

The Relationship Between Oxidative Stress Responses and Lung Inflammation with Cigarette Smoking

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Introduction

Cigarette smoking represents a major world health hazard. In fact, chronic cigarette smoking is the leading risk factor for the development of chronic obstructive pulmonary disease (COPD), the world's third leading cause of death and accounts for 90 % of lung cancers [1, 2]. Cigarette smoking produces adverse respiratory effects by exposing the airways and lung parenchyma to a variety of reactive oxygen species (ROS) and other toxic compounds. Although the molecular mechanisms underlying lung and airway damage in response to cigarette smoke remain incompletely understood, ROS are believed to produce tissue injury by affecting the function and gene expression profiles of lung structural cells and inflammatory cells. In fact, cigarette smoke exposure alters the expression of >600 genes in human monocytes [3]. Specifically, ROS exert direct deleterious effects on cell structure and function by damaging protein, lipid and DNA macromolecules which impair cellular function, induce apoptosis, and stimulate dysfunctional matrix remodeling in the lung and in the respiratory tract. Furthermore, cigarette smoke-induced cell damage causes the release of

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alarmins, cytokines, chemokines and up-regulation of adhesion molecules by epithelial cells in the airway and lung which collectively serve to attract an inflammatory cell infiltrate. In addition, bacterial constituents present in cigarette smoke further shape the intensity and inflammatory response by activating PAMPs [pathogen associated molecular patterns] expressed by lung cells which, in turn, interact with the cell's oxidant defense mechanisms [4, 5]. Moreover, the inflammatory process generated by the innate immune system, in turn, increases oxidant stress in the lung through the production of the superoxide ion by infiltrating neutrophils. Accordingly, the inflammatory reaction in the lung induced by oxidants in cigarette smoke has the potential to act as a positive feedback loop or self-amplifying process which exacerbates both conditions.

This chapter will describe the composition of cigarette smoke and the mechanism by which its major constituents induce oxidant stress imposed in the respiratory tract. Furthermore, we will discuss the molecular mechanisms in the lung which deal with oxidant stress. Finally, we will discuss the manner in which antioxidant defense mechanisms in the respiratory tract interact with inflammatory signaling pathways to shape the intensity and nature of both responses to cigarette smoke.

Cigarette Smoke Composition

Cigarette smoke contains more than 4,700 separate compounds many of which are highly toxic and xenobiotic materials [6–9]. In particular, cigarette smoke contains a variety of aromatic and non-aromatic hydrocarbons (dioxin, benzopyrene); alpha and beta aldehydes (acrolein); heavy metals (cadmium, zinc, iron); toxic gases (nitrogen dioxide, nitric oxide, carbon monoxide); and bacterial-derived substances (lipopolysaccharides [LPS]) which induce important biological effects on the innate and adaptive immune systems.

The effects of many of these compounds on oxidant defenses and the immune system have been well characterized (see below). Of considerable importance, the effects of individual compounds of smoke produce effects which in some cases are opposite in sign to those produced by cigarette smoke per se suggesting that the effects of cigarette smoke cannot be predicted from the study of its individual components but are best assessed using cigarette smoke itself.

Reactive Oxygen Species (ROS)

Smoke from a burning cigarette contains approximately 10^{15} ROS per puff [6]. It has been estimated that the concentration of total reactive oxygen species contained in the average cigarette ranges from 16 to 55 nmol H_2O_2/L [10]. Chemical studies of cigarette smoke performed in the 1980s and 1990s have characterized the nature of the ROS generated by both the particulate phase which is retained on a filter (termed cigarette “tar”) and the gas or vapor phase which passes through the filter. In fact,

the differing materials in these two phases of cigarette smoke exert different biological effects. The majority of the toxic chemicals generated in the particulate phase are semiquinones, phenol, catechol and nicotine [11]. The tar phase also retains several heavy metal ions including cadmium, nickel, and zinc. The major chemicals in gaseous phase are carbon monoxide, nitrogen oxides, ammonia, formaldehyde, acrolein (aldehyde), toluene, benzene, hydrogen cyanide, and the short-chained amides, acrylamide, acetamide [11, 12].

Cigarette smokers deposit up to 20 mg of tar in their lungs per cigarette smoked and the levels of ROS in cigarette smoke, which correlate closely with the level of tar phase materials [10]. Semiquinones cause sustained production of superoxide (O_2^-), hydroxyl radical (OH \cdot), singlet oxygen ($^1\text{O}_2$) and hydrogen peroxide (H_2O_2) [9]. In the aqueous phase of the surface lining fluid of the respiratory tract, superoxide radicals react quickly to oxidize proteins, lipids or nucleic acid macromolecules. Superoxide also can be enzymatically dismutated to form the more stable oxidant, hydrogen peroxide, by superoxide dismutase. Hydrogen peroxide can also form the very highly reactive hydroxy radical via the Fenton reaction via the iron present in cellular fluids and cigarette tar.

Although free radicals in the gas phase are short-lived and affect primarily the upper respiratory tract, radical concentrations are maintained at high levels in gas phase cigarette smoke for more than 10 min and seem to increase in concentration as smoke ages. In fact, radicals are continuously formed and destroyed. Based on nitrogen oxide chemistry, nitric oxide is slowly oxidized to form the more reactive nitrogen dioxide which reacts with unsaturated compounds such as isoprene to form carbon radicals which then rapidly react with oxygen to form peroxy radicals. These in turn react with nitric oxide to produce more nitrogen dioxide. In general, the gas phase is believed to be less harmful to the lung than the tar phase [13].

CS also promotes the generation of ROS and reactive nitrogen species (RNS) in resident lung structural and inflammatory cells by activation of endogenous NADPH oxidase (NOX). NOX isoforms transport electrons from cytoplasmic high energy electron donor NADPH to generate O_2^- and hydrogen peroxide (H_2O_2) [14]. Of the family of NADPH oxidase (NOX) isoforms, NOX1, 2, 4, 5 and Duox 1 and 2 are expressed in lung epithelial and other cell types [14–19]. Moreover, NADPH oxidase (NOX) isoforms are activated by cigarette smoke in a variety of cell types including alveolar macrophages, airway smooth muscle and pulmonary artery endothelial cells and are believed to contribute importantly to oxidant stress in the lung [14, 20, 21]. LPS in cigarette smoke acting on TLR4 [21] and cytokines secreted from airway and alveolar epithelial cells and inflammatory cells in the lung such as TNF- α and IL-1 β , activate NADPH oxidase. Of considerable importance, NADPH oxidase-derived ROS can induce mitochondrial ROS production indicating the possibility of a positive feedback loop [22, 23]. Of interest, tar- and nicotine-free cigarette smoke is capable of activating NADPH oxidase in PKC-dependent fashion indicating that gaseous phase ROS in addition to cigarette tar may contribute to NADPH-induced oxidant stress in some cell types [24]. In fact, acrolein, a gas phase constituent of cigarette smoke (see below), activates NADPH oxidase and superoxide production in human pulmonary endothelial cells [25].

An additional mechanism can contribute to endogenous ROS production in the lung. Nitric oxide (NO) in cigarette smoke can be transformed to NO by nitric oxide synthase which is expressed by a variety of respiratory cell types. In turn, $\cdot\text{NO}$ can be oxidized to the more potent peroxynitrite (ONOO⁻) by superoxide anion. NO synthase expression can be up-regulated by TNF- α and IL-1 β .

Acrolein

Acrolein, a highly water-soluble gas which is highly irritating to eyes, nose and respiratory passages, is deposited mainly in the aqueous lining fluid of the lower respiratory tract when cigarette smoke is inhaled. Acrolein contains a highly reactive alpha carbon which forms carbonylated macromolecules and depletes reduced glutathione and antioxidants in the respiratory tract [26–29]. As such acrolein and other α , β unsaturated aldehydes are major contributors to the oxidative damage induced by gas phase cigarette smoke [30, 31].

Of interest, the concentration of acrolein in sidestream smoke is actually 17-fold greater than in mainstream smoke due to altered combustion chemistry and lower temperatures [32, 33]. Acrolein is also formed endogenously in the lung during inflammation via three separate pathways: (1) by myeloperoxidase oxidation of the amino acid, threonine; by the oxidation of membrane fatty acids; and by thiamine oxidase mediated catabolism of the polyamines, spermine and spermidine. In fact, acrolein concentrations in expired breath condensate and in induced sputum are higher in smokers and ex-smoking subjects with COPD than in healthy nonsmokers [34, 35].

Acrolein induces a variety of deleterious effects on the respiratory tract which mimic the effects of chronic cigarette smoke exposure. On balance, acrolein has a proinflammatory effect but its effects on individual components of the inflammatory response are complex. In rodents, chronic exposure to acrolein increases infiltration of macrophages, neutrophils, and CD8+ T cell into the lungs [36]. Moreover, acrolein exposure increases IFN- γ , IP-10 (CXCL10), IL-12, MCP-1 (CCL2), RANTES (CCL5) and metalloproteinase (MMP)-12 in BAL [36]. Of interest, macrophage accumulation, production of these cytokines and increased MMP12 in response to acrolein does not occur in CD8 deficient mice suggesting that the pro-inflammatory effect of acrolein is initiated by effects on CD8 cells. Acrolein inhibits neutrophil apoptosis [36] but augments alveolar macrophage apoptosis [37]. Acrolein also has novel pro-inflammatory effects by generating chemoattractant peptides from breakdown of lung connective tissue. For example, acrolein acetylates the proline-glycine-protein (PGP) tri-peptide degradation product of collagen breakdown rendering it resistant to breakdown by the aminopeptidase activity of LTA4 hydroxylase [38]. PGP is chemoattractive for neutrophils by acting as a ligand for CXCL1 and CXCL2 [38]. Acrolein does not affect the hydrolyase activity of LTA4 hydroxylase which converts LTA4 to the powerful neutrophil chemoattractant, LTB4 [38].

Acrolein also has direct effects on the master inflammatory gene transcription factor, NF- κ B which appear to be anti-inflammatory [39]. For example, acrolein induces alkalization of the p50 subunit of NF- κ B which inhibits its

binding to NF- κ B consensus DNA sequences. This effect appears to account for acrolein-mediated inhibition of cytokine gene expression induced by endotoxin and TNF- α treatment [40].

Acrolein also has complex effects on lung oxidant defense. It irreversibly inhibits important antioxidant proteins including thioredoxin reductase, thioredoxin 1 and thioredoxin 2 but increases heme oxygenase-1 (HO-1) expression in human pneumocytes [41, 42].

Cadmium

Cadmium (Cd^{2+}) is abundant in tobacco and, depending on tobacco growing conditions, may be present in μg amounts in each cigarette [43, 44]. In general, the higher binding affinity of heavy metal ions leads to replacement of physiological divalent ions like Zn^{2+} in native proteins thereby altering their structure and function [45, 46]. Cd^{2+} is highly toxic to the lung when inhaled as a vapor or fume or directly instilled [47–50]. In human subjects [51–53] and animal models [54–56], acute exposure induces lung inflammation; chronic exposure induces centrilobular emphysema [47, 48, 57] and pulmonary fibrosis [58]. Cd^{2+} is retained in the body for long periods with a half-life of >10 years [59]. Cd^{2+} binding to metallothioneins in lung cells mitigates its toxicity [60, 61].

It has been suggested that Cd^{2+} present in cigarettes contributes to the development of lung dysfunction and COPD in chronic smokers [62, 63]. In fact, Cd^{2+} concentrations are greater in the emphysematous lung (fourfold) compared to smokers without emphysema and never smokers [64] and in alveolar macrophages from smokers compared to non-smokers [65]. Epidemiological studies indicate that urinary Cd^{2+} levels are greater in smokers and ex-smokers than in never smokers [63, 66]. Moreover, FEV1 and FVC are inversely related urinary Cd^{2+} levels and correlate better with Cd^{2+} concentrations than pack years of smoking [63]. Studies of the effects of Cd^{2+} in cultured pneumocytes, airway epithelial cells and lung fibroblasts indicate that Cd^{2+} causes protein misfolding and may induce an unfolded protein response (UPR) response [see below] [67]. Specifically, Cd^{2+} induces heat shock 70 chaperone expression in rat pneumocytes and human airway epithelial cells [68, 69]. Moreover, Cd^{2+} dose-dependently decreases total protein synthesis in rat type II pneumocytes and a human pneumocyte cell line and procollagen and proteoglycan mRNA and protein expression in human lung fibroblasts [69].

Polycyclic Aromatic Hydrocarbons

Cigarette smoke contains a variety of biologically active, poly-aromatic hydrocarbons which act as ligands for an endogenous receptor, the aryl hydrocarbon receptor (AhR). The AhR is a member of the basic helix-loop-helix family of transcription factors which mediates the biologic and toxic effects of its xenobiotic ligands [70].

The AhR induces expression of a variety of genes including phase I and II enzymes which detoxify toxins contained in cigarette smoke, cytochrome P450 and other monooxygenase activities [71]. The AhR also regulates cell apoptosis and transition through the cell cycle [71].

When bound to its polycyclic aromatic hydrocarbon ligands such as dioxin (tetrachloro-dibenzo-dioxin [TCDD]) or benzopyrene, the AhR translocates from the cytoplasm to the nucleus, heterodimerizes with the AhR nuclear translocator (ARNT) and activates transcription through the xenobiotic response element (XRE). The XRE consists of a canonic motif of 5'-TNGCGTG-3'. After nuclear export, the AhR is degraded via the proteasome. Of interest, the lung contains the highest concentration of AhRs of any other organ in the body [72–74]. In fact, secretory proteins such as surfactant protein A (SP-A) and clara cell secretory protein (CC10) are highly regulated by the AhR [75].

TCDD the best characterized AHR ligand induces a variety of effects in cultured respiratory cells and the lungs of rodents. For example, TCDD induces expression of MUC5AC, COX-2, IL-1 β and MCP-1 mRNA in cultured clara cells [75]. When injected intraperitoneally, TCDD produced similar effects in the whole lung lysate of mice along with increases in TNF- α and reductions in SP-A mRNA. Of interest, the results obtained using AhR knock-out mice exposed to cigarette smoke suggest that the AhR exerts an anti-inflammatory effect. For example, AhR^{-/-} mice demonstrate increased numbers of total cells, neutrophils and lymphocytes in BAL in response to acute cigarette smoke inhalation [76]. Similar results were obtained with LPS treatment, which does not contain AhR ligands. Moreover, AhR^{-/-} fibroblasts demonstrate heightened COX-2 expression and prostaglandin production in response to cigarette smoke which could be rescued by transient expression of AhR [77]. These data suggest that AhR deficient animals are inflammation prone and that the inflammatory responses to TCDD may be a manifest of non-AhR mediated effects.

Nicotine

Nicotine is present in milligram amounts in cigarette tar and, like acetylcholine, is a cholinergic agonist that binds to and activates nicotinic acetylcholine receptors [78]. In cell types which express the $\alpha 7$ nicotinic acetylcholine receptor, nicotine exerts diverse, cell type specific effects on immune cells [79].

In general, nicotine induces anti-inflammatory effects in vivo [79–82]. For example, nicotine inhibits LPS-induced elevation of serum TNF- α in mice, an effect which is eliminated in $\alpha 7$ knockout mice [79]. Similar effects were produced in alveolar macrophages in vitro [79]. Nicotine treatment also reduced LPS-induced leukocyte infiltration and myeloperoxidase activity in the mouse lungs, and reduced lung MIP-1a, MIP-2, eotaxin, IL-1, IL-6, and TNF- α [81]. In contrast, nicotine augments dendritic cell capacity to stimulate T-cell proliferation and release TH1 cytokines like interleukin-12 by increasing expression of the co-stimulatory molecules, CD86, CD40, MHC class II receptor, and the adhesion molecules, LFA-1 and

CD54 [83]. These latter results suggest that in contrast to its effects on innate immune responses activated by toll-like receptor stimulation, nicotine may augment adaptive immune responses. The mechanisms by which nicotine exerts these cell type specific effects and the signaling processes involved are unknown.

Antioxidant Defense Systems Involved in the Response to Cigarette Smoke

The respiratory system contains a variety of non-enzymatic and enzymatic antioxidant systems which protect against the injurious effects of oxidants. These systems function to affect electron transfer, enzymatically degrade the chemical compound, as well as scavenge and sequester transition metal ions. The non-enzymatic system scavenges free radicals via electron transfer to electrophilic thiol or carbon groups. This system is comprised of low molecular weight molecules and proteins including glutathione, thioredoxin, peroxiredoxin, α -tocopherol (vitamin E), uric acid, and vitamin C in the extracellular compartment of the lung. Cigarette smoke alters the concentrations of anti-oxidants in lung and other tissues [6, 30, 84 and reviewed by 85]. For example, smokers have lower concentrations of vitamin C in their blood plasma and vitamin E in lung lavage than nonsmokers [86–88].

The enzymatic system comprises the superoxide dismutase (SOD) family, catalase, glutathione peroxidase and heme oxygenase-1 and is also altered by chronic cigarette smoke exposure. SOD which transforms superoxide into hydrogen peroxide includes copper/zinc SOD ($\text{Cu}^{2+}/\text{Zn}^{2+}$)-SOD in the cytoplasm, manganese (Mn^{2+})-SOD in mitochondria, and extracellular SOD in the interstitial space of the lung [89, 90]. Catalase and glutathione peroxidase catalyze hydrogen peroxide to oxygen and water. Catalase is primarily located in peroxisomes, and glutathione peroxidase is distributed in cytoplasm and extra-cellularly [91]. Heme oxygenase-1 (HO-1) inactivates redox generating heme groups by converting heme to biliverdin-IX α , carbon monoxide (CO) and iron in the presence of O_2 and an electron donor, NADPH/cytochrome p450 reductase [92]. Heme cleavage by HO-1 prevents hydroxyl radical formation through iron. In fact, the importance of the enzymatic systems involved in anti-oxidant stress in the prevention of cigarette smoke induced lung inflammation and injury has been demonstrated repeatedly. The expression of SOD, catalase, glutathione peroxidase, and HO-1 is inducible by chronic oxidative stress including cigarette smoke exposure [93–95] and proinflammatory cytokines [96, 97]. Finally, the phase I enzymes which decarbonylate endogenous proteins and detoxify reactive aldehydes such as acetaldehyde and acrolein and other xenobiotics, such as aldehyde dehydrogenase, aldo-keto reductase, and NQO1 reductase, are also up-regulated in response to chronic cigarette smoke exposure [98]. Up-regulation of these enzymes in response to cigarette smoke-induced oxidant stress is largely accomplished via the transcriptional activity of the master antioxidant transcription factor, Nrf2 (nuclear factor-erythroid 2-related factor-2) [99].

The importance of the enzymatic anti-oxidant enzymes in protecting the respiratory system from cigarette smoke-induced injury has been demonstrated repeatedly. For example, exogenous expression of Cu^{2+} - Zn^{2+} - SOD protects CS, elastase and ceramide-induced emphysema in mice [100, 101]. Conditional knockout of extracellular SOD results in the elevation of lung superoxide levels, infiltration of inflammatory cells, and histological changes similar to those observed in adult respiratory distress syndrome [102]. In contrast, increased expression of extracellular SOD attenuates CS-mediated lung inflammation and emphysema in mice [103]. Administration of the SOD mimetic (i.e., MnTBAP) and intranasal administration of SOD-containing microparticles which act to increase lung superoxide levels, reduces mortality and prevents histological alterations [102].

The relevance of antioxidant enzymes in the prevention of cigarette smoke-induced chronic obstructive pulmonary disease in man is strongly suggested by epidemiologic data as well as observations that levels of antioxidant enzymes such as HO-1 are reduced in COPD [104]. Moreover, COPD patients demonstrate a high frequency of mutation of several genes of antioxidant enzymes such as extracellular SOD [105, 106], glutathione S-transferase M1 (GSTM1), GSTT1, GSTP1 and glutamate cysteine ligase (GCL) [107–112].

Nrf2/Keap

Nrf2, a transcription factor that mediates a broad-based set of adaptive responses to intrinsic and extrinsic cellular stresses, regulates expression of enzymes that inactivate oxidants; increase NADPH synthesis; and enhance toxin degradation and export [113, 114]. Nrf2 also enhances the recognition, repair and removal of damaged proteins; augments nucleotide repair; regulates expression of other transcription factors, growth factors, receptors and molecular chaperones; and inhibits cytokine-mediated inflammation [113, 114]. Of particular interest in the setting of cigarette smoke exposure, Nrf2 binds to anti-oxidant response elements in the promoter region of a variety of genes coding for important anti-oxidant enzymes (e.g., heme oxygenase-1 [HO-1], glutathione-S-transferase [GST], glutathione peroxidase [GP], superoxide dismutase [SOD], etc.) [99, 115–117]. In fact, Nrf2 regulates two major redox systems, the glutathione and thioredoxin systems, by promoting expression of enzymes involved in glutathione synthesis, transfer and reduction and thioredoxin synthesis and reduction [99, 115–117]. In addition, Nrf2 regulates several glutathione-dependent (e.g., UDP-glucuronosyl transferase) and glutathione independent enzymes (e.g., NAD(P)H:quinone oxidoreductase1[NQO1]), which are important in the detoxification of tobacco smoke products [116, 117].

Nrf2 and its actin-tethered redox-sensitive inhibitor, Keap1 (Kelch like-ECH-associated protein 1), are widely expressed in bodily tissues [118]. When present in the cytoplasm attached Keap1, Nrf2 has a short half-life as a result of its susceptibility to ubiquitination and proteasomal degradation [118]. Oxidation of Keap1 allows

Nrf2 to dissociate and migrate to the nucleus where it binds to a specific DNA consensus sequence found in the antioxidant response element [5'- NTGAG/CNNNGC-3'] [119]. Nrf2 activity is also regulated by the cytosolic protein, DJ-1, and the nuclear protein, Bach1 [120]. DJ-1 enhances Nrf2 expression by preventing its degradation by the proteasome thereby acting to stabilize Nrf2 in the cytoplasm [121]. The transcriptional inhibitor, Bach-1, on the other hand, inhibits Nrf2 transcriptional activity [122] by competing with Nrf2 for available transcriptional co-factors in the nucleus such as Maf K [119, 120, 123]

Of importance, post-translational modifications of Nrf2 (i.e., phosphorylation and acetylation) affect its functional activity in terms of binding to its inhibitors, its nuclear import and export, and its DNA binding affinity and transcriptional activity [124–127]. For example, phosphorylation of Nrf2 facilitates its dissociation from KEAP1 and its translocation to the nucleus [124–126]. Kinases which phosphorylate Nrf2 include PKC, PI3K and PERK [PKR-like ER resident kinase] [124–127]. At present, however, the Nrf2 phosphorylation sites targeted by kinases which may be activated by cigarette smoke e.g., PERK, PKC, PI3K, etc. and their functional consequences are completely unstudied.

Nrf2 is also acetylated by histone acetyltransferase (HAT) and deacetylated by histone deacetylase (HDAC) 2 [128]. Acetylation of Nrf2 diminishes its transcriptional activity and enhances its export from the nucleus [128]. Accordingly, increases in the level of acetylated Nrf2 are associated with decreases in Nrf2 activity. Specifically, reductions in HDAC2 expression or activity which occur in the setting of cigarette smoke exposure, reduce Nrf2-regulated HO-1 expression and increase sensitivity to oxidative stress in BEAS2B cells and mice [128]. Moreover, HDAC2 knock-down by RNA interference reduces H₂O₂-induced Nrf2 protein stability and activity in cells.

Nrf2 also interacts with the NF- κ B family of transcription factors which regulate the innate and adaptive inflammatory response and cell apoptosis (see below). For example, Nrf2 knockout mice demonstrate increased NF- κ B activity after treatment with TNF- α , LPS and respiratory syncytial virus [129, 130]. Nrf2 attenuates I κ B phosphorylation and increases IKK activity in response to TNF- α or LPS [130]. It is not clear if greater expression of NF- κ B and its targets in Nrf2 deficient animals is a result of diminished ability to scavenge ROS or to a direct interaction between the two transcription factors.

Direct evidence of the importance of Nrf2 in the pathogenesis of cigarette smoke-induced lung inflammation and emphysema has been provided in animal models and in cultured lung cells and human subjects [99, 131]. For example, Nrf2 knockout mice are more susceptible to CS-induced emphysema and inflammation while transcriptional induction of Nrf2 by CDDO (2-cyano-3,12-dioxooleana-1,9(11)-dien-28-oic acid) reduces oxidative stress and alveolar destruction in wild-type mouse but not in Nrf2 knockout mice [15, 99, 132, 133]. Mice deficient in Nrf2 demonstrate increased numbers of macrophages in BAL and lung tissue following cigarette smoke exposure [119]. Nrf2 knockout mice demonstrate increased lung infiltration with macrophages, lymphocytes, eosinophils, and neutrophils after

ovalbumin inhalation [134]. Moreover, type II pneumocytes from Nrf2 knockout mice demonstrate impaired growth and increased sensitivity to oxidant-induced cell death [99, 131]. In addition, deletion of KEAP1 in Clara cells in the airways of mice attenuates CS-induced inflammation and oxidative stress [135]. On the other hand, knockdown of DJ-1 in mouse lungs, mouse embryonic fibroblasts and human airway epithelial cells (BEAS2B) impairs antioxidant induction in response to CS [133]. Of considerable interest, expression of Nrf2 and several Nrf2-regulated antioxidant enzymes e.g. NQO1, HO-1 and glutamate cysteine ligase modifier subunit, is reduced in subjects with advanced COPD [133]. The potential importance of Nrf2 in cigarette smoke-induced lung inflammation and tissue injury have recently prompted trials of substances which increase anti-oxidant gene expression in respiratory cells in subjects with COPD. For example, sulforaphane, a derivative of broccoli sprouts, and resveratrol, a polyphenolic phytoalexin in grapes, regulate Nrf2 expression [136, 137].

Heat Shock Proteins (HSP)

The HSP family of proteins (e.g., HSP27, 60, 70, 90 and 100) participate in protein homeostasis in the cytoplasm and mitochondria and interact closely the ER chaperones in protein folding and transport [138]. For example, HSP90 interacts with and stabilizes IRE1 and PERK kinases [139].

Hsps (e.g., Hsp27, 60, 70, 90 and 100) are induced in response to cigarette smoke and are highly expressed in the lungs of chronic smokers and subjects with COPD [140]. In addition, serum levels of Hsp27 [141], Hsp70 and Hsp90 are elevated in COPD [142]. In vitro, ROS induce HSP expression in lung structural cells. For example, H₂O₂ increases the levels of Hsp60 in bronchial epithelial cells through a pathway involving NF- κ B-p65 [143]. Of interest, however, in animal models, the effects of cigarette smoke exposure on the expression of Hsps are complex and appear to be related to the duration of CS exposure. For example, 1-month exposure of rats to CS increases expression of Hsp70 in airway smooth muscle while a 3-month exposure dramatically reduced it [144]. Hsp expression is also controlled by corticosteroids. For example, dexamethasone increases Hsp72 mRNA and protein expression in the presence of cigarette smoke extract resulting in increased survival of alveolar epithelial cells [145].

Release of HSPs into the extracellular milieu may promote inflammation. For example, HSP60 released by epithelial cells in the setting of oxidative stress stimulates neutrophil activity in COPD patients [143]. Hsp60 also is a key target of T cell responses in chronic inflammation and induces expression of TNF- α and Th1-promoting cytokines, IL-12 and IL-15 in macrophages [146]. In addition, oxidative stress inducers such as CS induce the secretion of Hsp70 from lung structural cells and promote IL-8 release [147, 148], probably through acting as ligand for TLR4 [149].

Molecular Mechanisms of Oxidant Stress Induced Inflammation

Mitogen Activated Protein Kinases (MAPK)

The major redox sensitive signaling system presented in the lung is the MAPK system. MAPKs affect molecular targets which ultimately alter gene transcription in response to environmental stress. MAPK kinases include extracellular signal-regulated kinases (ERK), c-Jun-terminal kinases (JNKs), and p38 kinases. These kinases target a variety of immune effector molecules. For example, MAPK signaling pathways affect T-cell activation and differentiation [150, 151]. MAPK signaling regulates the influx of inflammatory cells into the respiratory tract. Specifically, p38 activation enhances lung inflammation by increasing the expression of inter-cellular adhesion molecule-1, tumor necrosis factor (TNF)- α , and MIP-2. P38 MAPK inhibitors decrease the expression of these pro-inflammatory cytokines and inhibit neutrophil influx in animal models of COPD [152].

Reactive oxygen species in cigarette smoke such as superoxide, hydrogen peroxide and peroxynitrite induce phosphorylation and activation of ERK [153], P38 [154], and JNK [155]. In part, MAPK activation is mediated by activation of the epidermal growth factor receptor and its tyrosine kinase activity [156]. Oxidants can also enhance MAPK signaling by inactivating tyrosine protein tyrosine phosphatase such as PP2a which inactivate MAPK such as JNK and p38 [157]. The importance of ROS-induced activation of the protein tyrosine phosphatases (PTPS) has been demonstrated recently in studies in which PP2a knockdown increases the intensity of cigarette smoke-induced inflammation in the lungs of mice. PTPS may be activated as a result of oxidation of cysteine residues within their catalytic domains. In addition MAPK phosphatases (MKPs) which inactivate MAPK are also inactivated by ROS [158].

Nuclear Factor Kappa B (NF- κ B)

A redox sensitive transcriptional factor NF- κ B, is an important regulator of the inflammatory and cell stress responses [159, 160]. Specifically, NF- κ B regulates expression of a variety of cytokines, chemokines, immunoreceptors, cell-adhesion molecules, stress response genes, regulators of apoptosis, growth factors, and transcription factors. NF- κ B is a family of homo- or heterodimers which contain a conserved Rel homology domain responsible for dimerization and binding to the consensus sequence [5'-GGGRNNYCC-3'] [159, 160]. The NF- κ B family of proteins can be divided into two distinct families based on the presence of a transactivation domain. RelA (p65), RelB and c-Rel all contain transactivation domains while p50 and p52 do not and require heterodimerization with the Rel proteins for

this function. In the absence of stimulation, NF- κ B is inhibited in the cytosol by association with I κ B [161–163]. In response to appropriate stimuli, I κ B is phosphorylated by I κ B kinases (IKKs) at two separate serine residues which leads its ubiquitination and subsequent proteasomal degradation. Release of NF- κ B from I κ B allows its translocation to the nucleus and subsequent binding to the promoter region of over 100 target genes [164]. In particular, NF- κ B regulates the expression of over 30 cytokines and chemokines, immune recognition receptors and cell adhesion molecules required for neutrophil migration including TNF- α , inducible NOS (iNOS), interleukin-1 (IL-1), intra-cellular adhesion molecule-1 (ICAM-1), and cyclooxygenase (COX-2) [165]. A wide range of agents involved in oxidant stress, immune system activation and bacterial infection stimulate IKK to activate NF- κ B including H₂O₂, TNF- α , IL-1, phorbol esters, microbial infection or PAMPs [165].

The importance of NF- κ B in the inflammatory response of the lung is demonstrated by the fact that NF- κ B knockout mice manifest less lung inflammation and cytokine levels in the BAL compared to wild-type animals in response to inhaled toxic substances. For example, NF- κ B knockout mice demonstrate less neutrophil infiltration and cytokine expression in the lung in response to LPS [166]. Moreover, ROS in cigarette smoke such as hydrogen peroxide activate NF- κ B in several cell lines in vitro [167–169]. In fact, H₂O₂ treatment leads to phosphorylation and activation of IKK. Oxidants may also directly phosphorylate the p65 subunit of NF- κ B.

Of interest, NF- κ B is also regulated by Nrf2. For example, NF- κ B activity is increased in Nrf2 knockout mice after treatment with TNF- α , LPS and respiratory syncytial virus [129, 130]. In fact, Nrf2 attenuates I κ B phosphorylation and increases IKK activity in response to TNF- α or LPS [130]. In addition, Nrf2 appears to regulate expression of at least subsets of the NF- κ B family directly. For example, p50 and p65 are reduced in Nrf2^{-/-} fibroblasts while c-Rel is increased in Nrf2^{-/-} fibroblasts [170]. Greater expression of NF- κ B and its targets in Nrf2 deficient animals may be a result of diminished ability to scavenge ROS and, hence, to greater oxidant stress or to more direct interactions between the two transcription factors. Of note, since a variety of stimuli such as ROS and LPS induce both Nrf2 and NF- κ B activity, an entirely antagonistic relationship between the two transcription factors under all circumstances is unlikely [171–174].

Of note, NF- κ B appears to be negatively regulated by the AhR. For example, AhR^{-/-} mice demonstrate increased NF- κ B DNA binding activity in whole lung lysates [76]. Moreover, heightened prostaglandin responses to cigarette smoke in AhR^{-/-} fibroblasts appear to be explained in part by loss of RelB protein. These data suggest that the AhR represses the NF- κ B complex by interacting with RelB.

AP-1

AP-1, another redox sensitive transcription factor, exerts a pro-inflammatory effect by inducing the expression of a variety of chemokines, in particular, C-X-C chemokines [175] in alveolar macrophages [176] and lung epithelial cells [177, 178].

AP-1 is a heterodimer composed of Fos, Jun and activating transcription factor (ATF) subunits interacted with c-Jun, the most potent activator of the group. Fos stabilizes Jun thereby enhancing its binding to promoter region in target genes.

MAPK signaling is an important pathway for AP-1 activation by phosphorylation of Fos, JUN, or ATF subunits [179, 180]. PERK (protein kinase R-like ER resident kinase) activation also induces Fos expression [181]. ROS can activate AP-1. For example, hydrogen peroxide induces phosphorylation of FOS and JUN and increases the expression of Fos, an effect which is attenuated by the use of ERK or JNK inhibitors indicating the importance of the MAPK signaling pathway [182]. Cigarette smoke induces phosphorylation of c-Jun which in turn promotes the expression of CXCL8.

Histone Deacetylases (HDAC)

The HDAC enzymes deacetylate lysine groups on histones thereby interfering with the binding of transcriptional activators. As such, the HDAC family of enzymes generally inhibits immune responses in the lung [183]. In fact, corticosteroids act by recruiting HDACs to transcriptional co-activators such as p65-CBP thereby inhibiting their activity by inducing deacetylation of the histone complex. HDACs also attenuate inflammation by deacetylating and, hence, inactivating the RelA subunit of NF- κ B [184]. Acetylation of RelA inhibits I κ B- α binding [184] and augments binding to IKK α causing export of the NF- κ B complex from the nucleus [184]. The effect of HDAC activity, therefore, is to attenuate NF- κ B transcriptional activity.

Of considerable interest, HDAC activity is affected by the redox state of the cell and is inhibited under conditions of oxidative stress. For example, cigarette smoke and H₂O₂ augment histone acetylation by decreasing the expression and activity of HDAC in human bronchial epithelial cells [185–187]. In the rodent model, cigarette smoke exposure increases histone acetylation, decreases HDAC activity and enhances NF- κ B mediated signaling [188, 189]. In contrast, cigarette smoke increases HAT activity contributing to increased acetylation of histone proteins [186]. Of interest, reduced HDAC2 activity in COPD may contribute to increases in Nrf2 acetylation, reduced Nrf2 stability and impaired anti-oxidant defense [128].

The Unfolded Protein Response (UPR)

The UPR alters the activity of signaling pathways which control protein synthesis, transport and degradation [125, 126, 190]. Moreover, the UPR up-regulates expression of a wide array of genes vital for cell survival including genes which promote oxidant defense (e.g., Nrf2, ATF4, HO-1). The UPR is activated in response to ROS and protects against oxidant-induced cell injury and death while defective function of UPR activity impairs the response to oxidant stress, increases ROS burden and diminishes cell survival [125, 126, 190–195]. Of considerable importance, signaling

pathways activated by the UPR also enhances the activity of pro-inflammatory pathways which regulate the immune response and thus have the potential to augment the innate inflammatory response to cigarette smoke [196].

Oxidant stress in general and cigarette smoke exposure, in particular, cause protein oxidation and misfolding in the lungs [197, 198] and cultured respiratory cells [197, 199]. The effects of cigarette smoke on protein oxidation appear to be largely due to the action of acrolein, superoxide and H_2O_2 . In addition, nicotine induces a UPR response in several cell types presumably by increasing cytosolic calcium [200]. Protein misfolding induced by cigarette smoke can be attenuated by ROS scavengers and by pre-treatment with an anti-oxidant, the glutathione precursor, n-acetyl cysteine [190, 194, 201–204].

Misfolded proteins are non-functional and potentially cytotoxic when present in sufficient amount. Accordingly, cells have evolved mechanisms to refold misfolded proteins using a variety of chaperones, protein disulfide isomerases and oxidoreductases to isomerize, oxidize and reduce thiol groups on target proteins [196]. The processes involved in protein refolding are energy dependent and require oxidation of thiol groups and the formation of intramolecular and intermolecular disulfide bonds [205]. Electron transport during disulfide bond formation involves two ER-resident enzymes: protein disulfide isomerase [PDI] and ER oxidoreductase 1 [ERO1] [206]. PDI accepts electrons resulting in cysteine oxidation and disulfide bond formation. Electrons are then transferred by ERO1 to reduce molecular oxygen (O_2) and form H_2O_2 , thereby increasing the oxidant burden of the cell.

The presence of misfolded proteins is sensed by a triad of ER resident proteins [i.e., PERK (protein kinase R like-ER resident kinase); ATF6 (activating transcription factor 6); and IRE1 (inositol requiring enzyme-1)] [191, 192, 207–209]. Although the precise mechanism by which an increase in the load of misfolded proteins is sensed is uncertain, dissociation of an inhibitor protein, the chaperone, GRP78, from the luminal surface of the sensors increases their activity and triggers a UPR. IRE1 α and IRE1 β (which is present in the lung and gut only), are transmembrane kinases with RNase activity, which splice XBP1 mRNA into a transcription factor (sXBP1) which also up-regulates the above ER resident chaperones, as well as genes involved in protein ubiquitination and degradation, lipid biosynthesis and expansion of ER mass. Activation of IRE1 induces a conformational change which leads to its formation of a complex with the adapter protein, TRAF2 [TNF- α receptor associated factor-2] which recruits IKK leading to the phosphorylation and degradation of I κ B [210, 211]. The IRE1-TRAF2 complex can also recruit JNK which phosphorylates and activates AP-1 [212].

PERK is a transmembrane kinase which phosphorylates and thereby inhibits eIF2 α , the eukaryotic translation initiation factor-2 α . Phosphorylation of eIF2 α is a crucial feature of the UPR since it inhibits protein translation globally, but facilitates translation of selected mRNAs containing appropriate open reading frames. In fact, inhibition of eIF2 α up-regulates translation of Nrf2 and ATF4, a basic zipper transcription factor which enhances ER chaperone expression, and which up-regulates expression of HO-1 and NQO1 metabolizing enzymes [116, 117]. Of interest, phosphorylation of eIF2 α and attenuated translation increases expression of NF- κ B [213]. Since I κ B, which has a much shorter half-life than NF- κ B, attenuating expression of

I κ B increases the ratio of NF- κ B to I κ B thereby freeing NF- κ B to translocate to the nucleus. PERK also directly phosphorylates Nrf2, which facilitates its dissociation from the cytoplasmic inhibitor, KEAP1, and its translocation to the nucleus [124–126]. ATF4 also induces expression of the pro-apoptotic transcription factor, CHOP (CCAAT/enhancer protein-homologous protein) which contributes to a UPR driven apoptosis pathway of cell death in lung structural and inflammatory cells [214, 215].

ATF6 is a proto-transcription factor, which upon proteolytic cleavage of its N-terminal transcriptionally active form in the Golgi apparatus, traffics to the nucleus where in conjunction with sXBP1, it activates genes encoding GRP78, calreticulin, calnexin, and PDI (protein disulfide isomerase).

Cigarette smoke induces a UPR response in the lungs of chronic cigarette smokers and in cultured human airway epithelial cells as reflected by up-regulation of expression of the hallmark UPR effector proteins, GRP78, calreticulin, calnexin and PDI [197]. Of interest, the UPR response to cigarette smoke appears to be partially reversible with smoking cessation since expression of these proteins is significantly less in ex-smokers than in active smokers. Cigarette smoke exposure also increases the expression of genes involved in protein folding and the ubiquitin-proteasome pathway in human monocytes suggesting impaired protein folding in this cell type [3]. Moreover, *in vitro* studies in human airway epithelial cells [202, 203, 215, 216] indicate that the cigarette smoke induced UPR is rapid in onset (within hours) and dose-dependent [197, 202, 203, 215, 216]. Furthermore, PERK activity is increased since phospho-eIF2 α , ATF4 and Nrf2 are up-regulated [197, 203]. In contrast, the IRE1 signaling pathway is not activated by cigarette smoke since XBP1 mRNA splicing is unchanged [202, 203, 215]. Activation of the PERK pathway without increase in activity of the IRE1 pathway in the setting of cigarette smoke exposure appears to be explained by active suppression of XBP1 splicing by cigarette smoke [203].

Of considerable interest, cross-talk between components of the UPR and components of both the MAPK pathway (i.e., JNK) and Toll-like receptor pathways (i.e., TLR4) affect the intensity of the inflammatory response and inflammatory cell survival [4, 5, 217]. These interactions may augment the intensity of the inflammatory process in the lung. For example, activation of the kinase activity of the IRE-1 arm of the UPR by misfolded proteins activates both JNK and NF- κ B and increases IL-8 mRNA and protein in human alveolar pneumocytes and airway epithelial cells [218–220]. Moreover, the IRE1 arm of the UPR can be activated by PAMPs to amplify the intensity of the innate immune response to pathogens. For example, LPS-induced activation of TLR 2 or 4 acting through the TRAF6 adapter protein activates the endonuclease activity of IRE1 with resultant increases in sXBP1 [5]. In turn, sXBP1 augmented production of IL-6 thereby magnifying the innate immune response to microbial infection in human monocytes [221]. Prior activation of the UPR by inducing protein misfolding using the canonical stimulus, thapsigargin, potentiated IRE activation of potentiated the IL-6 response to LPS. Of interest, the PERK and ATF6 arms of the UPR were inhibited. These data suggest that the UPR may potentiate the innate inflammatory response to PAMPs. Specifically, the combination of cigarette smoke exposure and TLR activation may act cooperatively to increase lung inflammation. In fact, mice treated with a combination of cigarette smoke and the viral PAMP and TLR3 ligand, poly (I:C),

demonstrate synergistic augmentation of lung inflammation and emphysema compared to either treatment alone [222].

Of interest, TLR4 activation by LPS also inhibits translation of ATF4 through a TRIF-dependent pathway in mouse monocytes [4, 217]. Inhibition of ATF4 expression diminishes expression of its downstream target, the pro-apoptosis transcription factor, CHOP, thereby promoting cell survival. Of interest, CHOP also appears to induce IL-8 expression at the transcriptional level by binding to the IL-8 promoter in human airway epithelial cells [218]. Inhibition of CHOP expression by LPS may therefore reduce IL-8 expression. Nonetheless, enhanced survival of TLR4-activated monocytes in the lung is likely to augment the inflammatory response to LPS present in cigarette smoke. Moreover, the combination of cigarette smoke exposure and activation of a TLR may act cooperatively to increase lung inflammation. In fact, mice treated with a combination of cigarette and the TLR3 ligand, poly (I:C), demonstrated synergistic augmentation of lung inflammation and emphysema compared to either treatment alone [222].

Oxidant stress is heightened in subjects with COPD and persists for prolonged periods even after subjects have stopped smoking [104, 133, 223]. In part, oxidant stress is heightened because Nrf2 expression is reduced in subjects with COPD [15, 122, 133, 223]. Reductions in Nrf2 in lung tissue and in alveolar macrophages appears to explain reductions in both glutathione dependent and glutathione-independent anti-oxidant defense, in particular, HO-1, which is transcriptionally regulated by Nrf2 and ATF4 [92, 224]. Nrf2 up-regulates the expression of the components of the 26 S proteasome [223]. Accordingly, decreased Nrf2 expression decreases proteasomal activity, impairs protein degradation and leads to accumulation of misfolded proteins in the lung of subjects with COPD [223]. Accumulation of misfolded proteins in the lungs of subjects with COPD may be expected to enhance UPR activity and contribute to the NF- κ B-induced inflammatory process. However, UPR activity in the lungs of subjects with COPD is unstudied.

Variations in Antioxidant Gene Expression and Susceptibility to Lung Inflammation

Of considerable importance, the propensity to develop lung disease varies widely across cigarette smokers and correlates only weakly with the smoking history as reflected in the number of cigarette pack years [225, 226]. In fact, it is estimated that only a minority (i.e., 15–35 %) of chronic, continuous cigarette smokers develop COPD [226, 227]. That the majority of long-term smokers do not develop lung damage or COPD suggests that compensatory mechanisms protect the lung from RONS or xenobiotic materials. In this regard, the magnitude of up-regulation of mRNA for several anti-oxidant genes e.g., glutathione peroxidase, glutathione synthase, HO-1, etc., varies considerably across individual cigarette smokers [228, 229]. The mechanism(s) underlying this inter-individual variability in important anti-oxidant gene expression is unknown.

In this regard, the expression of UPR related genes in response to pharmacological stimuli like thapsigargin or tunicamycin also varies widely in healthy human subjects but is concordant in monozygotic twins [230]. Moreover, polymorphisms in the PERK promoter affect PERK function and expression [231]. These findings suggest that UPR responses are genetically determined and that inter-individual differences in UPR function may affect the response to cigarette smoke and the development of lung inflammation in chronic smokers. This issue is unstudied, however.

Conclusion

The complex mix of compounds present in cigarette smoke exposes the respiratory tract to oxidant stress. Many of these compounds induce an inflammatory response by activating redox sensitive, pro-inflammatory pathways including NF- κ B, AP-1 and MAPKs and by inhibiting redox sensitive anti-inflammatory pathways such as HDACs. Conversely, an elaborate network of protein and small molecule anti-oxidants exist to scavenge ROS in the respiratory tract and maintain redox balance in the cell. The regulation of anti-oxidant defense is largely under the control of the redox sensitive transcription factor, Nrf2. Moreover, the UPR which is activated when proteins are oxidized and misfolded in the ER, regulates anti-oxidant defense per se by both Nrf2 dependent and Nrf2-independent mechanisms. Of considerable importance, the NF- κ B mediated pro-inflammatory and Nrf2 mediated anti-oxidant pathways interact to shape the intensity of the inflammatory response to cigarette smoke. Moreover, the UPR acting through its IRE1 arm appears to paradoxically have a pro-inflammatory aspect as well by affecting cytokine expression directly and indirectly via the NF- κ B and AP-1 signaling pathways. Of considerable importance, genetically determined inter-individual responses to oxidant stress and UPR activation vary considerably and are likely to contribute to differences in susceptibility to cigarette smoke-induced lung inflammation and lung damage. Further studies will be required to characterize the effects of cigarette smoke on the Nrf2 and UPR systems in the lung and their role in the development of cigarette smoke-induced lung inflammation and tissue damage.

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