

FORUM REVIEW ARTICLE

Dual Role of Hydrogen Peroxide as an Oxidant in Pneumococcal Pneumonia

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Abstract

Significance: *Streptococcus pneumoniae* (*Spn*), a facultative anaerobic Gram-positive human pathogen with increasing rates of penicillin and macrolide resistance, is a major cause of lower respiratory tract infections worldwide. Pneumococci are a primary agent of severe pneumonia in children younger than 5 years and of community-acquired pneumonia in adults. A major defense mechanism toward *Spn* is the generation of reactive oxygen species, including hydrogen peroxide (H_2O_2) , during the oxidative burst of neutrophils and macrophages. Paradoxically, *Spn* produces high endogenous levels of H₂O₂ as a strategy to promote colonization.

Recent Advances: Pneumococci, which express neither catalase nor common regulators of peroxide stress resistance, have developed unique mechanisms to protect themselves from H2O2. *Spn* generates high levels of H_2O_2 as a strategy to promote colonization. Production of H_2O_2 moreover constitutes an important virulence phenotype and its cellular activities overlap and complement those of other virulence factors, such as pneumolysin, in modulating host immune responses and promoting organ injury.

Critical Issues: This review examines the dual role of H_2O_2 in pneumococcal pneumonia, from the viewpoint of both the pathogen (defense mechanisms, lytic activity toward competing pathogens, and virulence) and the resulting host–response (inflammasome activation, endoplasmic reticulum stress, and damage to the alveolar– capillary barrier in the lungs).

Future Directions: An understanding of the complexity of H_2O_2 -mediated host–pathogen interactions is necessary to develop novel strategies that target these processes to enhance lung function during severe pneumonia. *Antioxid. Redox Signal.* 34, 962–978.

Keywords: hydrogen peroxide, pneumococci, pneumonia, pyruvate oxidase, virulence factor, ARDS

Introduction

INFECTIONS OF THE LOWER RESPIRATORY TRACT represent
the main cause of infectious disease mortality and represent the fifth highest cause of death overall. In 2015, pneumonia accounted for 2.7 million deaths worldwide (47). *Streptococcus pneumoniae* (*Spn*) is a major etiologic agent of community-acquired pneumonia and the leading cause of death in children younger than 5 years, worldwide (50, 51). It is a facultative anaerobe gram-positive bacterium that can

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colonize the upper respiratory tract as a commensal bacterium in healthy individuals. This asymptomatic transitory phase can lead to severe pneumonia upon migration of bacteria to the lower respiratory tract (119). Infections with *Spn* can lead to meningitis after crossing the blood– brain barrier and the following entry into the blood stream can contribute to heart disease by causing microlesions in the myocardium (14).

Currently, two main types of vaccines have been developed to reduce or eliminate the burden of infections, that is, the unconjugated 23-valent polysaccharide vaccine and a 10 or 13-valent-conjugated polysaccharide vaccine. However, their serotype coverage is not universal and they are limited with respect to noncapsulated *Spn* (12, 97). Once symptoms of pneumonia are diagnosed, antibiotic therapy with amoxicillin for ages under five, and azithromycin or clarithromycin for ages over five is indicated (38, 71). Antibiotic therapy, however, needs to be initiated before breakdown of the alveolar–capillary barrier and systemic inflammation in pneumococcal pneumonia (8). Unfortunately, in view of emerging pathogens, demographic shifts toward older populations, and increasing antibiotic resistance, the occurrence of pneumonia is poised to worsen rather than improve in the coming years (30, 119).

Significance

Bacterial pneumonia represents one of the major comorbidities that occur with the acute respiratory distress syndrome (ARDS) (23, 48, 81). One of the major lethal complications of ARDS is the development of pulmonary edema. Indeed, pathological specimens from ARDS patients reveal diffuse alveolar damage, and animal studies of bacterial pneumonia-associated ARDS have demonstrated both alveolar epithelial and lung endothelial injury with accumulation of protein-rich fluid in the alveolar space (27, 55, 78, 88). The ability of *Spn* to promote lung disease in the human host depends not only on microbial virulence factors, such as the pore-forming toxin pneumolysin (Ply) (77, 79, 111, 137), but also on variables in the host (age, genetic, and environmental factors). These affect the capacity of the immune system to clear bacteria and the susceptibility to develop tissue damage (30, 61).

While there has been focus on the pathogens causing pneumonia in recent years, for example, on *Spn*, there is a high and urgent need for research from the perspective of the host. The absence of alveolar neutrophilia was shown to be deleterious in murine pneumonia models (8, 101) and has a high negative predictive value for bacterial pneumonia in critically ill patients with suspected infection (129). Reactive oxygen species (ROS), such as hydrogen peroxide (H_2O_2) , play an important but highly complex role in pneumococcal pneumonia-associated ARDS. On the one hand, they are involved in neutrophil- and alveolar macrophage-mediated antibacterial defense, but on the other hand, they can contribute to the dysfunction of the alveolar–endothelial barrier and impair alveolar liquid clearance mechanisms. The following chapters discuss the actions of H_2O_2 from the viewpoint of the pathogen as well as in the host and outline its roles in driving the unfolded protein response (UPR), in blunting immune defense mechanisms, and in promoting acute lung injury.

Recent Advances: Actions of H_2O_2 on Spn

Spn generates and exploits H_2O_2

Spn, which grows predominantly in an aerobic environment of the oxygen-rich airway surface, can endogenously generate millimolar levels of H_2O_2 as a by-product during aerobic growth (90, 104). Here we describe those enzymes involved in pneumococcal H_2O_2 generation and examine how the pathogen exploits these high H_2O_2 levels to promote its colonization and enhance its virulence.

Enzymes involved in H_2O_2 generation in Spn. Pyruvate oxidase (SpxB) is considered the main source of H_2O_2 in *Spn*, as strains lacking this enzyme produce 87% less H_2O_2 (74). SpxB catalyzes the conversion of pyruvate to the phosphoryl donor, acetyl phosphate, and releases $CO₂$ and $H₂O₂$ as byproducts (104). Lactate oxidase (LctO), which converts lactate to pyruvate, positively impacts pyruvate flux through SpxB. *Spn* mutants lacking lactate oxidase also produce significantly lower levels of H_2O_2 (38% of the total H_2O_2) (74, 90, 104, 122) (Overview in Table 1).

Deletion of *spxB* and *lctO* significantly reduces bacterial H2O2 production. The absence of these enzymes renders *Spn* highly susceptible to the presence of exogenous H_2O_2 stress generated by host phagocytic cells to facilitate clearance of bacteria at infection sites (74, 104). This suggests a link between endogenous bacterial H_2O_2 generation and resistance to exogenous H_2O_2 produced by cells of the immune system. Levels of adenosine triphosphate (ATP) decreased more rapidly in $\Delta spxB$ pneumococcal mutants than in the wild-type strain during H_2O_2 exposure, suggesting that the increased killing of these mutants is due to their inability to limit depletion of ATP during H_2O_2 stress (104).

High levels of secreted H_2O_2 promote Spn colonization. Endogenously generated H_2O_2 diffuses rapidly through cell membranes and accumulates in the extracellular milieu of *Spn* cultures in concentrations high enough to kill or inhibit other common inhabitants of the respiratory tract, such as *Haemophilus influenzae*, *Staphylococcus aureus*, *Neisseria meningitidis*, and *Moraxella catarrhalis* (103). Using an *in vitro* model mimicking *Spn*/*S. aureus* contact during colonization of the nasopharynx, pneumococcal SpxB/LctOproduced H_2O_2 was shown to be converted into the more potent oxidant hydroxyl radical (- OH) that rapidly kills *S. aureus* (139). Thus, high levels of H_2O_2 provide a competitive advantage to *Spn* over other pathogens and commensal bacteria. A similar strategy is also applied by lactic acid bacteria at other epithelial interfaces, such as in the gut or the vagina. Thus, excretion of high levels of H₂O₂ by vaginal lactobacilli (*e.g.*, *L. gasseri*, *L. acidophilus*, and *L. johnsonii*) represents one of the most important defense mechanisms against vaginal colonization by undesirable microorganisms (58, 85).

Adaptation to endogenously generated H_2O_2 in Spn. Lisher *et al.* (74) revealed that SpxB/LctO-generated H_2O_2 functions as an intracellular signaling molecule in *Spn* that modulates glycolytic-, nucleotide-, and capsule-biosynthesis *via* protein sulfenylation. The authors demonstrated a clear correlation between sulfenylation levels and endogenous $H₂O₂$ production, with SpxB and LctO being among the identified targets of protein sulfenylation. Sulfenylation of

a PerR-regulated in other bacteria (*Spn* lacks PerR).

ATP, adenosine triphosphate; CiaRH, two-component system composed of CiaH histidine kinase and CiaR response regulator; ClpP, caseinolytic ATP-dependent proteases; CodY, GTP-sensing transcriptional pleiotropic repressor; CTM proteins CcdA, putative cytochrome *c*-type biogenesis protein homologue; Dpr, Dps-like peroxide resistance; H₂O₂, hydrogen peroxide; HtrA, high-temperature requirement A; LctO, lactate oxidase; MerR, mercury-sensing regulatory protein; MsrAB, methionine sulfoxide reductase A/B protein; ND, not determined; NmlR, Neisseria merR-like regulator; NOX, NADH oxidase; SodA, superoxide dismutase; *Spn*, *Streptococcus pneumonia*; SpxB, pyruvate oxidase; spxR, *Streptococcus* pyruvate oxidase regulator; TlpA, thioredoxin-like protein family; TpxD, thiol peroxidase.

SpxB was proposed to allow it to function as an H_2O_2 "sink," which is consistent with the fact that $\Delta spxB$ strains are more sensitive to exogenous H_2O_2 (74). Similarly, the thiol peroxidase (TpxD), which limits sulfenylation, was also shown to play a critical role in the adaptation to endogenous H_2O_2 *in Spn* (74).

A serine/threonine kinase StkP phosphorylates the response regulator ComE to control different cellular processes, including H₂O₂ production (107). Deletion of *comE* and *stkP* reduced the expression of *spxB* and *tpxD* and significantly decreased H_2O_2 generation (107).

A role for pneumococcal flavin reductase in resistance to oxidative stress has also been suggested, since an inactive mutant of the enzyme significantly increased susceptibility to H2O2, compared with wild-type *Spn*. Flavin reductase activity in *Spn* might also to be involved in bacterial virulence, as its absence does not affect *Spn* phagocytosis by primary mouse peritoneal macrophages, but it blunts adhesion to the type II alveolar-like cell line A549 (94).

Endogenous H_2O_2 promotes release of the pore-forming toxin Ply. The 53-kDa cholesterol-dependent pore-forming cytolysin (cholesterol-dependent cytolysin [CDC]) Ply (77, 79, 111, 137) can be released in the lungs by autolysis or upon antibiotic-mediated lysis (2). Although Ply lacks the N-terminal signal sequence found in other CDCs, which allows for extracellular release *via* the Sec-dependent pathway (128), the toxin's release has also been suggested in the absence of autolysis (4). Interestingly, *Spn* mutants that lack the pyruvate oxidase gene (*spxB*) are defective in Ply release. However, whereas complementation of *spxB* restored Ply release, exogenous addition of H_2O_2 failed to induce it. Since catalase supplementation prevented Ply release in some strains, these results indicate that intracellularly generated rather than secreted H_2O_2 promotes Ply release in some *Spn* strains (17).

Another link between SpxB and Ply release has been recently described. Deoxycholate-induced autolysis of *Spn* was significantly reduced in an SpxB-deficient strain, indicating a possible weakening of the cell membrane when SpxB is expressed (17). Endogenous H_2O_2 was found to control membrane fatty acid composition, by specific oxidation of the active site cysteine thiol residue of FabF (7). Nevertheless, it remains to be shown as to whether H_2O_2 generated by SpxB

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affects the Ply release directly or rather indirectly, by affecting the expression of yet unknown pneumococcal activators or repressors.

Protective pneumococcal mechanisms against H_2O_2

Generation of ROS is a conserved strategy of host phagocytic cells, primarily neutrophils, monocytes, and macrophages, to facilitate clearance of bacteria at the infection site. Bacteria can be engulfed and enclosed in phagosomes, into which superoxide is released by activated NADPH oxidase 2 (Nox-2). The resulting superoxide O_2 ^{-•} can then be dismutated to H_2O_2 by superoxide dismutase (SOD) in macrophages, and H_2O_2 can further be converted by myeloperoxidase (MPO) in neutrophils to generate the highly microbicidal species, hypochlorous acid (64, 136). Combating endogenous and host innate immune cellmediated oxidative stress is an integral aspect of colonization and virulence of the facultative anaerobe *Spn*.

Pneumococcal enzymes involved in defense from high $H₂O₂$ levels. Common proteins known to protect against oxidative stress in other bacterial species, such as the H_2O_2 scavengers catalase and NADPH-peroxidase, are absent in *Spn* (62, 123). However, previous studies have identified other pneumococcal enzymes implicated in the defense against oxidative stress (Table 1; Fig. 1), such as TpxD (53), Nox (3), SOD (143), and alkyl hydroperoxidase (alkyl hydroperoxide reductase [AhpD]) (100). The pneumococcal TpxD plays an important role in H_2O_2 elimination by catalyzing its reduction (53, 54).

Exposure to exogenous H_2O_2 (10–1000 μ *M*) significantly upregulated the expression of *tpxD* in *Spn*, whereas deletion of *tpxD* decreased the growth rate and survival of pneumococci in the presence of exogenously added H_2O_2 . Addition of the H_2O_2 scavenger catalase in the culture medium reversed the attenuated growth of the *tpxD* deletion mutant (53, 54). However, *Spn* lacks the transcription factors OxyR and PerR found in other bacteria such as *Escherichia coli*, which are described to regulate the expression of *tpxD* in response to $H₂O₂$ (18, 21, 62, 92). Instead, the transcription factor CodY was recently identified to be an activator of *tpxD* expression, triggering its upregulation in *Spn* under H_2O_2 stress (54).

The pneumococcal Nox is suggested to be indirectly involved in H_2O_2 scavenging, as it converts O_2 to H_2O and thereby prevents the generation of superoxide anion (O_2^{\bullet}) and H_2O_2 , which occurs when O_2 is not fully reduced. Pneumococcal Nox is necessary for *Spn* virulence in the murine respiratory tract and in Mongolian gerbil otitis media infection models (146). Unexpectedly, Nox mutations are linked to changes in virulence after intraperitoneal infection, where oxygen tension is low (3). However, Nox has also been associated with other functions such as *Spn* adhesion to A549 epithelial cells (96).

SODs protect cells from the toxic effects of O_2 ^{$-$} by converting it into the more diffusible and less reactive H_2O_2 and

FIG. 1. Mechanisms of pneumococcal defense against H_2O_2 . Schematic overview of the three defense mechanisms involved in the resistance against H_2O_2 : (i) defense enzymes that directly or indirectly degrade H_2O_2 , (ii) repair mechanisms, and (iii) regulators linked to H_2O_2 stress response. H2O2, hydrogen peroxide. Color images are available online.

 $O₂$ (73). In prokaryotes, SODs are distinguished by their metal cofactors: Fe³⁺, Mn²⁺, Cu²⁺/Zn²⁺, and Ni²⁺ (31, 37, 140). Previous studies demonstrated that *E. coli* mutants deficient in both the manganese- and iron-containing SODs are more sensitive to $H_2O_2(21)$. Furthermore, the expression of MnSOD (SodA) from *S. thermophiles* in bacteria not expressing SODs, such as *L. gasseri* and *L. acidophilus*, provided protection against H_2O_2 stress (16). It seems that SOD protects cells against H_2O_2 by removing O_2 ⁺⁻ and preventing the redox cycling of iron.

Although *Spn* contains two types of SODs—MnSOD and FeSOD—only MnSOD (SodA) levels were increased during aerobic growth, and deletion of *SodA* lowered the growth of the bacterium in aerobic conditions. Virulence studies revealed attenuated growth of the *sodA* deletion mutant in intranasally infected mice, with growth rates in the lung and bloodstream comparable with wild type (143). In conclusion, the mechanism by which SOD provides protection of *Spn* against H_2O_2 is indirectly targeted at removing O_2 ⁺⁻ and preventing the redox cycling of iron.

A putative gene for *ahpD*, a group of enzymes known to degrade H₂O₂, was detected in *Spn* (92, 100). However, AhpD does not seem to provide H_2O_2 resistance in *Spn*, as its depletion rather increased the resistance of *Spn* against H_2O_2 (100).

Pneumococcal proteins involved in repair of H_2O_2 -induced damage. Cellular damage caused by oxidative stress is multilayered and rapid. Therefore, in addition to enzymatic degradation of H_2O_2 , immediate repair of damaged proteins and lipids is essential for the survival of the bacterium. *Spn* is equipped with a number of proteins known to be involved in the repair of H_2O_2 -induced damage. These proteins include the following: (i) high-temperature requirement A, a serine protease, and chaperone protein, (ii) Clp ATP-dependent proteases, and (iii) CTM proteins consisting of CcdA (putative cytochrome *c*-type biogenesis protein homologue), thioredoxin-like protein family (TlpA), and methionine sulfoxide reductase A/B protein (MsrAB). All of these proteins participate in the recovery from H_2O_2 -induced oxidative stress, as their progressive removal leads to an increased susceptibility of Spn to H_2O_2 [reviewed in ref. (142)]. Table 1 and Figure 1 summarize the mode of action and the regulators of proteins involved in pneumococcal defense against H_2O_2 .

Impact of H₂O₂ on iron homeostasis. Transition of *Spn* from the nasopharynx to the lungs requires adjustment to a variety of environmental conditions, including availability of transition metal ions (98). Iron $(Fe²⁺)$ potentiates oxidative stress. Expression of Fe^{2+} transport systems and proteins that protect against oxidative stress is regulated by the orphan response regulator RitR. Deletion of *ritR* impaired *Spn* growth in high- $Fe²⁺$ medium, which could be reversed upon addition of manganese (Mn^{2+}) , the latter of which caused a reduction in the amount of H_2O_2 produced by *Spn*.

In *Spn*, excess levels of Zn^{2+} prevent the uptake of Mn^{2+} by irreversibly binding to the extracellular Mn^{2+} -binding protein pneumococcal surface adhesin A (89, 124). As a consequence, *Spn* becomes hypersensitive to oxidative stress, due to a decrease in the activity of MnSOD, which plays an important role in protecting the pathogen against high exogenous H_2O_2 levels (125). It is likely that many of the enzymes involved in resistance to ROS in *Spn* metallate with manganese rather than with iron.

 $H₂O₂$ can interact with ferrous ions (Fe²⁺⁾ and form a highly reactive hydroxyl radical ('OH) through the Fenton reaction, causing DNA damage and increased toxicity to the cells. *Spn* contains only a small number of iron-containing proteins, in contrast to most other bacteria, such as *E. coli*, and thereby avoid poisoning themselves during radical attack. This is consistent with findings showing that H_2O_2 mediated killing of *Spn* is unaffected by iron chelators and appears to be independent of the Fenton reaction (104).

A homologue of DNA-binding protein from starved cells (Dps) and of Dps-like peroxide resistance (Dpr) is present in the pneumococcal genome. Unlike Dps, which protects DNA through direct association, Dpr was found to be an important factor for mediating resistance of oxidative stress caused by H_2O_2 through chelation of free iron, thereby inhibiting the Fenton reaction. Furthermore, a *dpr* mutant has a reduced ability to colonize and is more rapidly cleared from the nasopharynx in a mouse model (65). In *S. suis*, Dpr can bind ferrous ions as well as other divalent cations, such as Cu^{2+} , Mn²⁺, and Zn²⁺ (52).

Critical Issues: Actions of H_2O_2 on the Host's Lung Cells

Spn-derived H_2O_2 induces the UPR in host cells

Endoplasmic reticulum (ER) stress, resulting from the accumulation of unfolded proteins, increased protein load, or calcium gradient dysregulation, can trigger the UPR. This fundamental stress response is used by eukaryotic cells to match demand for protein synthesis with the capability to fold proteins within the ER, to maintain cellular homeostasis (148). In lower organisms, such as *Caenorhabditis elegans*, the UPR was demonstrated to participate in the defense against pathogens, since loss of this pathway was shown to induce hypersensitivity to certain pore-forming toxins, but not to other toxic insults (10).

UPR signaling is mediated by three transducers that are inserted into the ER membrane: activating transcription factor 6 (ATF6), protein kinase R (PKR)-like ER kinase (PERK), and inositol-requiring enzyme 1 (IRE1). The ERresident chaperone immunoglobulin heavy chain-binding protein (BiP) binds to the luminal domain of the ER stress sensors and keeps them in a monomeric inactive state. Accumulation of unfolded proteins leads to release of BiP from the ER stress sensors and induces its subsequent binding to the unfolded proteins (20, 24). PERK and IRE1 become activated by dimerization (or oligomerization) and subsequent phosphorylation (19, 26). Phosphorylated IRE1 activates its own endoribonuclease, which mediates splicing from X-boxbinding protein 1 (XBP1) mRNA. Translation of the spliced transcript produces active XBP1 protein that translocates to the nucleus, where it induces the transcription of several ERresident chaperones and protein-folding enzymes (57, 70).

PERK activation induces phosphorylation of serine 51 of eukaryotic translation initiation factor 2α (eIF2 α). As a consequence, translation is inhibited and protein folding stress in the ER is decreased. However, PERK activation also increases the translation of the transcription factor activating transcription factor 4 (ATF4). ATF4 mRNA possesses internal ribosome entry site sequences in its 5'-untranslated regions and as such escapes translational suppression. Upon

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entering the nucleus, ATF4 regulates the expression of UPR target genes (20). Dissociation of BiP from ATF6 initiates its translocation to the Golgi compartment where it can be cleaved by two proteases. The activated transcription factor ATF6 then migrates to the nucleus and activates the expression of genes encoding proteins, which enhance ER capacity and function (including BiP) (138, 145).

Although UPR signaling can alleviate ER stress, it can also—when sustained—activate deleterious cell death pathways if homeostasis cannot be restored (99). Recently, activation of the UPR was even suggested to mediate vascular disease (105, 112). Indeed, the p22phox subunit, an essential component of most Noxs, was shown to be a novel target of the UPR transcription factor ATF4 under ER stress conditions, thereby increasing ROS generation from Noxs and promoting pathogenesis of cardiovascular disease. Hence, the UPR plays an important role in physiology, but can also contribute to development of cardiovascular disease. Infection with *Spn* can induce the UPR (6, 70, 93). This was demonstrated by the expansion of ER membranes in the H441 cell line (human lung adenocarcinoma similar to club-like lung epithelial cells) upon infection (75), a common feature observed during the UPR (106).

Secretion of *Spn*-derived H_2O_2 leads to activation of PERK, ATF-6, and IRE1 (Fig. 2). Dimerization and phosphorylation of activated PERK induce phosphorylation of $eIF2\alpha$ leading to inhibition of protein translation and ATF4 modulating expression of target genes (Fig. 2). Activated ATF-6 translocates to the Golgi, where it is cleaved by site-1 protease and site-2 protease. The processed ATF-6 enters the nucleus acting as a transcription factor of target genes. Activation of IRE1 leads to splicing of *xbp1* mRNA, which acts as transcription factor of target genes. IRE1 activation can also lead to regulated Ire1-dependent decay (RIDD of mRNA) or c-Jun N-terminal kinase (JNK) signaling activation. Induction of the UPR slows down ongoing protein synthesis and increases the folding capacity of the ER.

Although a number of bacterial virulence factors, including lipopolysaccharide (LPS) and some pore-forming toxins, such as listeriolysin-O, were shown to induce the UPR (10, 24, 75), infections with *Spn* in H441 cells revealed that H_2O_2 , rather than the pore-forming toxin Ply, is the main trigger of UPR, mainly by means of activating the PERK pathway (Fig. 2). The important role of H_2O_2 in the induction of the UPR during pneumococcal infection is documented by the observation that a mutant *Spn* strain lacking pyruvate oxidase

FIG. 2. Actions of Spn-derived H_2O_2 on the UPR in host cells. Infection with *Spn* induces the activation of the UPR. Secretion of *Spn*-derived H₂O₂ leads to activation of PERK, ATF-6, and IRE1. Dimerization and phosphorylation of activated PERK induce phosphorylation of eIF2a leading to inhibition of protein translation and ATF4 modulating expression of target genes. Activated ATF-6 translocates to the Golgi, where it is cleaved by S1P and S2P. The processed ATF-6 enters the nucleus acting as a transcription factor of target genes. Activation of IRE1 leads to splicing of *xbp1* mRNA, which acts as transcription factor of target genes. IRE1 activation can also lead to RIDD of mRNA or JNK signaling activation. ATF4, activating transcription factor 4; ATF6, activating transcription factor 6; eIF2 α , eukaryotic translation initiation factor 2 α ; ER, endoplasmic reticulum; IRE1, inositol-requiring enzyme 1; JNK, c-Jun N-terminal kinase; PERK, protein kinase R (PKR)-like ER kinase; RIDD, regulated IRE1-dependend decay; S1P, site-1-protease; S2P, site-1-protease; *Spn*, *Streptococcus pneumonia*; UPR, unfolded protein response; xbp1, X-box-binding protein 1. Color images are available online.

(SpxB), which secretes a very low level of H_2O_2 , does not induce UPR in H441 cells (75).

Induction of DNA damage by pneumococcal-secreted H_2O_2

Spn not only generates large amounts of H_2O_2 endogenously (34), but also releases large quantities of H_2O_2 *in vitro* and *in vivo* (42). Host cells typically trigger an antioxidant stress response during *Spn* infection, to prevent oxidative injury. This protective response occurs by inducing the production of the transcription factor nuclear factor erythroid 2-related factor 2, which plays a crucial role in the transcriptional activation of antioxidant enzymes and ROS scavengers. These include heme oxygenase 1, NADPH dehydrogenase, and SOD (73, 83).

At excessive concentrations, H_2O_2 can, however, induce toxic DNA double-strand breaks, which precede apoptosis, as was shown using cultures of the human A549 cell line (a model for type II pneumocytes) exposed to three serotypes of *Spn*. Catalase reduced the frequency of DNA damagepositive cells in these studies by 50% or more (109).

Another consequence of bacterial H_2O_2 release is an increased production of mitochondrial ROS in the host cells, as observed during infection with wild-type *Spn*, with a Plynegative mutant strain $(\Delta p l y)$, but not with a SpxB-negative *Spn* strain (63, 75) (Fig. 3). *Spn*-secreted H_2O_2 can also cause oxidative damage to mitochondrial DNA (mtDNA) and lead to the release of mtDNA into the cytoplasm, which in turn induces type I interferon expression in the A549 cell line, involving the stimulator of interferon gene signaling pathway (46) (Fig. 3).

Pneumococcal H_2O_2 affects inflammation in host cells

Apart from activating mtROS generation, DNA damage, and UPR in host cells, H_2O_2 secreted by *Spn* can also induce activation of all three mitogen-associated protein kinase subfamilies, that is, p38, JNK, and ERK, and cause nuclear factor kappa-light-chain-enhancer of activated B cell $(NF-KB)$ translocation and transcription of proinflammatory chemokines and cytokines (interleukin [IL]-8 and IL-23a) (Fig. 3) (9, 75). Canonical activation of the transcriptional regulatory factor NF- κ B protein complex involves phosphorylationinduced proteolysis of the inhibitory protein $I \kappa B \alpha$, which is bound to NF- κ B subunits RelA and p50 by I κ B kinase. Proteolysis of $I \kappa B \alpha$ leads to subsequent translocation of RelA/p50 protein complex to the nucleus (Fig. 3).

The ability of lung parenchymal cells to contribute to proinflammatory cytokine production has also been demonstrated in response to other pathogens, including *Legionella pneumophila*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *H. influenza* (22, 69, 110, 114). A mutation in pyruvate oxidase (SpxB), causing reduced H_2O_2 secretion, was shown to diminish adhesive properties of *Spn* to type II pneumocytes and capillary endothelial cells, which may contribute to diminished virulence *in vivo* (118).

Despite activating certain inflammatory pathways, pneumococcal-secreted H_2O_2 does not necessarily activate the host's immune defense. By contrast, recent results indicate that H2O2 released by *Spn* inhibits inflammasomes, key components of the innate immune system, as such further contributing to virulence and to colonization of the host (36). Thereby, H_2O_2 , which is secreted in millimolar quantities by some *Spn* strains,

FIG. 3. H_2O_2 -induced responses in the host cell. Spn produces large amounts of H_2O_2 , which induce a plethora of host cell responses. This includes oxidative and ER stress (*red*), activation of all three MAPK subfamilies (*green*), translocation of NF- κ B-complex into the nucleus (*violet*), and inflammasome inhibition (*blue*). Oxidative stress leads to production of mtROS and release of mtDNA and subsequent STING-dependent type I IFN (IFN- β) expression. Translocation of $NF- κ B-complex$ into the nucleus leads to expression of proinflammatory chemokines and cytokines (such as IL-8 and IL23a) and H_2O_2 -dependent production of Nrf-2, which induces expression of HO-1. HO-1, heme oxygenase 1; IFN, interferon; IL, interleukin; MAPK, mitogen-activated protein kinase; mtDNA, mitochondrial DNA; mtROS, mitochondrial reactive oxygen species; $NF-\kappa B$, nuclear factor kappa-light-chain-enhancer of activated B cells; STING, stimulator of interferon genes. Color images are available online.

has the capacity to counteract the NLRP3 inflammasomeactivating effect of Ply, the main virulence factor of *Spn* (91). On the contrary, pneumococcus-derived H_2O_2 was shown to directly promote aggregation and activation of platelets, cells orchestrating the systemic inflammatory response (1).

Dose-dependent effects of H_2O_2 on vectorial Na⁺ transport in alveolar epithelial cells

The level of fluid in alveoli represents a critical balance between the rate of fluid movement from pulmonary

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capillaries and lung interstitium across the alveolar barrier into the alveolar space and the transport of salt and water out of the alveoli. Vectorial $Na⁺$ transport out of the alveoli by the apically expressed epithelial sodium channel (ENaC) and the basolaterally expressed $\text{Na}^+\text{--}\text{K}^+$ pump in flat type I (cover 90% of alveolar surface) and cuboidal type II alveolar epithelial cells (cover 5% of alveolar surface) is the major mechanism to maintain an optimal level of airway and alveolar surface liquid (35, 86, 87, 116, 126, 127).

ENaC, whose activity is defined by its surface expression (*N*) and its open probability time (*Po*), is critically involved in alveolar fluid clearance (AFC) (35, 87). Indeed, genetic deletion of the crucial α subunit in neonatal mice prevents them from clearing fluid from their lungs, leading to respiratory distress and death shortly after birth (66). The observation that single-nucleotide polymorphisms rs4149570 and rs7956915 of ENaC-a are associated with neonatal respiratory distress syndrome and lung fluid absorption disorders indicates that ENaC-a (*SCNN1A*) also has a significant role in fluid clearance in man (72). When these mechanisms become impaired, as is the case in severe pneumonia, alveolar flooding occurs, which can precipitate a lethal hypoxemia by impairing gas exchange.

Concentrations of H_2O_2 in the alveolar space in healthy individuals were estimated to be in the micromolar to tens of micromolar range (25). Physiological concentrations of endogenous, dual oxidases $1/2$ -mediated and exogenous H_2O_2 were shown to increase ENaC activity (39, 60, 82). This occurs at least partially through a reduction in ubiquitination of the $ENaC-\alpha$ subunit, which blunts the subunit's degradation and thus increases its surface expression *N* (33). At physiological concentrations, H_2O_2 also activates PI3-kinases that produce the anionic phospholipids, phosphatidylinositol-4,5-bisphosphate and phosphatidylinositol-3,4,5-trisphosphate, which were shown to increase the amount of time that ENaC spends in an open state, transporting Na⁺ (*Po*) (60, 67, 108, 147). Physiologic levels of H_2O_2 also stimulate the Na⁺-K⁺ pump in alveolar epithelial cells (29, 49, 127).

However, during pneumococcal pneumonia, near millimolar concentrations of H_2O_2 can be secreted by *Spn* in the alveolar space, in addition to the H_2O_2 generated by activated neutrophils and alveolar macrophages (Fig. 4). These high levels suppress $ENaC-\alpha$ transcription, in an ERK-dependent manner, and can inhibit the Na⁺-K⁺ pump (29, 49, 127, 131, 141). As a consequence, vectorial $Na⁺$ transport is impaired and alveolar flooding can occur, which can precipitate a

FIG. 4. The complex actions of H_2O_2 in alveoli during pneumococcal pneumonia. *Spn* will migrate into the lower respiratory tract, and since it lacks catalase will generate millimolar levels of H_2O_2 , through the actions of pyruvate oxidase (SpxB) and lactate oxidase (LctO), which will diffuse into the alveolar space (1). Moreover, an early neutrophil-mediated and a later macrophage-derived generation and secretion of μ molar levels of H₂O₂ will occur (2, 3). High ROS levels in the alveolar space will promote alveolar endothelial barrier function (4) and will impair AFC (5), which is mainly mediated through vectorial sodium transport, involving the apically expressed ENaC and the basolateral Na^+K^+ pump in type II pneumocytes. AFC, alveolar fluid clearance; ENaC, epithelial sodium channel; ROS, reactive oxygen species. Color images are available online.

lethal hypoxemia by impairing gas exchange (Fig. 4). *Spn* release of Ply can aggravate this further, since this toxin has also been shown to impair ENaC activity (77).

Impact of H_2O_2 on alveolar–capillary barrier function

A tight barrier structure of only $0.3 \mu m$ thickness separates capillary blood from alveolar gas and is a crucial interface for efficient gas exchange (133, 135). A disruption of the alveolar–capillary barrier, if not resolved, can result in alveolar flooding and poor alveolar gas exchange, both of which lead to hypoxia and hypercapnia, hallmarks of ARDS (127). During pneumococcal pneumonia, high H_2O_2 levels accumulate in the alveolar space, originating mainly from *Spn* secretion, and to a lesser extent also from inflammatory neutrophils and alveolar macrophages, which first generate superoxide from Nox-2, which is then further converted into H_2O_2 by SOD.

An important role of H_2O_2 in the pathogenesis of acute lung injury was first recognized by the observation that both catalase and SOD protected sheep lungs from air emboliinduced increased vascular permeability (42). Moreover, intravascular H_2O_2 challenge in intact lungs was shown to cause both capillary endothelial and alveolar epithelial barrier dysfunction, characterized by increased actin stress fiber formation, intercellular gaps, and intracellular Ca^{2+} levels. These effects on barrier function could be partially inhibited by increasing cAMP or cGMP levels (102, 115, 117).

 H_2O_2 can mediate alveolar epithelial–endothelial paracrine signaling. As such, increased H_2O_2 levels in the alveolar space and pneumocytes can contribute to capillary endothelial barrier dysfunction (63). Recently, an important role for transient receptor potential (TRP) channels was suggested in the actions of ROS. This family of cation channels depolarizes the membrane potential and regulates intracellular concentrations of cations such as Ca^{2+} , the latter of which is known to regulate barrier function (113). Several TRP channels, including transient receptor potential melastatin 2 (TRPM2), transient receptor potential vanilloid-4 (TRPV4), and transient receptor potential channel 6 (TRPC6), are redox sensors that can be activated by H_2O_2 (5, 32, 84, 95). Micromolar levels of H_2O_2 were shown to stimulate ADP ribose formation in human pulmonary artery endothelial cells and to activate the Ca^{2+} permeable and oxidant-activated TRPM2 channel. H_2O_2 mediated Ca^{2+} entry and diminished transendothelial electrical resistance in these cells were blunted by TRPM2 siRNA depletion or by a neutralizing antibody (59). TRPM2 is also expressed in alveolar epithelial cells, and TRPM2 knockout mice were shown to be less susceptible to bleomycin-induced lung inflammation, which is known to be accompanied by increased H_2O_2 levels (144).

Phosphorylation of TRPV4 by the Src family kinase Fyn, which is tethered to the cell membrane by the fatty acid transporter CD36, was recently shown to significantly contribute to H_2O_2 -induced Ca^{2+} influx in lung microvascular endothelial cells (120). Proposed molecular mechanisms of $TRPV4-mediated$ edema formation include $Ca²⁺$ -induced activation of myosin light-chain kinase in endothelial cells (11) and the opening of Ca^{2+} -activated K⁺ channels (KCa3.1) in epithelial cells, which induce hyperpolarization (130).

Finally, TRPC6 was shown to be critically involved in the regulation of pulmonary vascular permeability and lung edema formation during LPS or ischemia/reperfusioninduced acute lung injury (134).

Clinical significance of endogenous H_2O_2 generation during pneumococcal pneumonia

The *SpxB* gene found in nearly all *Spn* strains encodes pyruvate oxidase, an enzyme that converts pyruvate to acetyl phosphate and generates near suicidal levels of H_2O_2 . These high levels of endogenous H_2O_2 would normally cause bacterial death in the absence of catalase, yet *Spn* is able to resist them and to even use them as a factor to outcompete *S. aureus* in the nose and to foster colonization in the host. As indicated above, a general strategy used by *Spn* and lactic-acid bacteria to avoid the toxic effects of the Fenton reaction is replacing iron with manganese. Also, the production of high levels of ferritin-binding proteins keeps free-iron levels low enough to suppress damage to DNA.

The complex role of H_2O_2 in pneumococcal-infected patients was clearly documented by recent observations with clinical isolates of serotype 1 belonging to 2 major clonal complexes (CCs), that is, CC228, associated with low mortality, and CC217, associated with high mortality (15, 121). Mutations in *SpxB* resulted in larger colony variants unable to produce endogenous H_2O_2 . Intravenous challenge of mice with these mutants revealed that early macrophage-mediated clearance was lower than that of wild-type bacteria, and resulted in a higher bacterial load (121). Nevertheless these mutants were less efficient in the colonization process when compared with the wild-type strain. Thus, a requirement for H_2O_2 in the infection process varies as the bacteria moves from niches that are oxygen rich to those that have low oxygen tension.

Alcoholics are at increased risk for developing pneumococcal pneumonia and a role for pneumococcal H_2O_2 for this predilection has also been postulated. The *Spn* type 2 D39 strain, which is ethanol-tolerant due to increased alcohol dehydrogenase E (*adhE*) expression, exhibits increased H_2O_2 generation. Thus, ethanol-fed mice were more susceptible to infection with the D39 wild-type bacteria than with the Δ *adhE* strain (80).

Future Directions

Pulmonary permeability edema as a consequence of the ARDS is a main cause of morbidity and mortality of pneumococcal pneumonia. In the absence of proven pharmacologic treatments, clinicians have to rely on ventilation strategies to deliver oxygen to patients, which can sometimes make the situation worse if the ventilation pressure is too high and causes ventilator-induced lung injury. Permeability edema is characterized by hyperpermeability of the alveolar– capillary barrier, combined with a deficiency to clear liquid from the alveolar space. Vectorial $Na⁺$ transport through the apically expressed ENaC and the basolateral $Na^+ - K^+$ pump is crucial for AFC. ARDS patients with an impaired capacity to clear alveolar fluid were shown to be at significantly higher risk to die (132).

During pneumococcal pneumonia, the pathogen can generate millimolar amounts of H_2O_2 that can rapidly diffuse through cell membranes and accumulate in the alveolar space. Whereas endogenous H_2O_2 clearly represents a colonization advantage to the pathogen, exogenous H_2O_2 in the \sim 10 μ *M* range generated by the Nox-2/MPO or Nox2/SOD

pathways in neutrophils and alveolar macrophages promotes bacterial clearance. Although the detailed mechanism by which the catalase-negative pneumococci can withstand high concentrations of endogenous and phagocyte-derived exogenous H_2O_2 is incompletely understood, several well-defined enzymatic pathways in the pathogen and in phagocytic cells of the host are involved, as summarized in Figure 5.

Excessively high levels of exogenous H_2O_2 in the alveolar space during pneumococcal pneumonia can be damaging to the pathogen, they also have effects on host cells of the alveolar space. Because H_2O_2 is membrane permeant, it can promote DNA damage and apoptosis, induce the UPR and blunt inflammasome-mediated host defense, and increase inflammation. In particular, type 1 and 2 alveolar epithelial cells and the microvascular endothelial cells make up the alveolar–capillary barrier in the lungs affected by high H_2O_2 concentrations. As a consequence of reduced subunit expression, impaired Na⁺-transport by ENaC and the Na⁺-K⁺ pump in AT1/2 cells will lead to a dysfunctional AFC. Moreover, impaired barrier function in both the epithelial and endothelial compartments will promote fluid, protein, and cell accumulation in the alveolar space.

Future therapeutic approaches for pneumococcal pneumonia should potentially aim at reducing the harmful effects of ROS in lung cells, without impairing host defense. As findings with SpxB mutants have indicated, strategies to blunt endogenous H_2O_2 generation in the pathogen seem challenging. However, agents able to impair endogenous $H₂O₂$ generation or promote their downstream effects on iron homeostasis could decrease the harmful effects of the pathogen and improve macrophage-mediated host defense.

In view of their role in barrier function, TRP channel inhibitors could represent attractive therapeutic candidates to counteract the actions of high levels of H_2O_2 during pneumococcal pneumonia. However, their rather ubiquitous expression and the multitude of their functions (regulation of the inflammatory response, pulmonary vasomotor control, and systemic blood pressure) may render also this approach challenging.

As such, therapeutic candidates that reduce the deleterious effects of oxidative stress on barrier function and AFC specifically in the host cells, without impairing antipneumococcal host defense, might hold the key to developing a successful pharmacological approach to the potentially lethal permeability edema associated with severe pneumonia.

The alpha-tocopherol form of vitamin E was shown to boost elastase activity of human neutrophils as well as their ability to kill *Spn* (13). Especially noteworthy are promising preclinical data with the potent antioxidant ascorbic acid (vitamin C), which in preclinical studies was shown to attenuate systemic inflammation and blunt sepsis-induced coagulopathy and vascular injury (40, 41, 43). In a recent phase 2 clinical trial in severely ill patients with sepsis and ARDS, high-dose intravenous administration of vitamin C did not significantly improve the primary endpoint, that is, modified Sequential Organ Failure Assessment (mSOFA) score at 96 h (44). Yet, taking into account mSOFA scores from patients who died during the trial, the mSOFA score at 96 h was significantly lower in patients on the test drug than in the placebo group (45).

A tumor necrosis factor (TNF)-derived peptide—the TIP peptide (a.k.a. AP301, solnatide), which mimics the lectin-

FIG. 5. Overview of positive (green) and negative (red) actions of endogenous and secreted H_2O_2 in the pathogen and in the host lung during pneumococcal pneumonia. In *Spn*, endogenous H_2O_2 promotes nucleotide, glycolytic, and capsule biosynthesis and increases Ply secretion. Secreted $H₂O₂$ kills competing pathogens in the respiratory tract and serves as a virulence factor, since it reduces NLRP3 inflammasome activation in the host. In the alveolar space, *Spn-*secreted H_2O_2 can induce activation of the UPR and cause DNA damage, which can precede apoptosis. Moreover, H_2O_2 can impair the alveolar–capillary barrier, induce inflammation, and blunt vectorial Na⁺ transport, crucial for AFC in pneumocytes. All of these actions of H_2O_2 on the host lung cells can promote the development of pulmonary edema during pneumococcal pneumonia. Ply, pneumolysin. Color images are available online.

like domain of the cytokine and directly binds to the α subunit of ENaC, the latter of which is expressed in both epithelial and endothelial lung cells (27, 28), was shown to significantly reduce oxidative stress in pulmonary artery endothelial cells under hypoxia/reoxygenation and in transplanted rat lungs (55, 56). The peptide significantly blunted bacterial toxininduced capillary leak and pulmonary edema in mice, rats, rabbits, and pigs and was moreover shown in a phase 2 clinical trial to significantly reduce extravascular lung water index in acute lung injury patients (a measure for edema) (68). Interestingly the lectin-like domain of TNF was shown not to interfere with antibacterial activities of the cytokine in a murine model of septic peritonitis (76).

In conclusion, H_2O_2 plays a complex role during pneumococcal pneumonia. On the one hand, its generation by the host's phagocytes can reduce bacterial burden. On the other hand, excessive endogenous generation of H_2O_2 by the pathogen provides a means to outcompete other pathogens inhabiting the respiratory tract and to increase resistance to exogenous levels of H_2O_2 . Moreover, excessive levels of ROS can significantly impair host defense and foster the formation of permeability edema in the lungs, through the impairment of alveolar–capillary barrier function and AFC capacity.

Strategies that specifically blunt H_2O_2 's deleterious actions on the host and promote pathogen susceptibility could represent a promising approach to reduce the high mortality associated with pneumococcal pneumonia.

Acknowledgments

Figures 1–4 were prepared using BioRender. The authors acknowledge funding institutions.

Author Disclosure Statement

R.L. is inventor on patents related to the use of the TIP peptide in ARDS. The other authors have no conflict of interest.

Funding Information

The study was funded by the National Institutes of Health HL134934 (Y.S.), HL125926 (D.F.), DK110409 (D.C.E.), and HL138410 (R.L.), by the Lungen- und Atmungsstiftung Bern, Switzerland (J.H., R.L.), and by the German Research Foundation SFB-TR 84 ''Innate Immunity of the Lung: Mechanisms of Pathogen Attack and Host Defense in Pneumonia'' (M.A.M. and T.C.).

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Date of first submission to ARS Central, November 28, 2019; date of final revised submission, March 17, 2020; date of acceptance, April 3, 2020.

Abbreviations Used

 $Ac-P = acetyl\ phosphate$ $AdhE = aldehyde-alcohol$ dehydrogenase E $ADP = adenosine diphosphate$ $AFC = alveolar fluid$ clearance $AlphaD = alkyl$ hydroperoxide reductase $ARDS = acute$ respiratory distress syndrome $ATF4 =$ activating transcription factor 4 $ATF6 =$ activating transcription factor 6 $ATP = adenosine triphosphate$ $BiP = \text{immunglobulin}$ heavy-chain-binding protein $Ca^{2+} =$ calcium $cAMP = cyclic adenosine monophosphate$ $CAP = community$ -acquired pneumonia $CC =$ clonal complex $CcdA = cytochrome$ *c*-type biogenesis protein homologue $CD36 = cluster of differentiation 36$ $CDC = cholesterol-dependent cvtolysin$ $cGMP = cyclic$ guanosine monophosphate $CiARH = ciaH =$ histidine kinase gene $ClpP = ATP$ -dependent Clp protease proteolytic subunit $CO₂ =$ carbon dioxide $CodY = GTP$ -sensing transcriptional pleiotropic repressor $ComE =$ response regulator ComE $CTM = CcdA$, TlpA, MsrAB $Dpr = Dps$ -like peroxide resistance $Dps = DNA$ -binding protein from starved cells $DUOX1/2 = dual oxidase 1/2$ eiF2 α = eukaryotic translation initiation factor 2 α $ENaC = epithelial sodium channel$ $ER = endoplasmic$ reticulum $ERAD = endoplasmic-reticulum-associated$ protein degradation $ERK =$ extracellular signal-regulated kinases $FabF = 3$ -oxoacyl-[acyl-carrier-protein] synthase 2 $Fyn = proto-oncogene tyrosine-protein$ kinase Fyn $H_2O_2 =$ hydrogen peroxide $HO-1$ = heme oxygenase 1 $HtrA = high-temperature requirement A$ $I \kappa B \alpha$ = nuclear factor of kappa light polypeptide gene enhancer in B cell inhibitor, alpha $IFN-I = type I$ interferon $IL =$ interleukin $IRE1 =$ inositol-requiring enzyme 1 $JNK = c$ -Jun N-terminal kinase

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LctO =lactate oxidase
      LPS =lipopolysaccharide
   MAPK = mitogen-associated protein kinaseMerR = mercury-sensing regulatory protein
   MLCK = myosin light-chain kinase
     MPO = myeloperoxidasemSOFA = modified sequential organ failure
              assessment
   MsrAB = methionine sulfoxide reductase A/Bprotein
  mtDNA = mitochondrial DNAmtROS = mitochondrial ROSNa<sup>+</sup>-K<sup>+</sup> pump = sodium-potassium pumpND = not determinedNF-\kappa B = nuclear factor kappa-light-chain-
              enhancer of activated B cells
    Nox-2 = NADPH oxidase 2
    Nrf-2 = nuclear factor erythroid 2-related factor 2
       O_2 = oxygen
    OxyR = hydrogen peroxide-inducible genesactivator
    PERK = protein kinase R (PKR)-like ER kinase
     PerR = ferric uptake regulator
PI3-kinase = phosphoinositide 3-kinase
      PIP_2 =phosphatidylinositol-4,5-bisphosphate
      PIP_3 =phosphatidylinositol-3,4,5-trisphosphate
      P1y = pneumolysin
     PsaA = pneumococcal surface adhesin A
     RelA = nuclear factor NF - kappa-B p65 subunitRIDD = regulated Ire1-dependent decay
     RitR = orphan response regulator
     ROS = reactive oxygen species
      S1P = site-1-protease
      S2P = site-2-protectsiRNA = silencing RNASOD =superoxide dismutase
      Spn =Streptococcus pneumoniae
    SpxB = pyruvate oxidase
   STING = stimulator of interferon genes
     StkP = serine/threonine kinaseTCS04 = two-component system 4
     TlpA = thioredoxin-like protein familyTNF = tumor necrosis factor
    TpxD = thiol peroxidase
      TRP = transient receptor potential
   TRPC6 = transient receptor potential channel 6
   TRPM2 = transient receptor potential melastatin 2
   TRPV2 = transient receptor potential vanilloid
     UPR = unfolded protein response
     VILI = ventilator-induced lung injuryXBP1 = X-box-binding protein 1
```