechanisms critical to cellular and ER homeostasis. This can cause unfolded proteins to accumulate in the ER lumen, resulting in ER stress [29]. Hypoxia-induced ER stress activates the PERK, ATF6, and IRE1α UPR sensors [128]. Furthermore, hypoxia induces HIF1α-independent transcription and splicing of XBP1 mRNA [128]. XBP1s, once translated, creates a transcriptional complex with HIF1α and recruits RNA polymerase II. The assembled XBP1s-HIF1α complex regulates the HIF1α transcriptional program and eventually the expression of HIF1α target genes, which ultimately augments and sustains HIF activity and the adaptive response to hypoxia [37].

17.4.3.1 Hypoxia- and ROS-Induced UPR^{mt}

Hypoxia-induced ROS production in mitochondria may interfere with mitochondrial protein folding, causing the accumulation of misfolded or unfolded mitochondrial proteins. This leads to further ROS imbalance and mitochondrial stress, resulting in the UPR^{mt} [70, 125, 136, 161, 174, 177, 211]. The major sensor of mitochondrial stress that triggers the UPR^{mt} is ATFS-1, which under normal conditions is trafficked from the nucleus to the mitochondrial matrix where it is degraded. This import process is disrupted under mitochondrial stress, and ATFS-1 accumulates in the nucleus where it triggers the expression of genes associated with restoring mitochondrial homeostasis, including mitochondrial antioxidant, protease, chaperone, and import machinery [177]. Mitochondrial stress also promotes the phosphorylation of eIF2α, inhibiting cellular translation while augmenting translation of the transcription factors CHOP, ATF4, and ATF5 [13, 256]. All three transcription factors upregulate the expression of UPR^{mt}-associated genes. Additionally, CHOP and ATF4 further induce transcription of ATF5 [8, 62, 125, 161, 174, 191].

17.4.4 The UPR Differentially Employs NOX2 and NOX4 to Mediate Pro-Apoptotic and Pro-Survival Responses with Implications in PH Pathogenesis

Hypoxia and other ER stressors [60, 128] may increase ROS generation through several sources in the cell, including NADPH oxidases (NOXs) [132, 185]. Elevated ROS can activate the UPR to promote both pro-oxidant and antioxidant mechanisms described in detail later in this chapter [181, 205].

UPR Pro-Oxidant Response ROS-activated UPR signaling may mediate a pro-oxidant response that may either confer cell death or survival [80, 82, 181]. A UPR pro-oxidant response may involve a host of ROS sources, including, for example, NOX2 and NOX4. NOX2 is subject to induction through the CHOP-ERO1α-inositol 1,4,5-triphosphate receptor (IP3R)-calcium/calmodulin-dependent kinase II (CaMKII)-NOX2 signaling axis or through JNK-mediated upregulation [131]. NOX2 may contribute to mitochondrial-driven pro-apoptotic signaling pathways, resulting in cell death [82, 131–133, 150, 205]. On the other hand, a UPR pro-oxidant response may also induce NOX4 through the IRE1α-JNK signaling pathway [185]. NOX4 activity is associated with H_2O_2 generation in addition to superoxide, which mediates adaptive signaling and cell survival.

UPR Antioxidant Response Conversely, ROS-activated UPR signaling may promote an antioxidant response through, for example, the upregulation of NRF2. NRF2 attenuates ROS levels through negative feedback, contributing to redox and cellular homeostasis [97, 229].

17.4.4.1 NOX2 and NOX4 Signaling in Pulmonary Vascular Endothelial Cells

Chronic exposure to hypoxia may result in endothelial injury and dysfunction, which is the initial step in PH development and progression.

Prominent mechanisms contributing to endothelial injury include the upregulation of ROS-producing NOX2 and NOX4 to the detriment of the underlying smooth and adventitial cell layers (Fig. 17.2) [2].

NOX2-Mediated Endothelial Cell Apoptosis in HIV-Induced Pulmonary Arterial Hypertension

During the early phases of the HIV-induced pulmonary arterial hypertension (HIV-PAH) disease model, human pulmonary microvascular endothelial cells (HPMECs) upregulate NOX2, which is native to the plasma membrane. NOX2 upregulation is associated with induced augmentation of Ras-Raf-ERK1/2 signaling, resulting in the disruption of endothelial tight junctions to elevate endothelial permeability and dysfunction and contribute to ROS-mediated apoptosis [2].

NOX4-Mediated Endothelial Cell Survival and Proliferation in HIV-PAH

As the disease progresses, HIV-PAH HPMECs upregulate NOX4, which is localized to

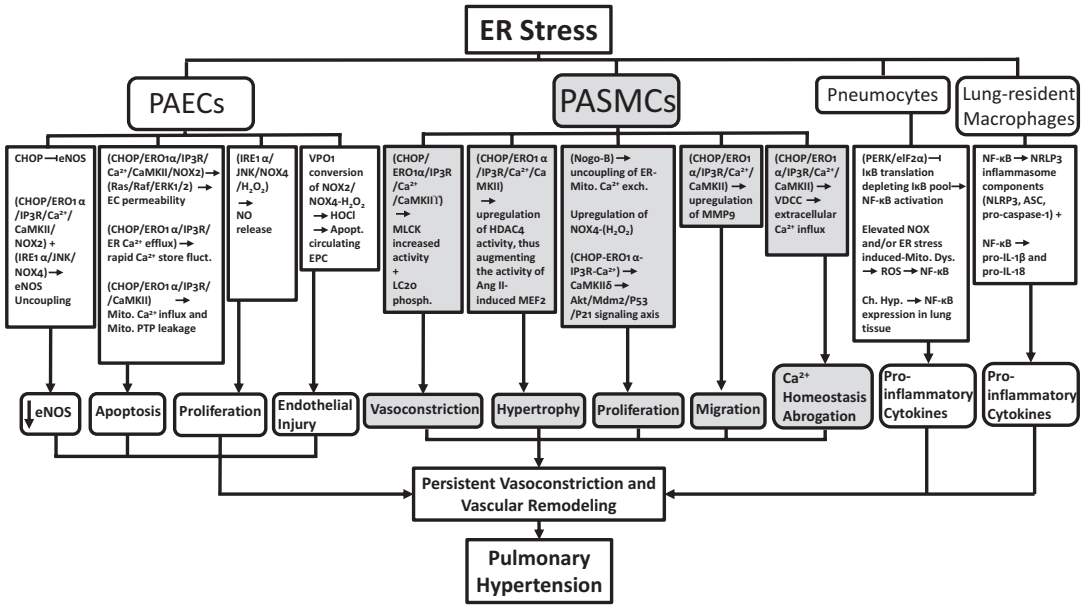

Fig. 17.2 Potential roles for redox-modulated UPR in PH pathogenesis. Increased endoplasmic reticulum (ER) stress initiates a cascade of signaling events in pulmonary arterial endothelial cells (PAECs), pulmonary artery smooth muscle cells (PASMCs), pneumocytes, and lung-resident macrophages. In PAECs, redox-modulated unfolded protein response (UPR) signaling can result in decreased nitric oxide (NO) production, apoptosis, maladaptive proliferation, and injury. In PASMCs, redox-modulated UPR signaling cascades can result in vasoconstriction, hypertrophy, proliferation, migration, and increased cytosolic calcium. In pneumocytes and lung-resident macrophages, these signaling events may result in elevated production of pro-inflammatory cytokines. All together, these signaling pathways converge and culminate in persistent vasoconstriction and vascular remodeling, contributing to the pathogenesis of pulmonary hypertension (PH). Ang II angiotensin II, Apopt. apoptosis, ASC apoptosis-associated speck-like protein containing a CARD, CaMKII Ca2+/calmodulin-dependent protein kinase II, Ch. Hyp. chronic hypoxia, CHOP C/EBP-homologous protein, eNOS endothelial nitric oxide (NO) synthase, ERO1α endoplasmic reticulum oxidoreductin-1α, HDAC4 histone deacetylase 4, IL-1β/IL-18 interleukin-1β/18, IP3R inositol 1,4,5-trisphosphate receptor, IRE1α inositol-requiring protein 1α, JNK c-Jun N-terminal kinase, LC20 20-kDa regulatory light chain of myosin II, Mdm2 mouse double minute 2 homolog, MEF2 myocyte enhancer factor-2, Mito. mitochondria, MLCK myosin light-chain kinase, MMP9 matrix metallopeptidase 9, NOX2/4 NADPH oxidase-2/4, PTP permeability transition pore, IκB inhibitor of κB, NF-κB nuclear factor kappa-light-chain-enhancer of activated B cells, NLRP3 NOD-, LRR- and pyrin domain-containing protein 3, ROS reactive oxygen species, VDCC voltage-dependent calcium channel, VPO1 vascular peroxidase 1

intracellular membranes including the ER and mitochondria. NOX4 upregulation in the late stages of HIV-PAH is associated with ROS-mediated autophagy, which switches the cells to an apoptosis-resistant hyper-proliferative state conferring cell survival and protection. NOX4 upregulation also promotes vascular structural integrity due to the release of NO secondary to NOX4-produced H_2O_2 [2, 181, 205]. NOX4 upregulation eventually results in ROS-induced maladaptive vascular remodeling that has been observed in the monocrotaline- and chronic hypoxia-induced models of PAH, as indicated by the proliferation of adventitial cells and SMCs, elevated right ventricle systolic pressure (RVSP), and right ventricle hypertrophy [12].

17.4.4.2 NOX2 and NOX4 Signaling in Circulating Endothelial Progenitor Cells

Endothelial injuries are mended by either local endothelial cell (EC) replication or by circulating endothelial progenitor cells (EPCs). NOX2 and NOX4 upregulation is not confined to ECs upon exposure to pro-PH conditions such as hypoxia; it is extended to the EPCs that are normally tasked with endothelial repair and homeostasis [28, 247]. In a hypoxia-induced PH rat model, vascular peroxidase 1 (VPO1) mediates the conversion of NOX2- and NOX4-generated H_2O_2 to hypochlorous acid (HOCl), a stronger and more destructive oxidant than H_2O_2 [247]. This HOCl-induced oxidative stress may induce EPC apoptosis and dysfunction interfering with EPC-mediated endothelial homeostasis, further compounding endothelial injury and dysfunction in hypoxia-induced PH.

17.4.4.3 NOX2 and NOX4 Signaling in Pulmonary Vascular Smooth Muscle Cells

Hypoxia, through the activation of ATF6, upregulates the ER structural protein Nogo-B in PASMCs in vitro. Nogo-B promotes the uncoupling of ER-mitochondria calcium exchange, attenuating mitochondrial ROS-mediated pro-apoptotic pathways to confer cell survival and proliferation [224]. Additionally, PASMCs showed elevated NOX4 expression in chronic hypoxia-induced PH animal models [166]. NOX4 knockdown augmented the IRE1α pro-apoptotic effectors JNK-ASK1 and attenuated PASMC proliferation in vitro [166, 185, 200]. Increased NOX4 expression was accompanied by increased ROS production. Interestingly, increased ROS generation was attenuated through GADD34 plasmid transfection, which interfered with UPR signal transduction (Fig. 17.2) [200]. Indeed, NOX4-generated ROS appears to be associated with promoting a pro-survival, and in the case of PH-PASMCs, maladaptive, UPR response, the mechanism of which is not yet clear.

Furthermore, chronic hypoxia may deplete the cartilage oligomeric matrix protein (COMP), which may result in the loss of the bone morphogenic protein type 2 receptor (BMPR2) in isolated bovine pulmonary arteries (BPAs) [268]. Depleted COMP and BMPR2 loss are associated with NOX2 and NOX4 upregulation that contributes to redox imbalance in isolated BPAs [268]. UPR signaling, BMPR2 loss, and other signaling pathways appear to converge at the NOX2 and NOX4 level to drive pro-PH signaling mechanisms in the pulmonary vasculature.

17.5 UPR Signaling Induces Pro-PH Calcium Signaling

17.5.1 Redox Modulation of Calcium Release from the Stressed ER

The ER is the major site of calcium storage in the cell, and ER calcium stores play a significant role in ER stress-response mechanisms. Most ER calcium ions are bound to foldases, chaperones, and other luminal proteins and may aid in protein folding [204]. ER stress leading to prolonged UPR signaling through CHOP induces ERO1α-mediated hyper-oxidation of the ER lumen and may promote IP3R-mediated calcium efflux to the cytosol [86, 150]. This altered ER redox state contributes to rapid fluctuations in calcium stores that may interfere with calcium-mediated protein folding [253], inhibit normal chaperone function, disrupt protein folding, alter protein conformation,

and affect protein-protein interactions in the ER [270]. This promotes further UPR signaling leading to apoptosis in ECs [52, 103, 111, 131, 144, 240, 277] and proliferation in SMCs (Fig. 17.2).

17.5.1.1 ER Stress-Induced Calcium Signaling and ROS Generation Mediate Apoptosis in Pulmonary Vascular ECs

Calcium released from the stressed ER through the CHOP-ERO1α-IP3R signaling pathway as described above [86, 150] binds to CaMKII, which then forms a node for several pro-apoptotic signaling mechanisms [52, 63, 126, 149, 240, 277]. One example is CaMKII-mediated mitochondrial calcium influx, which abolishes the mitochondrial inner membrane potential, promotes mitochondrial ROS generation, and increases mitochondrial permeability through the opening of mitochondrial permeability transition pores (PTPs) [52]. Open PTPs allow leakage of pro-apoptotic mediators such as cytochrome *c* into the cytosol [52, 73, 124, 232]. CaMKII activity is sustained through autophosphorylation and by calcium-CaMKII-independent ROS-mediated oxidation of Met281/282 [59]. Mitochondrial dysfunction-induced ROS can be viewed as part of a positive feedback loop amplifying CaMKII-mediated apoptosis triggered by the stressed ER [232]. In ECs, this aberrant calcium flux-induced apoptosis may result in vascular injury and arteriolar remodeling, contributing to the progression of PH (Fig. 17.2).

17.5.1.2 ER Stress-Induced Calcium Signaling Mediates Remodeling in Pulmonary Vascular SMCs

Contrary to its pro-apoptotic role in ECs, CHOP-ERO1α-IP3R-calcium-activated CaMKII may assume a pro-remodeling role in PASMCs. CaMKII promotes extracellular calcium influx into the cytosol through its modulation of the β3 subunit of voltage-dependent calcium channels [189]. CaMKIIδ also stimulates Akt activation [130] which results in high mouse double minute 2 homolog (Mdm2) phosphorylation at the Akt-specific Ser166 site [273]. This process results in p53 degradation and decreased p21 expression to prevent apoptosis, ultimately conferring vascular SMC proliferation [134, 142]. Moreover, CaMKII may contribute to increased vasoconstriction through the activation of myosin light chain kinase (MLCK) and subsequent phosphorylation of 20-kDa regulatory light chain of myosin II (LC20) [108]. CaMKII also modulates histone deacetylase 4 (HDAC4) activity, contributing to myocyte enhancer factor 2 (MEF2) activation by angiotensin II to promote SMC hypertrophy [133]. Furthermore, CaMKII regulates matrix metalloproteinase 9 (MMP9) expression, which aids in ECM degradation that may allow for PASMC migration [71, 206, 271]. Taken together, ER stress-activated CaMKII assumes divergent roles in ECs and PASMCs, both of which ultimately result in pulmonary arteriolar remodeling contributing to the pathogenesis of PH (Fig. 17.2).

17.6 UPR and ROS Signaling Modulate eNOS, Contributing to PH Pathogenesis

Decreased nitric oxide (NO) in pulmonary arterial ECs promotes endothelial dysfunction, causing persistent vasoconstriction and PASMC proliferation [24, 188]. This increases pulmonary vascular resistance and contributes to PH pathogenesis. NO bioavailability in ECs is regulated by endothelial NO synthase (eNOS) activity, expression, and uncoupling [7, 48, 188, 242].

17.6.1 Calcium-Dependent Regulation of eNOS May Contribute to PH Pathogenesis

eNOS activity is regulated by several factors, including CaMKII. Activated CaMKII mediates Ser1177 phosphorylation in eNOS, increasing NO release [116]. Additionally, calcium-bound calmodulin binds to its specific domain in eNOS,

aligning the eNOS oxygenase and reductase domains and inhibiting protein kinase C (PKC)-mediated phosphorylation of Thr495, both of which promote NO synthesis [116]. Additionally, UPR signaling and ROS generation may negatively modulate eNOS through several mechanisms.

17.6.2 CHOP Inhibits eNOS Expression, Contributing to PH

The ER stress-induced PERK effector CHOP regulates cellular responses including immune and inflammatory responses, cellular differentiation and proliferation, and apoptosis [140]. Under normal physiological conditions, CHOP is minimally expressed, but transcriptional upregulation during ER stress mediates ischemia and hypoxia-induced apoptosis [259]. CHOP inhibits eNOS transcription in ECs through the postulated binding to an optimal CHOP-responsive element at the eNOS promoter [140], directly inhibiting eNOS transcription to confer a wide range of antiangiogenic effects. Inhibited eNOS expression interferes with normal endothelial cell growth, migration, vasodilation, and bone marrow-derived cell-related functions [140]. ER stress-induced CHOP inhibition of eNOS expression underscores its role in modulating postnatal vessel formation and maturation [140] and potential contribution to PH pathogenesis.

17.6.3 ROS Induces eNOS Uncoupling in Endothelia During Chronic Hypoxia and Reoxygenation Injury

In addition to CHOP, chronic exposure to hypoxia and hypoxia/ischemia and reoxygenation (H/R) injury interfere with eNOS function in ECs [48, 140, 259]. Chronic hypoxia and H/R injury elevate oxidative stress in ECs through NOX2 and NOX4, mitochondrial ROS leakage, and ischemia-induced conversion of xanthine dehydrogenase to xanthine oxidase. This conversion hinders the FAD-binding site and allows O_2 to act as an alternative electron acceptor to NAD^+, resulting in superoxide generation [48].

Chronic hypoxia and H/R-mediated ROS generation also result in eNOS uncoupling in which eNOS generates superoxide instead of NO causing endothelial dysfunction and contributing to a variety of cardiovascular diseases [48, 65]. eNOS uncoupling is mediated by ROS through two mechanisms. One is ROS-mediated oxidation of the eNOS cofactor tetrahydrobiopterin (BH_4) to dihydrobiopterin (BH_2), resulting in both forms of biopterin competing for a single eNOS-binding site. The second mechanism is ROS-mediated S-glutathionylation of eNOS, in which elevated ROS disrupts the ratio of reduced to oxidized glutathione in the cytosol. This shift toward GSSG promotes disulfide exchange between GSSG and Cys689 and Cys908 in the eNOS reductase domain, resulting in eNOS S-glutathionylation and uncoupling [48].

In the chronic hypoxia-induced pulmonary hypertension animal model, it has been shown that eNOS is subject to uncoupling [7, 48, 65]. Moreover, eNOS uncoupling exacerbates and further compounds existing oxidative stress in endothelial cells through its aberrant generation of superoxide [65]. Decreased NO bioavailability and increased ROS production may ultimately result in persistent vasoconstriction and SMC proliferation in small pulmonary arteries and arterioles, increasing pulmonary vascular resistance and ultimately contributing to PH pathogenesis [48, 247].

17.7 ROS and NF-κB Signaling Regulate Inflammatory Processes Leading to PH

17.7.1 NF-κB Mediates ER-Based Signals and Is Subject to ROS-Induced Activation

NF-κB is a redox-sensitive transcription factor that regulates the expression of a multitude of genes implicated in inflammatory and immune responses, cell proliferation, and tumorigenesis [81, 245, 260]. NF-κB can be activated through

IκB kinase (IKK)-mediated phosphorylation and subsequent disassociation and degradation of the inhibitory IκB subunit in a polyubiquitin-dependent manner. Active NF-κB subsequently dimerizes and undergoes nuclear translocation [162, 183]. NF-κB can be activated by elevated ROS, which may occur through NOX signaling as well as ER stress induced-mitochondrial dysfunction [183]. NF-κB also promotes increased ROS production [170], enabling a feed-forward loop. Importantly, ER stress and UPR signaling activate NF-κB [181]. PERK phosphorylation of eIF2α inhibits IκB translation, depleting the IκB pool to promote NF-κB activation [258].

Prolonged exposure to hypoxia upregulates the expression of NF-κB in lung tissue [138]. In the nucleus of lung cells, NF-κB regulates the expression of several pro-inflammatory mediator-encoding genes, contributing to pulmonary vascular remodeling and PAH disease state [207, 270]. Moreover, NF-κB regulates inflammatory processes through inflammasome activation [74, 157].

17.7.2 NF-κB Is Critical for Inflammasome Activation to Regulate Inflammation Leading to PH

In response to intra- and extracellular stress signals, a number of multi-protein complexes termed inflammasomes mediate macrophage-driven immune responses that culminate in the production of the pro-inflammatory cytokines IL-1β and IL-18, contributing to the regulation of inflammatory processes [122, 155]. The nucleotide-binding oligomerization domain (NOD)-like receptor (NLR) family, leucine-rich repeat (LRR), and pyrin domain (PYD)-containing protein-3 (NLRP3) inflammasome has been implicated in the progression of several diseases, including PH [123]. NLRP3 activation requires two steps, priming and activation initiation, which attests to the highly regulated nature of the inflammasome response in macrophages.

NF-κB is critical for the priming phase, which occurs in response to extracellular pathogen-associated molecular patterns (PAMPs) recognition by cell surface toll-like receptors (TLRs) and pro-inflammatory cytokine receptors on antigen-presenting cells [56, 66, 96, 148] and/or in response to intracellular damage-associated molecular patterns (DAMPs) such as tumor necrosis factor α (TNF-α) or monosodium urate and calcium pyrophosphate dihydrate crystals [41, 156]. NF-κB mediates upregulation of the NRLP3 inflammasome protein components NLRP3, an apoptosis-associated speck-like protein containing a CARD (ASC) and pro-caspase-1 as well as upregulation of pro-IL-1β and pro-IL-18 [16, 123].

Elevated ROS mediates NLRP3 inflammasome activation at both phases: indirectly during priming, through ROS-induced NF-κB activation [16], and directly during activation initiation, through ROS-induced activation of NLRP3 [241, 275, 276]. Interestingly, all known NLRP3 activators induce ROS production [56, 157, 241, 275]. ROS-induced TRx interacting protein (TXNIP) dissociation from the redox-sensitive domain of TRx allows free TXNIP to bind and activate NLRP3 [275]. In the macrophage-like cell line THP1, NLRP3 activators MSU and R-837 generate ROS and mediate TXNIP dissociation from TRX, which can be prevented by the ROS inhibitor APDC [56]. Elevated H_2O_2 mediates the association of TXNIP with NRLP3, further affirming the role of ROS in NLRP3 inflammasome activation [56, 275].

Upon activation, NLRP3 oligomerizes, then recruits, and activates pro-caspase-1 through ASC [148, 202]. Activated caspase-1 cleaves pro-IL-1β and pro-IL-18 [54], activating them to promote the release of several downstream cytokines that propagate the inflammasome-mediated inflammatory response [15].

17.7.3 NLRP3 Itself Promotes NF-κB Activation Through IL-1β in a Feed-Forward Manner

IL-1β is a pro-inflammatory cytokine activated by the NLRP3 inflammasome that elicits an expansive array of secondary cytokines to trans-

duce inflammatory signaling [239]. IL-1β mediates the feed-forward activation of NF-κB through two known pathways [154, 254]. First, through the activation of the phosphoinositide-3 kinase (PI3K)-Akt/protein kinase B (PKB) signaling axis, IKKα is activated to dissociate IκB from NF-κB as described earlier [25, 154, 254]. Second, IL-1β associates with TNFα and transforming growth factor β (TGFβ) to induce NF-κB inducing kinase (NIK), which in turn activates IKKα and NF-κB.

17.7.4 ROS-Induced Hyaluronan Fragmentation Plays a Major Role in Inflammasome Activation in Chronic Hypoxia-Induced PH

As mentioned, all known NLRP3 inflammasome activators generate ROS, which mediates NLRP3 activation in chronic hypoxia-induced PH [56, 241]. Exposure to hypoxia elevates ROS production, rendering the pulmonary vasculature, including the ECM in the outer adventitial layer, susceptible to oxidative stress [99, 137, 241]. Elevated extracellular ROS may promote the degradation of critical components of ECM such as glycosaminoglycan (GAG) and hyaluronan (HA). The degradation and biosynthesis of HA are implicated in rapid matrix remodeling during processes such as inflammation and tumorigenesis [26, 27, 164]. Chronic hypoxia-mediated ROS generation may cause HA fragmentation, generating biologically active HA fragments that form ligands for the macrophage cell surface receptors CD44, the receptor for HA-mediated motility (RHAMM), and TLR4 [167, 216, 226, 241]. Ligand-activated RHAMM induces macrophage recruitment [165, 241] and TLR4 promotes NF-κB activation and the eventual upregulation of pro-inflammatory cytokines [107, 165]. Interestingly, extracellular ROS-induced HA fragments bound to CD44 receptors trigger NLRP3 inflammasome activation to play a major role in chronic hypoxia-induced PH. In a chronic hypoxia-induced PH model, administration of the superoxide dismutase (SOD) mimetic MnTE-2PyP to reduce ROS production decreases NLRP3 activation, reducing vascular remodeling and attenuating PH development [241].

17.7.5 The Inflammasome Activates Pro-Inflammatory Cytokines Evident in PH

IL-6 is a pro-inflammatory cytokine that can be induced by several upstream pro-inflammatory mediators including IL-1β, TNFα, and TGFβ [25]. IL-1β promotes IL-6 transcription through the PI3K-Akt/PKB signaling axis and activator protein 1 (AP-1) [3, 40, 47, 152, 195], as well as the activation of IKKα-NF-κB and AP-1 to promote further IL-6 expression [25]. Long-term upregulation of IL-6 has been observed during PH [261].

CD4+CD25+ regulatory T cells (Tregs) impart anti-inflammatory effects in PAH and other diseases. Tregs suppress the expression of the pro-inflammatory cytokines IL-1β, IL-6, and monocyte chemoattractant protein 1 (MCP-1) while upregulating the expression of IL-10 in chronic hypoxia-induced PH [42].

17.8 Redox Signaling Via the UPR Sensors Drives PH Progression or Attenuation

17.8.1 UPR Signaling Modulates Oxidative Stress Through NRF2 Activation

NRF2 is an anti-inflammatory and antioxidant transcription factor that is targeted for degradation under non-stress conditions while bound to the ubiquitin ligase adaptor KEAP1 in the cytoplasm [188, 229]. Cellular oxidative stress promotes PERK phosphorylation of this complex to disassociate NRF2 and allow it to translocate to the nucleus [178], where it heterodimerizes to other bZIP proteins at the antioxidant response element (ARE), a specific

cis-acting regulatory element located in the promoter region of several antioxidant and anti-inflammatory genes, to upregulate transcription of target genes [145, 188, 229] including as glutathione S-transferase (GST) A1 and A2 subunits, heme oxygenase 1 (HO-1), sulfiredoxin-1 (SRXN-1), glutamate-cysteine ligase catalytic subunit (GCLC), UDP glucuronosyl transferase (UGT), and NAD(P)H: quinone oxidoreductase 1 (NQO1) [127, 159, 269]. NRF2 is the most important protein for inducing ARE-mediated transcription to counteract oxidative stress and activated inflammatory pathways in the cell (Fig. 17.3) [127, 178].

17.8.1.1 NRF2 Balances Activation and Repression of Antioxidant Gene Expression

Upon heterodimerization with other bZIP proteins, NRF2 and its binding partner form a transcriptional activator or repressor. Transcriptional activators are formed with c-Jun, Jun-B, Jun-D, and ATF4 [178]. Activator heterodimers may compete with transcriptional repressor protein complexes such NRF2-MafK or Maf homodimers for binding to the ARE, exerting transcriptional regulation over antioxidant gene expression [105, 106, 172, 178].

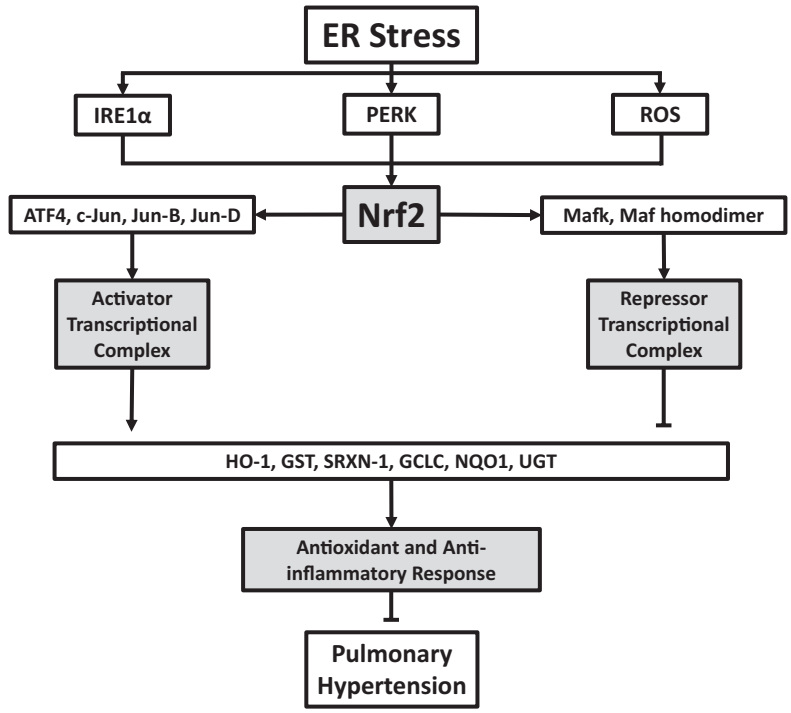

Fig. 17.3 ER stress potentially induces an antioxidant and anti-inflammatory UPR that attenuates the development of PH. Endoplasmic reticulum (ER) stress initiates inositol-requiring protein 1α (IRE1α)- and protein kinase RNA-like endoplasmic reticulum kinase (PERK)-mediated induction of nuclear factor erythroid 2-related factor 2 (NRF2), which can also be activated through elevated cytoplasmic reactive oxygen species (ROS) secondary to ER stress. Activated NRF2 undergoes nuclear translocation where it may form an activator transcriptional complex that binds to the antioxidant response element (ARE) at which it upregulates the transcription of antioxidant and anti-inflammatory genes. This signaling cascade is modulated through the formation of NRF2 transcriptional complex. NRF2-driven antioxidant and anti-inflammatory gene transcriptional upregulation attenuates oxidant stress and triggered inflammatory processes triggered by the initial ER stress, mitigating the pathogenesis of pulmonary hypertension (PH). ATF4 activating transcription factor 4, GCLC glutamate-cysteine ligase catalytic subunit, GST glutathione S-transferase, HO-1 heme oxygenase-1, Maf musculoaponeurotic fibrosarcoma, MafK musculoaponeurotic fibrosarcoma K, NQO1 NAD(P)H: quinone oxidoreductase 1, SRXN-1 sulfiredoxin-1, UGT UDP glucuronosyl transferase

17.8.1.2 NRF2 Activation Is Redox-Mediated

ARE gene expression may additionally be subject to redox regulation. Altered redox status during ER stress may promote ROS-induced modification of cysteine residues on KEAP1, allowing NRF2 dissociation and participation in ARE gene transcription [97, 178]. ARE-expressed proteins such as glutathione-S-transferase and thioredoxin may participate in a negative feedback mechanism. Both proteins are reactive cysteine-based inhibitors of ASK, which activates the JNK and p38 mitogen-activated protein kinase (MAPK) signaling pathways to induce ARE gene expression [1, 39]. Taken together, thiol redox modulation plays a pivotal role in regulating ARE gene expression in response to cellular oxidative stress.

The NRF2 antioxidant response is also promoted through another mechanism mediated by IRE1α. Elevated cytosolic ROS sulfenylate Cys715 at the IRE1α kinase activation loop [91, 117] and attenuate IRE1α kinase activity and canonical UPR signaling. However, sulfenylation also initiates the NRF2 antioxidant response (Fig. 17.3) [91]. The UPR and antioxidant response functions of IRE1α are mutually exclusive, such that elevated ER stress triggers IRE1α UPR signaling, while cytosolic ROS-mediated cytoplasmic stress initiates the IRE1α antioxidant response [91].

17.8.2 IRE1α Regulates and Is Regulated by Innate Immune Pathways

The IRE1α-XBP1 axis contributes to innate immunity by mediating lipopolysaccharide (LPS)-triggered TLR4 signaling in macrophages [158]. Both TLR2 and TLR4 activate NOX2 through the adaptor protein TRAF6, elevating ROS generation to promote IRE1α activation and XBP1 splicing. XBP1s translocates to the nucleus and binds to the promoter regions of pro-inflammatory genes such as IL-6, TNF, and IFN-β, upregulating their transcription [158]. IRE1α may also promote ROS production through NOX and the mitochondria during ER stress [158]. This ROS-IRE1α-ROS feed-forward loop may exacerbate UPR-mediated inflammatory pathways in the cell, contributing to metabolic deterioration and eventually disease [270].

17.8.3 PERK Signaling Contributes to ROS Production Through CHOP

17.8.3.1 CHOP Downregulates BCL-2 Transcription Via GSH Depletion to Promote ROS

Prolonged UPR signaling can result in overexpression of the PERK effector CHOP, which can complex with other transcription factors at the BCL-2 promoter to suppress its transcription and attenuate BCL-2-mediated anti-apoptotic signaling [140, 217]. Increased CHOP levels are also associated with depletion of GSH while GSSG remains unchanged, shifting this ratio to disrupt the cellular redox state and elevating intracellular ROS [160]. The mechanism by which overexpressed CHOP or suppressed BCL-2 may deplete cellular GSH remains unclear, but this ultimately promotes ER stress-induced apoptosis [160].

17.8.3.2 GADD34 Induces ROS Generation and Misfolded Protein Overload

GADD34, which is upregulated by the CHOP-ATF4 signaling axis, activates a PP1C complex to dephosphorylate elF2α. This attenuates the initial global translation inhibition imposed by PERK in the early stages of the UPR [23, 181]. Resuming translation contributes to increased cellular ROS along with misfolded and unfolded protein overload in the ER, while CHOP signaling promotes calcium efflux and apoptosis.

17.9 NRF2 Antioxidant and Anti-Inflammatory Signaling Attenuates PH

17.9.1 The Anti-Inflammatory Role of the NRF2-Induced Heme Degradation Pathway

As mentioned earlier, NRF2 promotes the expression of several antioxidant genes including HO-1, the inducible HO isoform that degrades free

heme, a pro-oxidant, into equimolar amounts of biliverdin, carbon monoxide (CO), and ferrous iron. Ferritin is co-induced with HO-1 to sequester HO-1-generated ferrous iron [93, 104].

Biliverdin reductase converts heme-derived biliverdin to bilirubin. Both biliverdin and bilirubin have antioxidant properties and can interfere with inflammatory cascades by altering the expression of endothelial adhesion molecules and blocking leukocyte adhesion to endothelial cells in the vasculature [11, 139, 222].

HO-1-generated carbon monoxide (CO) confers anti-inflammatory properties by interfering with AP-1 binding to the IL-6 promoter in LPS-activated macrophages through JNK-mediated signaling [104]. In LPS-induced systemic inflammation, CO inhibits the expression of pro-inflammatory IL1-β, macrophage inflammatory protein 1β (MIP-1β), and TNFα. CO also increases the expression of the antioxidant macrophage cytokine IL-10 [163]. Moreover, CO exhibits anti-inflammatory properties during vascular injury [182, 215]. CO, biliverdin, and bilirubin activate MAPK signaling, inhibiting SMC proliferation [274].

17.9.2 HO-1 Activity Attenuates PH Progression

Chronic hypoxia increases the expression of pro-inflammatory cytokines and chemokines in the lungs within the first 2–5 days of exposure, increasing vascular permeability to target ECs, epithelial cells, and monocytes. This leads to leukocyte recruitment, further releasing proteolytic and pro-oxidant mediators promoting vasoconstriction [4, 223, 262]. Chronic hypoxia-induced pro-inflammatory cytokines may induce proliferation in pulmonary vascular smooth cells contributing to vascular remodeling, eventually leading to PH [163]. Moreover, increased HO-1 activity promotes Th-2 cytokine expression, as opposed to Th-1, suggesting a key role for HO-1 modulation of lymphocyte maturation [104]. Interestingly, the lungs of HO-1 overexpressing mice exposed to chronic hypoxia showed attenuated levels of pro-inflammatory cytokines such as monocyte chemoattractant protein (MCP)-1, IL-1β, IL-6, and macrophage inflammatory protein (MIP)-2 [104]. Furthermore, in a monocrotaline (MCT)-induced PAH model, the immunosuppressant agent rapamycin mediates its vascular SMC anti-proliferative effects through HO-1 induction [274].

17.9.3 NRF2 Activation Is Protective Against PAH

NRF2 activation through sulforaphane (SFN) attenuates pulmonary vascular inflammation, remodeling, and fibrosis as well as preventing right ventricle hypertrophy and fibrosis in SU5416- and chronic hypoxia-induced PAH animal models [102]. These effects are associated with NRF2-mediated upregulation of NQO1 and downregulation of NLRP3 [102]. TGF1β-mediated endothelial-mesenchymal transition (EndMT), which contributes to vascular remodeling in PAH, is partially driven by oxidative stress to promote TGFβ1 and TGFβ2 expression and secretion [169]. The NRF2 activator salvianolic acid A may attenuate EndMT and reduce oxidative stress in the pulmonary vasculature through the NRF2 and HO-1 signaling mechanism in PAH [38].

17.9.4 NRF2 Deregulation in PAH Pathogenesis

17.9.4.1 Xenobiotic-Induced NRF2 Deregulation

Abuse of the inhaled form of methamphetamine (MA) may contribute to PAH by preventing NRF2 nuclear translocation, contributing to oxidative stress. This correlates with MA-induced PASMC proliferation, mediated by downregulation of the pro-apoptotic mediators BAX and caspase-3 and upregulation of the anti-apoptotic mediators BCL-2 and proliferating cell nuclear antigen (PCNA) [135]. Taken together, excessive oxidative stress-induced NRF2 deregulation may contribute to pulmonary arterial remodeling in chronic MA-induced PAH.

17.9.4.2 Viral Infection-Induced NRF2 Deregulation

NRF2-ARE activity and target genes are repressed in HIV-PAH concomitant with elevated oxidative stress evident in increased ROS production in human primary arterial endothelial cells (HPAECs) [213]. NRF2 levels were not altered in these HPAECs, but NRF2-ARE-regulated genes were transcriptionally repressed, suggesting differential regulation of NRF2-ARE through other mechanisms. It is possible that the pro-oxidant and pro-inflammatory HIV transactivator of transcription (Tat) can bind to the enhancer element or to AP-1 sequences proximal to the ARE in the promoter region, subverting the transcriptional expression of ARE-regulated genes [213]. Small Maf proteins (sMaf), co-transcriptional factors that normally heterodimerize with NRF2 or with BTB and CNC homology 1 (Bach1), the transcriptional repressor of ARE-regulated genes, contribute to the transcriptional regulation of ARE-driven genes [106]. Tat may modulate sMaf heterodimerization with NRF2 as well as Bach1, mediating the transcriptional repression of ARE-driven genes. This repressed antioxidant gene expression contributes to the impairment of redox homeostasis and elevated oxidative stress in HIV-PAH HPAECs, resulting in endothelial dysfunction, imbalance of endothelial proliferation and apoptosis, and pulmonary arterial remodeling, contributing to HIV-PAH development and progression [213].

17.10 Misfolded BMPR2 Implicates UPR Signaling in Familial PAH Pathogenesis

17.10.1 BMPR2 Mutation or Reduced Expression in FPAH and PAH Pathogenesis

Familial pulmonary arterial hypertension (FPAH), caused by an inherited autosomal dominant mutation, accounts for 6% of PAH cases. A clear association has been established between a heterozygous mutation or reduced expression of a gene that encodes for BMPR2 and with FPAH and PAH, respectively [143]. Interestingly, attenuated expression of the BMPR2 gene is closely linked with vascular inflammation [201]. BMPR2 is part of the TGF-β receptor superfamily, which through SMAD signaling modulates many critical cellular processes including cell differentiation, proliferation, migration, and apoptosis, as well as secretion and deposition of the ECM. BMPR2 is composed of three domains: a ligand-binding domain, a kinase domain, and a cytoplasmic tail [143]. Upon BMPR2 mutation, highly conserved cysteine residues in the ligand-binding domain of BMPR2 are prone to alteration, causing the aberrant protein to be retained and possibly build up in the ER. This accumulation of mutant proteins in the ER may trigger the activation of UPR, implicating it in the pathogenesis of FPAH [265].

17.10.2 Attenuated BMPR2 Expression Promotes Inflammatory Cell Recruitment and Vascular Remodeling in PH

Reduced BMPR2 expression in HPAECs prolongs p-p38-MAPK signaling in response to TNF stimulation. Augmented p-p38 signaling activates the GADD34-PP1 complex, dephosphorylating elF2α to disrupt stress granule formation. Translation resumes, amplifying the synthesis of granulocyte-macrophage colony-stimulating factor (GM-CSF), a powerful chemokine that stimulates stem cell production of granulocytes and macrophages [201]. GM-CSF also mediates macrophage polarization and increased production of the pro-inflammatory cytokines IL-6, IL-8, IL-12, TNF, and leukotriene B4 [64, 119]. Moreover, augmented GM-CSF mRNA translation in HPAECs may induce GM-CSFRα expressing HPAECs to express inflammatory cell adhesion molecules. Uninhibited GM-CSF mRNA translation in HPAECs may promote the recruitment of GM-CSFRα-expressing inflammatory cells to the pulmonary vasculature, mediating enhanced macrophage production of

inflammatory cytokines and increased MMP activity, all of which contribute to vascular remodeling [201]. Altogether, attenuated BMPR2 expression mediates p-p38-dependent deactivation of elF2α stress granule formation, allowing translation of GM-CSF mRNA in HPAECs to promote inflammatory cell recruitment, vascular remodeling, and ultimately the development of PAH.

17.11 Summary and Conclusion

Despite the mitigating role played by HIF, hypoxia can result in the deregulation of a number of mechanisms critical to cellular and ER homeostasis, resulting in ER stress and the onset of UPR. Elevated ER and mitochondrial ROS secondary to hypoxia trigger UPR and UPR^{mt}, respectively. ROS-activated UPR may mediate a pro-oxidant response that may either confer cell death through NOX2 as seen in EPCs in chronic hypoxia-PH and endothelial cells in early HIV-PAH or survival through NOX4 as observed in PASMCs in chronic hypoxia-PH and endothelial cells in late HIV-PAH. UPR-associated NOX4 may also mediate pro-proliferative signaling pathways in PASMCs. On the other hand, ROS-activated UPR may promote an antioxidant response through NRF2, for instance, contributing to redox and cellular homeostasis.

Prolonged ER stress may result in CHOP-induced ERO1α-mediated hyper-oxidation of the ER lumen resulting in IP3R-mediated ER calcium efflux. Rapid fluctuation of calcium stores may contribute to apoptosis. Elevated cytosolic calcium triggers CaMKII-mediated mitochondrial calcium influx contributing to apoptosis in ECs. On the other hand, calcium-triggered CaMKII can initiate an array of signaling cascades that culminate in proliferation and hypertrophy in PASMCs (Fig. 17.4).

Redox-sensitive NF-κB regulates the expression of a multitude of genes implicated in inflammatory/immune response, cell proliferation, and tumorigenesis. NF-κB mediates ER-based signals and is subject to ROS-induced activation. NF-κB promotes ROS production and regulates the expression of several pro-inflammatory mediator-encoding genes in lung cells, contributing to pulmonary vascular remodeling and PAH.

In response to intra-/extracellular stress signals, inflammasomes such as NLRP3 mediate macrophage-driven immune responses that culminate in the production of the pro-inflammatory cytokines IL-1β and IL-18, contributing to the regulation of inflammatory processes. NLRP3 has been implicated in the progression of several diseases, including PH. All known NLRP3 activators induce increased ROS production. Elevated ROS mediates NLRP3 inflammasome activation at both phases: indirectly during priming, through ROS-induced NF-κB activation and directly during activation initiation, through ROS-induced activation of NLRP3. NF-κB-activated NLRP3 promotes NF-κB activation through IL-1β in a feed-forward manner. IL-1β also promotes IL-6 transcription which if sustained may contribute to PH.

Chronic hypoxia-mediated ROS generation may cause HA fragmentation in pulmonary vascular adventitial ECM, generating HA fragment ligands that bind to the following macrophage receptors: RHAMM inducing macrophage recruitment, TLR4 promoting NF-κB activation and the eventual upregulation of pro-inflammatory cytokines, and CD44 triggering NLRP3 activation contributing to the development of chronic hypoxia-PH.

The anti-inflammatory and antioxidant transcription factor NRF2 is targeted for degradation under non-stress conditions. This process is prevented under cellular oxidative stress through PERK-mediated phosphorylation of Nrf2 ubiquitin ligase adaptor, allowing for NRF2 binding to ARE mediating the transcriptional upregulation of many antioxidant and anti-inflammatory genes such as glutathione S-transferase A1/A2 subunits, HO-1, ϒ-glutamyl cysteine synthetase, UDP glucuronosyl transferase, and NAD(P)H: quinone oxidoreductase. NRF2 antioxidant response is also promoted through another mechanism mediated by IRE1α, in which elevated cytosolic ROS sulfenylate Cys715 at the IRE1α kinase activation loop, initiating the NRF2 antioxidant response. HO-1, the inducible HO iso-

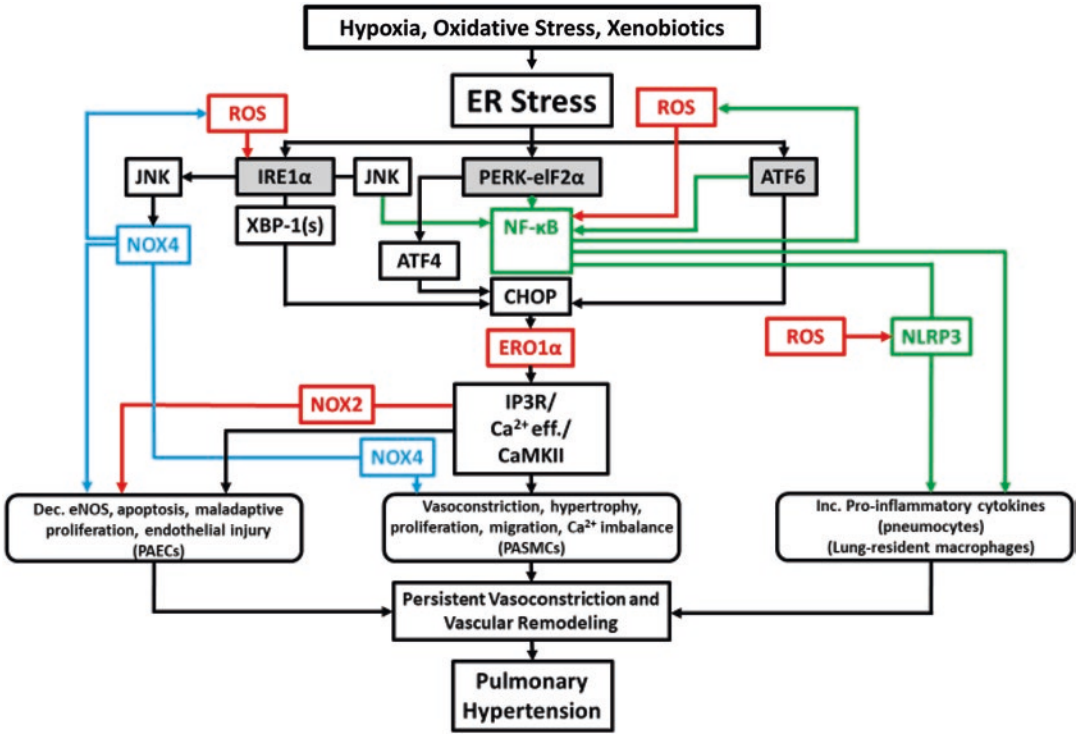

Fig. 17.4 Interplay among redox, inflammatory, and UPR signaling potentially contributes to PH pathogenesis. Hypoxia, oxidative stress, xenobiotics (chemicals and antigens), and other inducers of endoplasmic reticulum (ER) stress trigger the three arms of unfolded protein response (UPR), contributing to elevated reactive oxygen species (ROS) production through NADPH oxidases 2 and 4 (NOX2, NOX4) and the mitochondria, along with elevated cytosolic calcium and nuclear factor kappa-light-chain-enhancer of activated B cells (NF-κB)/nucleotide-binding oligomerization domain (NOD)-like receptor (NLR) family, leucine-rich repeat (LRR), and pyrin domain (PYD)-containing protein-3 (NLRP3)-mediated inflammasome activation. These signaling events result in decreased nitric oxide (NO) production, apoptosis, and maladaptive proliferation and injury in pulmonary arterial endothelial cells (PAECs), while potentially augmenting vasoconstriction, hypertrophy, proliferation, migration, and further cytosolic calcium imbalance in pulmonary artery smooth muscle cells (PASMCs). In pneumocytes and lung-resident macrophages, triggered UPR and elevated cytosolic calcium and ROS converge to activate NF-κB/NLRP3 which contribute to the upregulation of pro-inflammatory cytokines. These signaling events culminate to cause persistent vasoconstriction and vascular remodeling in pulmonary small arteries and arterioles, elevating pulmonary vascular resistance and contributing to the development of pulmonary hypertension (PH). Redox signaling mediators are represented in red and blue boxes, while inflammatory signaling mediators are shown in green boxes. ATF 4 and 6 activating transcription factor 4 and 6, CaMKII calcium-/calmodulin-dependent kinase II, CHOP C/EBP-homologous protein, ERO1α ER oxidoreductase 1α, IP3R inositol 1,4,5-triphosphate receptor, IRE1α inositol-requiring protein 1α, JNK JUN N-terminal kinase, PERK protein kinase RNA-like endoplasmic reticulum kinase, XBP1 X-box binding protein 1

form, is a key NRF2/ARE-driven antioxidant gene that degrades free heme, a pro-oxidant, into equimolar amounts of biliverdin, CO, and ferrous iron, all three of which have antioxidant and anti-inflammatory properties that attenuate the progression of PH. The NRF2 activator, salvianolic acid A, may attenuate EndMT and reduce oxidative stress in the pulmonary vasculature through the NRF2/HO-1 signaling mechanism in PAH. NRF2 mediates upregulation of NQO1 and downregulation of NLRP3, which are associated with attenuated pulmonary vascular inflammation, remodeling, and fibrosis in SU5416/chronic hypoxia-PAH. Furthermore, oxidative stress-induced NRF2 deregulation may contribute to pulmonary arterial remodeling in chronic

MA-induced PAH. NRF2/ARE activity and target genes are repressed in HIV-induced PAH concomitant with increased ROS production in HPAECs. This may result in endothelial dysfunction, endothelial proliferation/apoptosis imbalance, and pulmonary arterial remodeling contributing to HIV-induced PAH.

This repressed antioxidant gene expression contributes to the impairment of redox homeostasis and elevated oxidative stress in HIV-induced PAH PAECs, resulting in endothelial dysfunction, endothelial proliferation/apoptosis imbalance, and pulmonary arterial remodeling contributing to HIV-induced PAH development and progression.

ARE gene expression may additionally be subject to redox regulation. Altered redox status during ER stress may promote modification of cysteine residues on Keap1 and allow the dissociation of NRF2 to participate in ARE gene transcription. ARE-expressed proteins such as glutathione-S-transferase and thioredoxin may participate in a negative feedback mechanism. Both proteins are reactive cysteine-based inhibitors of ASK, an inducer of ARE gene expression.

LPS-triggered TLR2/TLR4 through TRAF6-NOX2-ROS signaling promote IRE1α-XBP1 UPR axis, upregulating transcription of pro-inflammatory genes such as IL-6, TNF, and IFN-β in macrophages. ROS-activated IRE1α may also promote further ROS production through NOX and the mitochondria in a feed-forward (ROS-IRE1α-ROS) loop which may exacerbate UPR-mediated inflammatory pathways in the cell.

ER-stress induction of PERK-CHOP downregulates the transcription of the pro-survival bcl2 gene via GSH depletion promoting elevated cellular ROS, which ultimately promotes ER stress-induced apoptosis. CHOP-ATF4 upregulation of GADD34 induces ROS generation through attenuating PERK-induced elF2α phosphorylation/inactivation, an event that may also result in overloading the ER with misfolded/unfolded proteins. Elevated ROS and ER overload promote cell death. ER stress-induced CHOP has been shown to inhibit eNOS transcription in ECs through the postulated binding to an optimal CHOP-responsive element at the eNOS promoter potentially contributing to PH pathogenesis.

Chronic hypoxia and H/R-mediated ROS generation results in eNOS uncoupling through oxidation of biopterin and eNOS S-glutathionylation. Decreased endothelial NO bioavailability and increased ROS production may result in persistent vasoconstriction and PASMC proliferation ultimately contributing to PH pathogenesis.

Upon BMPR2 mutation, highly conserved cysteine residues in the ligand-binding domain of BMPR2 are prone to alteration, causing the aberrant protein to be retained in the ER triggering UPR that may contribute to the pathogenesis of FPAH. Furthermore, attenuated BMPR2 expression deactivates elF2α stress granule formation, allowing translation of GM-CSF mRNA in HPAECs to promote inflammatory cell recruitment and vascular remodeling, contributing to FPAH.

Altered metabolic-redox states due to factors promoting PH within various cells at the different levels of the pulmonary vasculature induce UPR signaling to control processes such as autophagy, proliferation, feed-forward roles for inflammatory factors, and apoptosis. This signaling further activates NOX 2 and 4, promoting EC apoptosis and PASMC proliferation; uncouples eNOS to promote SMC proliferation; and promotes inflammation and IL-6 production as well as apoptosis – all of which may contribute to pulmonary vascular remodeling and PH development (Fig. 17.4). PH progression may be further exacerbated by dysregulation of NRF2 antioxidant signaling, causing EC and SMC dysfunction, as well as BMPR2 downregulation that promotes inflammatory cell recruitment and vascular remodeling. Interestingly, FPAH is caused by a BMPR2 mutation that may cause the misfolded BMPR2 protein to accumulate in the ER, triggering UPR signaling. In conclusion, there are several mechanisms through which cellular redox processes are able to modulate the UPR during ER stress, allowing these redox processes to have a major role in directing the subsequent expansive signaling events that participate as an

integral part of remodeling and PH pathogenesis. While many aspects of the role of UPR signaling in PH need to be better defined, it appears that multiple redox processes appear to be sensors for controlling the balance between UPR signaling mechanisms and the processes they influence in the progression of PH.

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