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The host response and molecular pathogenesis associated with respiratory syncytial virus infection

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Abstract

Since the isolation of respiratory syncytial virus (RSV) in 1956, its significance as an important human pathogen in infants, the elderly and the immunocompromised has been established. Many important mechanisms contributing to RSV infection, replication and disease pathogenesis have been uncovered; however, there is still insufficient knowledge in these and related areas, which must be addressed to facilitate the development of safe and effective vaccines and therapeutic treatments. A better understanding of the molecular pathogenesis of RSV infection, particularly the host-cell response and transcription profiles to RSV infection, is required to advance disease intervention strategies. Substantial information is accumulating regarding how RSV proteins modulate molecular signaling and regulation of cytokine and chemokine responses to infection, molecular signals regulating programmed cell death, and innate and adaptive immune responses to infection. This review discusses RSV manipulation of the host response to infection and related disease pathogenesis.

Keywords

adaptive immunity; disease; innate immunity; respiratory syncytial virus

Respiratory syncytial virus

The *Paramyxoviridae* family includes important human respiratory-tract pathogens, of which human respiratory syncytial virus (RSV) is a member. RSV is in the *Pneumovirinae* subfamily and type species member of the *Pneumovirus* genus. RSV was first isolated four decades ago from chimpanzees during an outbreak of respiratory illness [1]. Thereafter, RSV was isolated from infants with pneumonia and bronchitis [2], and was named RSV owing to its characteristic

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ability to induce syncytia in cell lines. RSV is a ubiquitous virus and the most important cause of serious lower respiratory-tract illness in infants and young children worldwide, as well as an important pathogen in the elderly and the immunocompromised [3–11]. RSV is the primary cause of hospitalization for respiratory tract illness in young children with infection rates approaching 70% in the first year of life [12]. In the USA, lower respiratory-tract disease develops in 20–30% of children infected with RSV, of which many require hospitalization [13].

RSV is a nonsegmented pleiomorphic negative-strand RNA virus containing two nonstructural (*NS1* and *NS2*) genes followed, in gene order, by nucleocapsid, phosphoprotein (*P*), matrix, small hydrophobic (*SH*), surface attachment glycoprotein (*G*), surface fusion glycoprotein (*F*), a *M2* gene, which encodes two proteins from *M2-1/M2-2* open reading frames that have roles in RNA transcription and replication, and RNA-dependent RNA polymerase (*L*). The virus consists of a nucleocapsid surrounded by a lipid envelope derived from the host-cell plasma membrane during the budding process [14–16]. There are three virally encoded surface transmembrane proteins: *G*, *F* and *SH*, and all three of these proteins have been associated with modifying aspects of the host response to infection. The *G* protein, or attachment protein, is a type II glycoprotein with a single N-terminal hydrophobic region (amino acids 38–66) that serves as a signal peptide and membrane-anchor [17–20]. Proximal to the membrane anchor region is an extracellular ectodomain containing four cysteine residues that are highly conserved in all RSV isolates [21,22]. This cysteine region contains a CX3C chemokine motif (amino acids 182–186) that may facilitate virus attachment to cells expressing the CX3C chemokine receptor, and modify CX3CL1 (fractalkine)-mediated responses as an immune evasion strategy [23]. The *G* glycoprotein is expressed as both a membrane-bound (G_m) and secreted form (G_s) by initiation of translation at an alternate in-frame AUG codon located in the middle of the hydrophobic transmembrane region [19]. Approximately 15% is synthesized in infected cells as a soluble form lacking the cytoplasmic but G_s retains the same characteristics domain, as G_m , for example, glycosylation and antibody reactivity [24,25]. The *SH* protein is a minor surface protein that has been shown to have the ability to form cation-selective ion channels in planar lipid bilayers [26] and interact with the *G* protein [27]. In addition, the *SH* protein may inhibit TNF- α signaling [28]. Considering the other RSV proteins with known immune modulatory activities, the function of *NS1* and *NS2* proteins appear to act cooperatively to antagonize the type I IFN antiviral response [29–33]. Studies with recombinant RSV with deletions in the *NS1* and *NS2* have shown that these genes are dispensable for virus replication *in vitro*, however, through type I IFN antagonism, they provide auxiliary functions for efficient RSV replication *in vitro* and *in vivo* [34].

RSV replication

RSV attachment to cells primarily occurs via heparin-binding domains on the *G* protein with cell-surface glycosaminoglycans [35–37]. The *G* protein itself is not required for virion attachment as RSV mutant viruses lacking *G* and/or *SH* genes have been shown to infect cells likely through interaction with the *F* protein [38–41]; however, *G* protein appears to be necessary for efficient virus replication *in vivo* [40]. Following cell fusion and penetration mediated by the *F* protein [42], the nucleocapsid is released into the cytoplasm [43–46] where the *L* protein initiates viral transcription and replication proceeds [47]. Transcription of mRNA occurs in a 3' to 5' order from a single promoter near the 3' end resulting in a series of subgenomic mRNAs [48–52]. mRNAs can be detected by 4 h postinfection with peak mRNA synthesis and protein expression occurring 12–20 h postinfection. Importantly, the level of protein expressed is related to mRNA abundance [49], thus there are decreased levels of mRNA proportional to the gene distance from promoter sequence. Virions assemble at the plasma membrane where nucleocapsids localize with the cell-membrane containing membrane viral

glycoproteins. The virions mature in clusters at the apical surface in a filamentous form associated with caveolin-1, and extend from the plasma membrane [53].

Regulation of the host-cell response to infection

RSV primarily infects respiratory epithelial cells lining the nasal passages and respiratory tract. RSV infection of host cells has been shown to alter the tempo and expression patterns of various genes related to protein metabolism, cell growth and proliferation, cytoskeleton organization, regulation of nucleotides and nucleic acid synthesis, and cytokine/chemokine genes linked with inflammation [54,55]. While a primary function of airway epithelium is to promote gaseous exchange, it also functions as the interface between the external environment and the host, thus acting as a first-line defense against pathogens. Given the unique position of airway epithelial cells in this regard, they also provide a close interface with various immune components including mucosal dendritic cells (DCs) and intraepithelial lymphocytes [56]. To overcome the repertoire of immune defenses encountered, it is not surprising that RSV enlists a variety of immune modulatory and evasion strategies to promote virus infection and replication.

RSV delays programmed cell death to facilitate virus replication

RSV infection does not induce substantial cytopathology in human airway epithelial cell models [57,58], a feature in part associated with the ability of RSV to delay programmed cell death or apoptosis of epithelial cells. It has been shown that RSV-infected cells have increased expression of the anti-apoptosis gene *IEX-1L* and increased expression of several Bcl-2 family members including myeloid cell leukemia-1 and Bcl-XL [59–62]. Recent studies have suggested other mechanisms that may contribute to delayed cell death that are linked to the inhibition of tumor suppressor p53 and Akt activation, leading to p53 proteasome degradation [63]. The delay of apoptosis has also been connected to the phosphatidylinositol 3-kinase-dependent pathway [64], and to increased ceramidase and sphingosine kinases leading to enhanced levels of anti-apoptotic proteins within cells [65]. In addition, the RSV NS and SH proteins have been shown to delay premature apoptosis, a feature that results in more robust viral titers [28,66].

Modulation of host-cell responses via pattern recognition receptors

A majority of respiratory epithelial cells express pattern recognition receptors (PRRs) or Toll-like receptors (TLRs), which aid in sensing infection and host-cell signaling and communication. RSV infection of respiratory epithelial cells has been shown to result in increased TLR4 expression on the cell surface within 24 h postinfection [67,68]. The upregulation of TLR4 leads to increased sensitivity to endotoxin, and upon stimulation with lipopolysaccharide, enhanced IL-6 and IL-8 production has been observed [67]. TLR4 expression in infants responding to RSV infection has also been examined. In one study, infants possessing two single-nucleotide polymorphisms encoding Asp299Gly and Thr399Ile substitutions in the TLR4 ectodomain were highly associated with symptomatic RSV disease, suggesting that heterozygosity of these two extracellular TLR4 polymorphisms is associated with symptomatic RSV disease in high-risk infants [69], supporting the role for TLR4 in host response to RSV infection. Furthermore, peripheral monocytes isolated from infants with severe RSV bronchiolitis also showed increased TLR4 expression [70]. Like lipopolysaccharide, the RSV F protein can interact with TLR4 and CD14 in human monocytes leading to the activation of NF- κ B and the production of proinflammatory cytokines TNF- α , IL-6 and IL-12 [71]. While the mechanism is not yet clear, the RSV G protein may also suppress TLR3/4-mediated cytokine production by interfering with the TLR adaptor, TNF receptor-associated factor/Toll IL-1 receptor domain-containing adaptor molecule-1 or NF- κ B activation, resulting in decreased proinflammatory cytokine production [72,73]. A recent study demonstrated that RSV promotes TNF- α , IL-6, monocyte chemoattractant protein (MCP)-1 and

RANTES via interaction with TLR2 and TLR6 [74]. These findings indicate that TLR4 has a role in sensing RSV infection and contributing to protection from RSV infection.

RSV interferes with the host antiviral cytokine response

Several studies have shown that RSV nonstructural proteins, NS1 and NS2, are important in antagonizing the type I IFN response in infected epithelial cells as well as suppressing DC maturation [30,32,33,75–78]. NS2 is the principal type I IFN antagonist linked to STAT-2 signaling [76,79,80]. The NS1 protein contains elongin-C- and cullin-2-binding sequences and can potentially act as an ubiquitin E3 ligase to target STAT-2 to the proteasome [80,81]. Bovine RSV nonstructural proteins have also been shown to interfere in type I IFN signaling via a mechanism involving IFN regulatory factor (IRF)3 phosphorylation and subsequent activation [75]. Aside from the role for NS1 and NS2 in governing type I IFN expression, a recent study in mice epithelial-15 lung cells showed that by 24 h postinfection, in the absence of NS1 and NS2 proteins, type I IFN mRNA and IFN- β protein expression were suppressed [31]. In this study, a role for RSV G-protein inhibition of IFN- β was revealed and linked to the induction of suppressor of cytokine signaling (SOCS)1 and SOCS3 expression. SOCS proteins are negative regulators of cytokine expression [82,83], and act to inhibit the JAK–STAT pathway to regulate cytokine expression via a kinase inhibitory region [84]. While it remains unclear whether NS1 and NS2 directly affect SOCS expression, the net result of SOCS expression leads to a decreased antiviral response within the cell. RSV can also interfere with JAK–STAT signaling and chemokine transcription by inducing Bcl-3, which complexes with STATs in the nucleus, resulting in enhanced infection [85].

RSV infection modulates respiratory epithelial cell function

A consequence of severe RSV disease is fluid extravasation into the lung air spaces [86]. RSV infection of murine and human airway cells results in decreased sodium transport across epithelial cells leading to reduced alveolar fluid clearance in mice [64,87,88]. Evidence suggests that the RSV F protein and TLR4 have a role in this effect [89], and one recent study found that RSV infection of primary bronchial cells resulted in a loss of plasma-membrane integrity and cytoskeletal rearrangement dependent on MAPK signaling via p38 and heat shock protein-27 activation [86]. p38 MAPK activation and heat shock protein-27 phosphorylation may result in actin reorganization and an altered shape of the infected cell [90].

RSV infection also results in reduced levels of surfactant proteins (SP), particularly SP-A and SP-D, in bronchoalveolar lavage [91,92]. Nonciliated cells of the respiratory tract produce SP-A and SP-D, which are important in promoting opsonization of pathogens as well as apoptotic cells [93]. SP-A has been shown to bind to the RSV F protein and promote uptake of RSV-infected cells by macrophages [94,95], while SP-D binds to the RSV G protein to inhibit infection [96]. Although SP-A and SP-D bind viruses as part of the clearance mechanism, it is possible that RSV may use these innate host-defense proteins to sequester surfactant proteins during infection to prevent antibody neutralization or to limit the immune cell response to infection, an effect that may be linked to the decreased levels of SP-A and SP-D found in the lungs of infected infants [92].

Matrix metalloproteinases are involved in the digestion of extracellular matrix components such as gelatin, collagens (types IV, V, XI and XVII) and elastin [97]. RSV infection can enhance the expression of matrix metalloproteinase-9, which increases the rate of syncytium formation, leading to more efficient viral replication [98]. Furthermore, prostaglandin, which are implicated in many regulatory events including the differentiation of immune cells and regulation of immunological and inflammatory responses, are increased via increased cyclooxygenase-2 expression, which occurs during RSV infection [99–101]. Prostaglandin E2

is considered a potent proinflammatory mediator, and in the lung, has a role in limiting the immune inflammatory response as well as the tissue repair processes [102].

RSV G protein immune evasion

The RSV G protein was first recognized as an attachment protein involved in the binding of RSV particles to the host cell surface. Following RSV infection, the G protein is produced in two forms, G_m and G_s [24,103]. G protein is one of two major RSV proteins recognized in the antibody response to infection, the other being the F protein [104,105]. While the antibody response primarily recognizes epitopes within the C-terminal region of the G protein [106, 107], the glycosylation pattern of the RSV G protein changes depending on the specific cell type infected [108–111]. Thus, the altered glycosylation patterns are likely to be a feature linked to immune evasion associated with changes in the G protein antigenic profile [112,113].

The G protein has known attributes that contribute to host protein mimicry and immune evasion. For example, the G_m and G_s proteins both contain a central-conserved cysteine-rich region, homologous to the fourth subdomain of the TNF receptor, which can modulate the innate immune response to infection [23,72,114–116]. TNF- α/β are proinflammatory cytokines implicated in a large range of inflammatory conditions [117] and in the antiviral response to RSV infection [118]. It is possible that the G_s protein may bind to TNF- α or other homologs modulating the host antiviral response [24,116]. The central-conserved cysteine-rich region also contains a CX3C chemokine motif at amino acid positions 182–186, which binds to CX3CR1, the CX3CL1 (fractalkine) receptor [23]. CX3CR1 mimicry by the G protein has been shown to facilitate RSV infection and alter CX3CL1 chemotaxis of human and mouse leukocytes [23]. Expression of the G protein during RSV infection of mice has also been shown to decrease the number of activated and RSV-specific pulmonary CX3CR1⁺ T cells, as well as natural killer (NK) cells [119]. Consistent with this finding, infection of mice with a RSV mutant virus lacking the *G* and *SH* genes results in enhanced numbers of NK cells recruited to the lung as well as increased IFN- γ and TNF- α production, suggesting that the G and/or SH surface proteins inhibit NK cell recruitment and proinflammatory cytokine production [41]. Together these studies suggest that RSV can modulate both the innate and adaptive immune responses to infection via G protein expression.

Cytokine response to RSV infection

Cytokines are a diverse group of secreted proteins produced *de novo* in response to immune stimuli that mediate and regulate immunity, inflammation and hematopoiesis. Chemokines, a constituent of the cytokine family, function to activate and attract leukocytes to sites of infection. Many cytokines are pleiotropic and may have multiple, overlapping or redundant actions that can be explained by the presence of receptors for a cytokine on multiple cell types or lineages, or by a cytokine having the ability to activate multiple signaling pathways that may differentially contribute to different cell functions. A wide range of cytokines and chemokines are produced by different cell types in response to RSV infection, some of which mediate proinflammatory functions to activate and recruit immune cells, and others that suppress or regulate the proinflammatory state. For example, RSV infection of airway epithelial cells has been shown to result in a cascade of signaling events mediated by NF- κ B leading to the expression of proinflammatory cytokines and chemokines including RANTES, MCP, eotaxin, IL-9, TNF- α , IL-6, IL-1 and CX3CL1 (fractalkine) [120–127]. It has been suggested that certain patterns of cytokine and chemokine expression in a RSV-infected individual may be an indicator of disease severity [128]. Studies with RSV-infected patients have shown that increased levels of macrophage inflammatory protein (MIP)-1 α , RANTES and IL-8 are often present in the upper and lower respiratory tract [121]. Likewise, bronchial epithelial cells infected with RSV have been shown to express high levels of IL-6, IL-8 and RANTES [129]. Blocking any one of these factors may result in less severe disease. For example, antibody-

mediated depletion of RANTES or eotaxin results in reduced airway hyper-reactivity and eosinophilia in mice infected with RSV [130,131]. Furthermore, the tempo and pattern of cytokine and chemokine expression has also been linked to age, as mice infected as neonates display higher illness scores, greater cell recruitment to the lungs and increased IL-4 production, and upon reinfection with RSV as adult mice, develop manifestations of severe disease associated with a Th2-type cytokine response [132].

RSV G-protein expression during acute infection in mice has been associated with altered CC and CXC chemokine mRNA expression and Th1/Th2-type cytokine responses by bronchoalveolar leukocytes [133,134]. Specifically, the G protein appears to inhibit early MIP-1 α , MIP-1 β , MIP-2, MCP-1 and IFN-inducible protein of 10 kDa mRNA expression, all important chemokines that attract immune cells to sites of infection or inflammation [133]. G-protein expression has also been linked with reduced IFN- β expression in mouse lung epithelial cells [31], thus RSV appears to modulate the balance or expression of cytokines to manipulate antiviral immunity, a feature that may contribute to RSV-mediated disease pathogenesis.

RSV activation & regulation of cellular transcription factors

Accumulating evidence suggests that RSV interacts with TLRs and PRRs and activates signaling and downstream cellular transcription pathways [68,71,73,74,135–138]. *In vitro* studies show that RSV infection upregulates TLR4 expression in A549 cells [68], and more specifically, that purified RSV F protein interacts with TLR4 in a CD14-dependent manner [71]. Signaling through TLR4 can lead to activation of TNF receptor-associated factor and the adaptor protein MyD88, which in turn activate downstream members IKK ϵ /TANK-binding kinase-1 and IL-1 receptor-associated kinase-4, thereby initiating signaling pathways leading to the induction of an array of transcription factors (IRF3, IRF7, NF- κ B, JNK, p38 MAPK and activator protein-1), which translocate to the nucleus and initiate transcription of various proinflammatory genes [139]. TLR3, the ligand of which is dsRNA, is upregulated in response to RSV infection [137,140]. Cellular signaling via TLR3 leads to the activation of downstream IKK ϵ /TANK-binding kinase-1, which in turn induces the nuclear translocation of transcription factors such as IRF3, IRF7 and NF- κ B. Activation of the TLR3 pathway in A549 airway epithelial cells was shown to control phosphorylation of RelA providing a mechanism for regulating RSV-induced NF- κ B-dependent gene expression at the late phase of infection [138]. Similarly, retinoic acid-inducible gene (*RIG*)-I, is a cellular cytoplasmic helicase protein that recognizes the 5' triphosphate ends of RNA generated by viral polymerases and when activated leads to the induction of IFN- α and IFN- β [141]. *In vitro* studies in A549 cells have shown that RSV infection induces RIG-I and TLR3 expression, and that TLR3 induction is regulated by RIG-I-dependent IFN- β and mediated by both IFN response-stimulated element and STAT sites within its proximal promoter [138]. These findings indicate distinct roles for RIG-I and TLR3 in mediating RSV-induced innate immune responses. Later stage signaling events suggest that paracrine signaling mechanisms may have an important role in the innate response to RSV infection. Recently, studies examining IFN-mediated monocyte-derived DC (mDC) TLR3/4 signaling showed that mDCs treated with live or UV-irradiated RSV showed no early (within 4 h) induction of IFN- β [73]. In this study, initial virus attachment to the cells blocked poly-I:C-mediated IFN- β induction. Furthermore, studies using IFN-stimulated response element reporter analysis in HEK293 cells demonstrated that RSV G protein inhibited TLR3/4-mediated IFN-stimulated response element activation. These findings are consistent with studies in mice epithelial-15 lung cells, which showed that RSV G protein modulates SOCS1 and SOCS3 expression associated with the type I IFN response, and in particular, inhibits IFN- β expression [31].

STAT proteins are a family of transcription factors that are activated following phosphorylation by JAK, translocated to the nucleus, where IFN- γ activation factor, a dimer of STAT1, binds

to, and initiates transcription of, genes containing IFN- γ -activated sites [142]. RSV proteins have been shown to modulate STAT signaling and transcription of IFN-regulated genes. For example, *in vitro* studies in A549 cells and human tracheobronchial epithelial cells have shown that RSV NS protein expression is linked to reduced levels of STAT2 [76,80], a feature that requires proteasomal activity. NS1 protein contains elongin-C- and cullin-2-binding consensus sequences, which allow NS1 to act as an E3 ligase, thereby targeting STAT2 for proteasome-mediated degradation [81]. Degradation of STAT2 suppresses formation of the IFN-stimulated gene factor-3 transcription factor complex [143,144]. The IFN-stimulated gene factor-3 transcription factor is a heterotrimer complex composed of STAT1, STAT2 and IRF9, which translocate to the nucleus and bind to ISRE leading to the transcription of IFN-regulated genes such as 2'5'OAS Mx, PKR, MHC, CD80, CD86, iNOS, *STAT1* and *IRF7* [145]. These studies provide a mechanism for NS antagonism of type I IFN responses to infection [76,78]. In addition, another mechanism that can negatively regulate type I IFN expression is SOCS regulation of the JAK-STAT signaling pathway [82]. Of the eight SOCS family members, SOCS1 and SOCS3 appear to be the most efficient at downregulating type I IFN expression [146], and SOCS1 and SOCS3 expression has been shown to be modulated during RSV infection, leading to type I IFN antagonism [31,147].

Innate immunity to RSV infection

Innate immunity constitutes an evolutionarily conserved, nonspecific primary defense strategy that is important for recruitment, activation and production of the virus-specific adaptive immune response that mediates long-lasting immunity. Viral recognition by the host is essential for regulating the functional consequences of infection. TLRs and PRRs recognize conserved pathogen-associated molecular patterns [148]. Viruses that trigger TLRs initiate a complex signaling cascade leading to the expression of a variety of genes and signaling through NF- κ B [149]. It is likely that multiple TLRs and/or PRRs are involved in detecting RSV or RSV components as several TLRs and PRRs have been shown to be affected by RSV infection [68,71,73,74,135–138], and although not all TLRs or PRRs may be required to facilitate RSV clearance, it seems that some, for example TLR3, may be important for maintaining an immune environment by avoiding the development of Th2-mediated pathology in the lungs [150].

TLRs are broadly distributed along the airways by various cell types including respiratory epithelial cells, alveolar macrophages and DCs. Virus infection sensed by TLRs results in NF- κ B activation and inflammatory chemokine and cytokine expression. These chemokines and cytokines can act directly or via an autocrine/paracrine feedback mechanism to regulate virus infection and replication. RSV has been shown to be a poor inducer of type I IFNs (IFN- α/β), and cells infected with RSV are resistant to the antiviral effects of IFN- α/β [30]. As noted previously, RSV NS1 and NS2 proteins have been shown to act cooperatively as type I IFN antagonists [30,32,33,75], and recent studies suggest that RSV G protein also inhibits IFN- β expression [31]. As type I IFNs have an important role in DC maturation, activation of NK cells, differentiation and function of T cells, as well as enhancing primary antibody responses [151,152], RSV-mediated inhibition of IFN production negatively impacts antiviral immunity and facilitates virus replication.

Dendritic cells

DCs are the major antigen-presenting cells following RSV infection [153,154]. The costimulatory or inhibitory surface molecules and cytokines secreted by DCs influence the T-cell response, such as whether T cells are activated or tolerized and whether they are polarized to Th1, Th2 or regulatory T cells [155]. Respiratory DCs are located within intraepithelial sites and below the respiratory epithelium where they encounter RSV and carry the RSV antigens to the draining lymph node. There are two main subsets of DCs: myeloid or conventional DCs expressing CD11b and CD11c, and plasmacytoid DCs (pDCs) expressing little or no CD11b

or B220 [156]. The balance between conventional DCs and pDCs in the lung and lymph nodes is essential for driving pulmonary immunity to RSV infection [157]. Increased pDC numbers have a protective impact on the nature of the overall immune environment, while depletion of pDCs from the lungs of RSV-infected mice results in a pathologic response characterized by increased Th2 cytokine profiles [157–159]. DCs in the lung can be infected by RSV. Although RSV-infected DCs can still differentiate and mature, they display impaired T-cell activation, an effect linked to altered IFN- α or IL-1 receptor- α expression [160,161]. It has also been shown that direct contact of T cells with RSV F protein expressed on cells inhibits T-cell activation [162]. Moreover, a recent study showed that RSV impairs T-cell activation by preventing T-cell receptor–DC synapse assembly on DCs [163]. Thus RSV-infected DCs expressing F protein may also inhibit T-cell activation by a related mechanism.

Macrophages

Macrophages, like DCs, are key effector cells in the innate immune response. The lower respiratory tract abounds with alveolar macrophages, which serve as significant sources of proinflammatory cytokines such as TNF- α , IL-6 and IL-8 following RSV infection [164]. In one study, a depletion of macrophages significantly inhibited the early release of inflammatory cytokines following RSV infection, an effect which resulted in enhanced virus titers in the lung [165]. In this study, a depletion of macrophages had little effect on the activated T-cell recruitment and overall lung disease, suggesting that macrophages may be more important in the earliest response to RSV infection. However, a recent study comparing RSV-mediated lung pathogenesis in BALB/c and New Zealand Black (NZB) mice showed that alveolar macrophages are central in the disease process because depletion of alveolar macrophages in BALB/c mice before RSV exposure resulted in airway occlusion, and a similar pathogenesis was observed in NZB mice deficient in alveolar macrophages [166]. In this study, RSV infection yielded an increased viral load and enhanced expression of type I IFN genes at the height of disease, suggesting that innate, rather than adaptive, immune responses are critical determinants of the severity of RSV bronchiolitis.

Natural killer cells

NK cells constitute a major component of the innate immune system where they have a major role in the clearance of tumors and virus-infected cells by virtue of their natural cytotoxic ability. Chemokines, such as MIP-1 α , are important for the recruitment of NK cells to the site of infection and inflammation [167]. During RSV infection, NK cells are recruited to the lungs very early after infection and reach peak levels at approximately day 3–4 postinfection [41, 114]. DCs are considered to be the primary cell types that potentiate NK-cell activation and cytotoxicity [168,169]; however, a recent study showed that alveolar macrophages are required to recruit and activate NK cells in response to RSV infection, and depletion of macrophages reduced the activation and recruitment of NK cells [165]. RSV G and/or SH proteins appear to regulate trafficking of NK cells to the lungs, as mice infected with a RSV mutant lacking G and SH genes exhibited greater pulmonary trafficking of NK cells compared with mice infected with wild-type RSV [41].

Natural killer T cells

Natural killer T (NKT) cells are a subpopulation of CD1d-restricted T cells that coexpress semi-invariant T-cell receptor and NK-cell markers [170]. NKT cells recognize glycosphingolipids presented by CD1d, an antigen-presenting molecule that is related to the classical MHC class I and class II glycoproteins [171,172]. These cells can produce Th1- and Th2-type cytokines and therefore have the potential to impact adaptive immune responses by governing aspects of the cytokine microenvironment. NKT cells have been implicated in immune responses against RSV infection; NKT cells were shown to have a role in early IFN-

γ production and efficient induction of CD8 T-cell responses during primary RSV infection [173].

Adaptive humoral immunity

RSV infection induces antibody responses against several viral antigens; however, only the two major surface glycoproteins (F and G proteins) induce antibodies that have a major role in protection [174]. Vaccination studies using recombinant vaccinia virus expressing various RSV proteins have shown that serum antibodies can be induced by F, G, M2 and P proteins, but only F and G proteins were the major determinants of protection [175]. The RSV F protein has two forms: a mature form, found in virions, and an immature folded form [176,177]. The immature F protein does not contain all the neutralizing epitopes found on the mature form of the F protein, thus if released from lysed cells or made available from a denatured mature F protein; it is possible that the immature form may induce an ineffective antibody response leading to the diversion or reduction of a protective antibody response. It has been shown that both forms of F protein are able to induce antibody responses of comparable magnitudes [178]. Comparing the F to G proteins among RSV isolates, reveals that the G protein is the more divergent protein [179]. Between the major antigenic subgroups of RSV, such as A and B strains, there is only a 53% identity for G protein but a 90% similarity for the F protein. Therefore, few G-specific monoclonal antibodies are cross-reactive, while the majority of F-specific monoclonal antibodies are cross-reactive [179]. Unexpectedly, very few individual G-protein-specific monoclonal antibodies efficiently neutralize RSV infectivity, and G-protein-specific antibody neutralization requires multiple antibodies [180]. Furthermore, the majority of G-protein-specific monoclonal antibodies are much less effective compared with F-protein-specific monoclonal antibodies in the neutralization of RSV. It appears that protective anti-G protein antibodies recognize the central-conserved cysteine-rich region of the G protein [181]. It is plausible that this feature may also be linked to antibody-mediated inhibition of G protein CX3C interaction with CX3CR1 and immune modulation [23].

Neutralizing antibodies have an important role in protection from RSV infection, although serum and mucosal neutralizing antibodies seem to provide different levels of protection. Serum antibodies, mainly composed of IgG, gain access to the lungs easier than to the nasal passages via transduction. Passive immunization studies in cotton rats have demonstrated that serum antibodies can provide complete protection against RSV replication in the lungs, but only a partial reduction in nasal virus titers [182]. Mucosal secretory IgA antibody may have a more important role in local protection, although this antibody is short-lived and has less neutralizing activity compared with serum IgG antibodies. Repeated RSV infection can induce a sustained antibody response associated with high levels of mucosal IgA in nasal secretions, a feature that can limit virus replication in the upper respiratory tract independent of the level of serum antibodies [183].

Cellular immunity

Although antibody responses are vital for protection against RSV infection, T-cell-mediated cellular immune responses have a greater role in virus clearance. In humans, CD8⁺ T cells recognize F, matrix, M2 and NS2 proteins, but there is little or no recognition of G, phosphoprotein or NS1 protein [184]. In BALB/c mice, CD8⁺ cytotoxic T lymphocyte primarily recognize F, nucleocapsid and M2 proteins [185]. Priming of different subsets of CD4⁺ T cells appears to contribute to the quality and magnitude of the CD8⁺ T-cell response and subsequent disease pathogenesis. Studies in BALB/c mice vaccinated with different recombinant vaccinia virus constructs expressing G or F proteins have shown that F and G proteins prime different subsets of CD4⁺ T cells [186]. In BALB/c mice, F protein primes both CD8⁺ and CD4⁺ T cells toward a Th1-type biased cytokine response while G protein primes

only CD4⁺ T cells that are biased towards the Th2-type cytokine response [187]. The Th1 and Th2 CD4⁺ T-cells elicited react to a single region comprising amino acids 183–197 of the G protein [188]. Antigen-specific Th2-type CD4 T cells from mice have also been shown to respond to non-glycosylated immunodominant epitopes in the ectodomain of G protein, however, these epitopes have been shown to be poorly recognized by human CD4⁺ T cells [189,190]. In a related study, it was reported that the immunodominant peptide in G protein is recognized by both Th1 and Th2 CD4⁺ T cells in humans [191,192].

The importance of CD4⁺ memory T cells to RSV reinfection has been investigated; however, the majority of studies have focused on the response to RSV G-protein priming. It has been shown that the memory CD4⁺ T-cell response to the RSV G protein in the lungs of primed BALB/c mice challenged with RSV is dominated by effector T cells expressing a single TCR V β chain, such as V β 14 [193]. CD4⁺ T cells expressing TCR V β 14 preferentially proliferate and expand into activated effector T cells in the lungs rather than the lymph nodes, which drain the site of infection [194]. Although this study is limited to a specific inbred strain of mice, these findings may be important as RSV-specific CD4⁺ memory T cells have been shown to have a major role in RSV-induced immunopathology, a feature linked to polarizing for a Th2-type cytokine response and pulmonary eosinophilia [114,153,195–197]. It has recently been shown that RSV-specific memory CD8 T cells, when present in sufficient numbers, inhibit Th2-associated chemokines, CCL17 and CCL22, and may alter the trafficking of Th2-type cells and eosinophils into the lung [198]. Interestingly, the memory CD4⁺ T-cell response to RSV F protein is much broader than that to RSV G protein. Immunization of mice with the F protein elicits a broad repertoire of RSV F-protein-specific CD4⁺ T cells that predominantly express Th1-type responses; however, in the absence of IFN- γ , RSV F-specific memory CD4⁺ T cells secrete IL-5 and develop pulmonary eosinophilia after RSV challenge, suggesting that IFN- γ can modulate the memory CD4⁺ T-cell response to secondary RSV infection [199].

CD8⁺ T cells have a major role in the clearance of a virus. RSV-specific CD8⁺ T cells are found in the lungs and peripheral tissues after RSV infection. Studies have demonstrated that virus clearance is temporally associated with an increase of RSV-specific CD8 cytotoxic T-lymphocyte activity in the lungs [200]. Although T-cell responses to RSV infection predominantly occur in the lungs, it has been demonstrated in a mouse model that T-cell subsets can redistribute to secondary sites following RSV infection [201]. A higher proportion of RSV-specific CD8⁺ T cells in the peripheral blood have been observed in older infants than younger infants, a feature that might be due to immune immaturity, the Th2-type environment in the lungs or the suppressive effect of maternal antibodies. It has been shown that young children are prone to develop a Th2-type cytokine biased response, which has also been associated with higher RSV pathology [202]. However, other studies have demonstrated a predominant Th1-type response [203].

CD8⁺ memory T cells are important for clearing RSV reinfection. Studies of RSV-specific CD8⁺ memory T cells in humans have demonstrated that most pulmonary CD8⁺ T cells are retained in the lungs and a minority in the peripheral blood [204]. Consistent with these findings, it has been shown, following acute RSV infection in mice, that approximately 20% of pulmonary CD8⁺ T cells secrete IFN- γ in response to immunodominant peptide stimulation compared with 2–3% in the draining lymph node [205]. It remains unclear whether resident or recruited RSV-specific CD8⁺ T cells may be more important to control RSV reinfection; however, it has been demonstrated that although there is a higher proportion of CD8⁺ memory T cells in the lungs, amplification of recall responses in the organized lymphoid tissue is more efficient [205]. These findings do not appear to be related to RSV-mediated suppression, as RSV does not impair the *ex vivo* functionality of RSV-specific CD8⁺ T cells isolated from the lung during the acute and memory phase of murine RSV infection [206], suggesting that

functionality is likely to be affected by the lung environment. Consistent with these findings, it was recently shown that RSV-specific CD8⁺ T cells isolated from the lungs were impaired in their ability to secrete IFN- γ compared with RSV-specific CD8⁺ T cells isolated from the spleen, providing strong evidence that the decreased functionality of CD8⁺ cytotoxic T lymphocyte is specific to a lung environment and is not dependent on the specific virus, viral antigen or route of infection [207]. The mechanisms contributing to pulmonary CD8⁺ T-cell functional impairment are not well understood, but the effect may be linked to the cytokine microenvironment or other features. One study suggested that the functional inactivation of CD8 T cells is independent of RSV infection and is mediated by immunosuppressive agents in a basal lung environment [208]. It has been shown that the functional inactivation of CD8⁺ T cells is associated with TCR signaling, and the activity could be improved by IL-2 expression in the lungs [209].

Disease pathogenesis

A variety of host factors affect RSV disease pathogenesis. Some of the known risk factors for severe disease include the age of the individual at the time of infection, congenital heart disease and immunodeficiency or suppression [210–212]. The state of immune maturation early in life is also important for susceptibility to RSV disease. Maternal antibodies appear to confer only partial protection from RSV infection, and have been shown to also suppress antibody and T-cell responses to primary RSV infection [213]. Furthermore, genetic-association studies have demonstrated that variations in certain genetic loci, such as haplotype and Th2-type cytokine genes, confer susceptibility to RSV disease [214–216]. RSV disease pathogenesis mechanisms are not well understood, but the virus itself likely contributes to the level of pathogenesis and there is abundant evidence that the early innate host response to primary infection is important. Although RSV disease phenotypes vary in humans and among animal models, inflammatory mediators have been strongly implicated in RSV pathogenesis. For example, numerous studies have established that RSV can cause asthma exacerbations and bronchiolitis [217], and that these conditions are associated with enhanced CD4 T-cell responses, inappropriate cytokine expression, inflammation and reduced immune regulation [217–219].

There is no single paradigm for how the cascade of inflammatory mediators and events that follow affect RSV disease pathogenesis. Numerous inflammatory mediators are expressed in the response to RSV infection in humans and in animal models, and there is controversy regarding the importance of inflammatory mediators, Th1- versus Th2-type cytokine responses and dysfunction induced by RSV. It appears that disease pathogenesis is a multifactorial process involving virus replication, innate responses to infection and aberrant immune responses linked to modification by RSV proteins. The often early onset of RSV disease severity suggests that features affecting innate immunity have an important role in the disease process, and it is likely that these features are linked to RSV activation of PRRs or TLRs [220]. How RSV recognition and the subsequent response is tailored by the individual PRRs or TLRs is not yet clear, but evidence suggests that RSV may be recognized by surface and cytoplasmic TLRs including TLR2, TLR3, TLR4 and RIG-I [71,74,137,138,221], and that RSV may inhibit TLR7- and TLR9-mediated type I IFN production in human pDCs [136].

Activation of the innate immune response to RSV infection is associated with the production of chemokines and cytokines, which signal and recruit immune cells to sites of infection. These cells and their constituents function to regulate virus replication, but over-exuberant or inappropriate production of immune mediators in the respiratory tract may exacerbate the inflammatory response and promote airway damage and pathogenesis during virus clearance. RSV has been shown to modify the tempo and magnitude of cytokine and chemokine expression patterns during infection [114,151,196,222–224], and these features likely contribute to immune dysregulation and aspects of disease pathogenesis. Consistent with this

view, *in vivo* chemokine blockade reduces RSV-associated lung pathology in mice treated with anti-RANTES antibodies [130], and treatment of RSV-infected mice with a competitor of the RANTES receptor (Met-RANTES) reduces recruitment of inflammatory cells to the lung [225].

The innate immune response interfaces with adaptive immunity and has an important role in defining the magnitude and quality of adaptive immunity to RSV infection and immunopathology. Inefficient or inappropriate innate and inflammatory responses triggered by RSV may contribute to the induction of inappropriate T-cell responses, and there is considerable evidence of a Th2-type biased immune response specific for some RSV antigens [151,196,224,226–228]. It is thought that efficient virus clearance requires Th1-type responses characterized by IFN- γ , IL-2 and IL-12 expression, and that Th2-type responses characterized by IL-4, IL-10 and IL-13 expression are mostly ineffective and can lead to allergic diseases and asthma. Th2-type cytokine responses have been linked to RSV vaccine-enhanced disease studies in mice and cotton rats immunized with formalin-inactivated RSV vaccine or vaccinia vectors expressing RSV F or G proteins [195,224,228–231]. In these studies, sensitization with the RSV G protein leads to Th2-type CD4⁺ T-cell responses, and in many cases pulmonary eosinophilia, during subsequent challenge with RSV. In small animal models, ablation of either CD4⁺ or CD8⁺ T cells after RSV infection has been shown to decrease disease severity and illness [224,232], indicating the important role of T cells in immune pathology. Interestingly, RSV-specific memory CD8⁺ T cells appear to have an important role in regulation of the aberrant CD4⁺ T-cell response associated with vaccine-enhanced disease [198,233,234], but may have less of a role in other allergy-related pathologies such as airway hyper-responsiveness to RSV infection [235].

Conclusion

Numerous host and several virus components have been connected with disease pathogenesis following RSV infection; however, the importance of a single component against the spectrum of mediators is difficult to identify as being singularly important. It is apparent that RSV causes an atypical host response to infection with attributes of altered innate and inadequate immune memory responses where individuals may be repeatedly infected with the same or different strains of RSV, and where RSV may reinfect despite the presence of specific neutralizing antibodies [153,236–239]. Experimental animal models and *in vitro* studies of RSV infection have helped to identify and differentiate aspects of the host response to infection, and to identify RSV proteins that modulate these responses, however, the features of molecular pathogenesis remain poorly understood. A better understanding of the interplay between RSV and the host response to infection is needed to facilitate vaccine and antiviral drug development, although accumulating evidence suggests that regulating aspects of innate immunity may be more important in controlling disease pathogenesis.

Future perspective

Understanding the host response and molecular pathogenesis of RSV infection is critical for the development of vaccines, antivirals and other disease intervention approaches. It is clear that we must understand the problem if we are to prevent or correct it. Fundamental to this understanding is the biology behind RSV infection. RSV first infects respiratory epithelial cells during infection. The host response to infection is sensed by PRRs or TLRs that induce a network of host cell gene products, which profoundly affect the cascade of inflammatory and immune signals and functions. RSV-specific gene products have been shown to modulate the tempo, pattern and magnitude of the signaling cascade in the early elements of innate immunity. These early elements in innate immunity are required to properly orchestrate the adaptive immune response as well as regulate airway inflammation and disease pathogenesis. It is clear

that the identification of host pathways affected by RSV proteins will be fundamental to achieving rationally designed antiviral drugs and vaccines. Despite decades of effort toward an efficacious RSV vaccine, there are still no clear contenders on the horizon. It is likely that the vaccine focus will shift from current vaccine approaches toward the development of mucosal RSV vaccine strategies and antiviral drug approaches toward novel strategies that encumber RNA interference or antisense approaches that could be used to specifically target the virus or airway epithelium host genes early after infection. It is likely that interceding in the earliest events following RSV infection may offer a clearer path toward drug-based disease intervention, and generating antibody responses that target RSV proteins more effectively may provide greater efficacy for RSV disease pathogenesis.

Executive summary

Respiratory syncytial virus

- Respiratory syncytial virus (RSV) is a paramyxovirus.
- Nonsegmented negative-strand RNA virus containing two nonstructural (*NS2* and *NS1*) genes followed, in gene order, by nucleocapsid, phosphoprotein, matrix, small hydrophobic, surface attachment glycoprotein (G), surface fusion glycoprotein (F), a M2 gene encoding two proteins from M2-1/M2-2 and RNA-dependent RNA polymerase.
- Transcription of mRNA occurs in a 3' to 5' order from a single promoter near the 3' end resulting in a series of subgenomic mRNAs.
- The level of protein expressed is related to mRNA abundance.
- Virions assemble at the plasma membrane where nucleocapsids localize with the cell membrane containing membrane viral glycoproteins.

Regulation of host-cell responses to infection

- RSV primarily infects respiratory epithelial cells lining the nasal passages and respiratory tract.
- Following infection, RSV delays apoptosis by enhancing IEX-1L, several Bcl-2 family members, proteins within the phosphatidylinositol 3-kinase pathway, and by inhibiting tumor suppressor p53 and oncogene Akt.
- RSV proteins modulate host-cell responses through pattern recognition receptors and Toll-like receptors (TLRs); RSV F protein interacts with TLR4; G protein potentially with TLR2.
- RSV interferes with the host antiviral cytokine response; NS1 and NS2 are important in type I IFN antagonists.
- RSV induces suppressor of cytokine signaling (SOCS)1 and SOCS3 negative regulation of type I IFNs.
- RSV infection modulates respiratory epithelial-cell function, surfactant protein (SP)-A and SP-D are decreased, and matrix metalloproteinases are increased.
- RSV G protein contains a CX3C chemokine motif which can bind to the CX3CR1 and impede CX3CR1 responses and CX3CR1-mediated leukocyte chemotaxis.

Cytokine responses to RSV infection

- RSV infection of airway epithelial cells results in a cascade of signaling events mediated by NF- κ B leading to the expression of proinflammatory cytokines and chemokines.
- RSV G-protein expression during acute infection in mice has been associated with altered CC and CXC chemokine mRNA expression and Th1/Th2-type cytokines.
- RSV G protein inhibits IFN - β and IFN-stimulated gene-15.

Regulation of cellular transcription factors

- RSV infection induces many transcription factors including IFN regulatory factor (IRF)3, IRF7, NF- κ B, p38 MAPK and AP-1.
- RSV G protein interferes with Toll IL-1 receptor domain-containing adaptor molecule-1 or NF- κ B activation leading to reduced levels proinflammatory cytokines.
- Interferon antagonism by NS1/NS2 is mediated by inhibiting STAT2 and IRF3 activation.
- NS1 contains elongin-C- and cullin-2-binding sequences that provide ubiquitin E3 ligase activity to target proteins, specifically STAT2, to the proteasome.
- RSV G protein induces SOCS1 and SOCS3 proteins which negatively regulate cytokine signaling cascades, particularly type I IFNs.

Innate immunity to RSV infection

- Host cells recognize RSV infection via TLR4, TLR3, TLR2 and retinoic acid-inducible gene-I resulting in the expression of proinflammatory cytokines and chemokines.
- The balance between conventional dendritic cells (DCs) and plasmacytoid DCs in the lung and lymph nodes is important for driving pulmonary immunity to RSV infection.
- DCs infected with RSV lose their ability to stimulate RSV-specific T cells.
- RSV G protein has a role in modulating natural killer cells and other cell trafficking to the lung through inhibition of cytokines and chemokines.

Adaptive humoral & cellular immunity

- RSV F and G surface proteins induce neutralizing antibody production, and these are the major antigenic determinants of protection.
- T-cell responses have an important role in viral clearance.
- RSV F protein may polarize both CD4⁺ and CD8⁺ T-cell responses toward a Th1-type response.
- RSV G protein may prime CD4⁺ T cells toward a Th2-biased response.

Disease pathogenesis

- A variety of host factors affect RSV disease pathogenesis; known risk factors for severe disease include the age of infection, congenital heart disease and immune deficiency or suppression.
- The state of immune maturation early in life is important for susceptibility to RSV disease.
- Genetic-association studies indicate that variations in certain genetic loci confer susceptibility to RSV disease.

- Disease pathogenesis is a multifactorial process.

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