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Rhinoviruses and Their Receptors: Implications for Allergic Disease

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Abstract

Human rhinoviruses (RVs) are picornaviruses that can cause a variety of illnesses including the common cold, lower respiratory tract illnesses such as bronchitis and pneumonia, and exacerbations of asthma. RVs are classified into three species, RV-A, B and C, which include over 160 types. They utilize three major types of cellular membrane glycoproteins to gain entry into the host cell: intercellular adhesion molecule 1 (ICAM-1) (the majority of RV-A and all RV-B), low density lipoprotein receptor (LDLR) family members (12 RV-A types) and cadherin-related family member 3 (CDHR3) (RV-C). CDHR3 is a member of cadherin superfamily of transmembrane proteins with yet unknown biological function, and there is relatively little information available about the mechanisms of RV-C interaction with CDHR3. A coding single nucleotide polymorphism (rs6967330) in CDHR3 could promote RV-C infections and illnesses in infancy, which could in turn adversely affect the developing lung to increase the risk of asthma. Further studies are needed to determine how RV infections contribute to pathogenesis of asthma and to develop the optimal treatment approach to control asthma exacerbations.

Keywords

Human rhinovirus; cellular receptor; ICAM-1; LDLR; CDHR3; asthma; allergy

Introduction

Human rhinoviruses (RVs) are non-enveloped positive-strand RNA viruses in the family *Picornaviridae*, genus *Enterovirus* classified into three species (RV-A, B and C) according to phylogenetic sequence criteria and distinct genomic features. Clinical isolates of RV-A and RV-B identified by 1987 [1] were classified into 100 serotypes based on their antigenic cross-reactivity in serum neutralization tests, while more recently isolated A and B (geno)types ($n = 15$) were assigned solely on sequence identity criteria [2]. The third species

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(RV-C) were identified beginning in 2006 [3, 4] with the development of highly-sensitive molecular detection techniques since RV-C clinical isolates did not propagate in standard cell culture (such as HeLa or embryonic lung fibroblasts) [5–8]. Current genetically-based classification assigns RV-C isolates into 65 types (including 10 provisionally assigned types) using sequence diversity thresholds in two capsid-coding genes (13% nucleotide divergence in VP1 and/or >10% divergence in VP4/VP2 when VP1 sequences are lacking) [2, 9].

RVs is the most frequent cause of the common cold, but can also induce more severe lower respiratory tract illnesses such as bronchitis and pneumonia and provoke exacerbations of asthma, cystic fibrosis and chronic obstructive pulmonary disease [10–13]. It is now recognized that wheezing illnesses in infancy caused by RV are strongly associated with a high risk of developing asthma in genetically predisposed children, however, the pathogenic mechanisms underlying both asthma inception and exacerbation are not yet clearly understood [14–16]. RV-A and RV-C isolates are more virulent in infants, and are more likely to cause exacerbations of childhood asthma compared to RV-B [17–25].

RV-A and RV-B serotypes were classified into two groups, major and minor, on the basis of cellular receptor specificity, utilizing either intercellular adhesion molecule 1 (ICAM-1) or low density lipoprotein receptor (LDLR) family members for cell entry [26], whereas RV-C receptor remained unknown until recently [27]. Failure of the conventional cell culture systems to support RV-C growth along with the unique amino acid composition profiles of the available RV-C capsid sequences in the putative ICAM-1 and LDLR receptor footprint sites, inconsistent with both major and minor group receptor interactions, suggested unique receptor specificity. After development of a first reverse genetics system for RV-C, we demonstrated that the full-length viral RNA transcripts synthesized *in vitro* were infectious when transfected into cell lines resistant to RV-C infection [8]. We and others also developed the first culture systems for RV-C (sinus mucosal organ culture and air-liquid interface (ALI) culture of differentiated airway epithelial cells) [8, 28–31], and recently discovered that cadherin-related family member 3 (CDHR3), a transmembrane protein with yet unknown biological function, mediates virus binding and replication [27].

Allergic diseases are caused by a hypersensitivity to normally harmless non-infectious antigens and mediated by allergen specific immunoglobulin E (IgE) antibody response and T helper type 2 (Th2) cells. Chronic allergic inflammation induced by prolonged or repetitive exposure to allergens is characterized by the presence of large numbers of eosinophils, mast cells and some other immune cells, as well as physiological changes in structural cells and extracellular matrix in the affected tissues. A number of cross-regulatory mechanisms between the antiviral and allergic immune responses that might play a role in the pathophysiology of allergic diseases have been revealed in both the *in vitro* and *in vivo* human studies [32–35]. RV may also directly induce specific IgE response in children with high total IgE levels, however, its role in promoting allergic response and inflammation is uncertain [36].

Rhinoviruses replicate their genome and produce progeny in epithelial cells of upper and lower respiratory tract. They have been recovered in specimens obtained from the nose, sinuses, larynx, nasopharynx, trachea, bronchi as well as conjunctiva and middle ear [37–

42]. Diseases of the respiratory tract, including rhinosinusitis, allergic rhinitis and bronchial asthma are one of the most common reasons for doctor visits in the United States and their prevalence and the impact on health care costs keep increasing [43]. About 80% percent of childhood asthma [44, 45] and more than 50% of adult asthma have been reported to be allergic [46], and respiratory viral infections are the most important triggers for exacerbations in asthmatic patients [10, 47].

The relationship between viral respiratory infections, allergic inflammation and asthma as well as possible molecular mechanisms of virus-allergen interactions in development and exacerbation of asthma have been extensively reviewed [32, 34, 35]. In this article, we will briefly discuss known cellular receptors utilized by RVs, molecular signaling induced by virus binding, entry and replication in host cells, and provide an update on CDHR3 protein recently implicated in RV-C entry.

Rhinovirus receptors and entry to host cells

Receptor-mediated endocytosis

Rhinoviruses can utilize several cellular receptors in order to cross the plasma membrane by endocytosis, release their genome from viral capsid via structural rearrangements, and deliver it to the site of polypeptide translation and replication in the cytoplasm. Endocytosis, a form of active transport of various molecules into the cell, describes the *de novo* production of internal membranes from the plasma membrane. It plays a key role in nutrient uptake, cell signaling, cell shape changes and often exploited by viruses for internalization into cells. There are several distinct endocytic pathways coexisting in mammalian cells that are best defined through their differential dependencies on certain lipids and proteins, including clathrin, caveolin, flotillin, kinases, small G proteins, actin, dynamin etc. [48]. Although some cargoes enter exclusively by one pathway, most cargoes can enter by several pathways. Endocytosis of transmembrane receptors upon binding to specific extracellular ligands removes them from the surface; this process generally occurs via clathrin-coated pits and vesicles.

Productive entry pathways of RV-A and RV-B have been extensively studied, mostly in established model cell lines such as HeLa [49, 50], whereas molecular mechanisms of RV-C entry and receptor-mediated signaling are unknown. Both the major and minor group RVs are internalized by a clathrin- and dynamin-dependent receptor-mediated endocytosis in HeLa cells [51, 52], however, minor group RV can also enter via clathrin- and dynamin-independent pathway [53]. The only other known receptor that can be alternatively exploited by some major group RV types (RV-A8, A54 and A89) in cultured ICAM-1-negative cells is heparan sulfate [54, 55], and virus entry in this case depends primarily on low endosomal pH and dynamin but not on clathrin, caveolin, or flotillin [56].

Identification of RV-A and RV-B receptors

The major group RV cellular receptor ICAM-1 was identified in 1989 by three independent research groups [57–59], and five years later followed by the discovery of LDLR family members as the receptors for minor group rhinoviruses, which includes only 12 known RV-

A types [60]. In both cases, the functional receptors were identified by screening monoclonal antibodies that inhibit RV infection and recognize cellular membrane proteins with binding activity to RVs *in vitro*, and validated by up- or downregulation of the target protein expression in cultured cells. These receptors belong to two different families of transmembrane glycoproteins with well-characterized properties.

ICAM-1 is a member of the immunoglobulin (Ig) superfamily of cell adhesion molecules expressed by several cell types including leukocytes, epithelial and endothelial cells. ICAM-1 is composed of five immunoglobulin (Ig) domains (extracellular part), a transmembrane region, and a short cytoplasmic domain [61]. It plays a major role in leukocyte migration from blood to the tissues in inflammatory sites via binding to two membrane-bound integrin receptors, leukocyte function-associated antigen (LFA-1) [62], and macrophage-1 antigen (Mac-1) [63].

The LDLR family comprises at least three members that can bind and internalize RV including the LDLR, the very low density lipoprotein receptor (VLDLR), and the LDLR related protein (LRP). Receptors in this family are recognized by the presence of several structural modules in their extracellular regions and overall similar domain arrangements that include ligand-binding repeats, epidermal growth factor precursor repeats, YMTD spacer domains (β -propeller modules), a single transmembrane domain, and a relatively short cytoplasmic tail [64, 65]. LDLR is responsible for uptake of its natural ligand, cholesterol-carrying lipoprotein particles, into cells by endocytosis via clathrin-coated pits, and their release upon delivery to the low pH milieu of the endosome [66]. The cytoplasmic tail of the LDLR family members contains motifs for interaction with a number of cytoplasmic adaptor and scaffold proteins, and mediates signal transduction [64].

ICAM-1 vs LDLR binding and entry in HeLa cells

There are some differences in the subcellular localization between major and minor group receptors. ICAM-1 is located at the plasma membrane and also in the cytoplasm on the apicolateral portions of the airway epithelial cells [67, 68], whereas LDLR family members are endocytic recycling receptors found mainly in recycling endosomes and, to a lesser extent, at the plasma membrane [69, 70]. Although the structural changes in the viral capsid of both major and minor group RVs similarly result in a stepwise transition from native virus to subviral particles and release of the RNA, some key virus binding properties are receptor specific [50, 71].

Members of the both receptor groups require low endosomal pH for structural changes, however, in case of ICAM-1, the changes are catalyzed by the receptor and occur before and during the endocytosis [72–74]; whereas LDLR family members do not provide sufficient uncoating signals upon binding [75, 76]. The receptor binding sites were mapped around the 5-fold axis of symmetry in viral capsid but they have also shown to be different between the major and minor group RVs. The first domain of ICAM-1 binds the virus inside the canyon (a 2.5-nm depression) surrounding the dome at the vertex [77], whereas the LDLR ligand binding domain, that composed of multiple ligand-binding repeats, attaches to the top of the star-like surface exposed structure at the vertex [78]. In contrast to LDLR proteins containing the NPxY internalization motif (x, any amino acid residue), ICAM-1 short

cytoplasmic tail lacks any known endocytosis signal and is not required for RV internalization [79].

RV entry in primary airway epithelial cells

The entry mechanism of major group RVs is thought to be cell-type specific because in contrast to HeLa cells, RV-B14 endocytosis in rhabdomyosarcoma cells is independent of clathrin, caveolin, flotillin, and lipid rafts [50, 56]. Since most of the work on RV receptors and cell entry was done in HeLa and some other established cell lines, the mechanisms of viral entry in airway epithelial cells, natural RV host cells, have not been fully elucidated. ICAM-1 and LDLR expression was confirmed in both ciliated and non-ciliated cells of airway epithelium [50, 67, 68]. Studies on major group RVs in primary airway epithelial cells revealed some contradicting results on virus entry pathways.

Lau and colleagues proposed that internalization of RV occurs via clathrin-mediated endocytosis (in agreement with data from HeLa cells) and is regulated by the non-receptor tyrosine kinase Syk, which is widely expressed in both leukocytes and airway epithelial cells and fibroblasts. Briefly, RV-A16 binding to ICAM-1 leads to the recruitment of Syk to the plasma membrane and formation of an ICAM-1/ezrin/Syk complex resulting in phosphorylation and activation of Syk and subsequent downstream signaling to the phosphoinositide-3 (PI3) kinase pathway, that ultimately regulates RV internalization [80, 81].

In contrast, studies from Gulbins group revealed that both major and minor group RV infection of nasal mucosa (as well as lung fibroblasts and HeLa cells) occur via ceramide-enriched and ganglioside type 1 (GM-1) positive membrane platforms, and is independent of clathrin and dynamin [82, 83]. This apparent discrepancy might indicate that several pathways can be used for RV uptake in both primary airway epithelial cells and cell lines. Further studies in fully-differentiated airway epithelial cells are needed to understand RV binding and entry mechanisms in vivo.

CDHR3 mediates RV-C binding and entry

We have recently discovered that human cadherin-related family member 3 (CDHR3) protein mediates virus binding and replication in normally unsuspceptible cultured cells [27]. Since both our group and others have demonstrated that only fully differentiated cultures of human airway epithelial cells support RV-C replication while undifferentiated monolayers (as well as many continuous cell lines) do not [28–30], we compared genome-wide gene expression profiles in these cells by microarrays and identified a total of 12 target genes encoding transmembrane proteins for functional validation. Transfection-induced expression of CDHR3 was sufficient to enable virus binding and subsequent replication in HeLa and 293T cell lines normally unsuspceptible to RV-C infection. In the absence of human CDHR3 crystal structure, we modeled the ectodomains 1–6 relative to other known cadherin family protein structures and identified a putative docking site for CDHR3 domains 1 and 2 binding RV-C15 across the adjacent protomers, in a 5-fold to 2-fold axis orientation in a region with multiple residues conserved among all RV-C types [27].

CDHR3 is a member of cadherin superfamily of transmembrane glycoproteins with yet unknown biological function. Other members of this family such as classical cadherins and desmosomal cadherins are responsible for communication between identical cells through calcium-dependent interactions, and protocadherins are implicated in neuronal plasticity and tissue development [84, 85]. The functional role of many related members of the family remains largely unknown. Cadherins are the principal components of adherens junctions and desmosomes and also have functions beyond adhesion, including roles in signaling, mechanical transduction and brain morphogenesis [86].

A study of Danish children provided the first hints about possible functions of CDHR3. In a genome-wide association study, CDHR3 was reported as a novel gene associated with an increased risk of developing severe childhood asthma [87]. The CDHR3 genotype (rs6967330) that converts residue cysteine to tyrosine at position 529 (Cys529→Tyr), significantly increased the risk of asthma hospitalizations and severe exacerbations in young children (2–6 years old) compared with the control group. Transfection experiments *in vitro* have also shown that this mutation in ectodomain 5 near a calcium binding site leads to a marked increase in cell surface expression of the CDHR3 protein, presumably, by altering the protein conformation. We then confirmed that this mutation also mediates enhanced RV-C binding and replication *in vitro* and developed a HeLa cell line (HeLa-E8) stably expressing the CDHR3-Y₅₂₉ variant that supports efficient propagation of RV-C by infection [27].

Although CDHR3 is the only cellular factor known so far that enables RV-C propagation in normally unsusceptible host cells, the loss-of-function and direct biochemical receptor-virus interactions have not yet been confirmed. Nevertheless, in agreement with its proposed RV-C receptor function, CDHR3 is highly expressed in differentiated human airway epithelial cells *in vitro* [27, 88] and in human lung tissue and bronchial epithelium *in vivo* [87, 89]. CDHR3 subcellular localization has not been mapped yet; however, high level of its expression was found in ciliated cells in differentiated airway epithelium [Griggs *et al.*, manuscript in preparation]. Recent RNA-seq analysis of RV-A16 infected ALI cultures found that CDHR3 mRNA expression at baseline was slightly lower in asthmatic epithelial cells compared to non-asthmatic cells ($p = 0.02$), however, the CDHR3 genotype was not provided for these donors [90]. Interestingly, in contrast to ICAM-1 and LDLR, CDHR3 expression was further decreased upon viral infection and its reduction was highly correlated with viral infection (Pearson correlation p -value = 1.6×10^{-4}) indicating different regulatory mechanisms. Rhinovirus-induced disruption of the barrier function of airway epithelial cells cultured at ALI along with downregulation of some tight and adherens junction mRNAs and proteins have been also documented [90–92].

The molecular mechanisms involved in RV-C binding to CDHR3 as well as subsequent entry and signaling pathways are not yet defined. Studies on epithelial (E)-cadherin (CDH1), which is the prototype and well-characterized member of cadherin family widely expressed in epithelial cells, and on other classical cadherins, revealed that they can use many pathways for internalization from the cell surface, including clathrin-, dynamin- and caveolin-dependent and clathrin-independent pathways [93, 94]. These pathways can ultimately lead to recycling it back to the cell surface, sequestration inside the cells or target

it for degradation in lysosomes. The cytoplasmic domain of E-cadherin binds to β -catenin and p120 bridging it to the cytoskeleton through additional binding interactions with α -catenin and actin. Tyrosine kinase (such as Src and receptor tyrosine kinase family) signaling regulates trafficking of E-cadherin, e.g. tyrosine phosphorylation of the E-cadherin-catenin complex results in endocytosis and disruption of cell-cell adhesion [95] but other mechanisms of regulating cadherin endocytosis could exist including actin polymerization. If CDHR3 can function similarly to E-cadherin, then by analogy with other known RV receptors, RV-C can presumably hijack one of these endocytic pathways to enable cell entry.

Assuming that CDHR3 can play a role in maintaining epithelial barrier function, it could be inaccessible to virus approaching from the apical surface if localized to adherens junctions in polarized airway epithelium. Other viruses, including some enteroviruses, bind to various cell-adhesion molecules located in intercellular junctions to gain entry to the host cell [96]. For example, coxsackievirus B, which utilizes coxsackievirus and adenovirus receptor (CAR) in tight junctions for internalization, also interacts with additional decay-accelerating factor (DAF) on the apical cell surface to activate actin rearrangements that permit subsequent virus movement to the tight junctions [97]. Some human cadherins (e.g. E-cadherin) are utilized by a number of fungal, bacterial and viral pathogens (e.g. *Candida albicans*, *Listeria monocytogenes*, *Leptospira interrogans* and adenovirus) as entry cellular receptors [98–100]. In a recent study it has been found that desmoglein-2 (DSG-2), a member of the cadherin protein superfamily and constituent of desmosomes, is the attachment receptor for human species B adenoviruses (Ad3, Ad7, Ad11 and Ad14), which cause respiratory and urinary tract infections [101]. Adenovirus interaction with DSG-2 in epithelial cells results in the opening of intercellular junctions, thus increasing access to other receptors (e.g. CD46) that are generally not accessible.

There is evidence that dysregulated epithelial barrier function may promote airway inflammation and allergic sensitization [102]. Tight junctions serve to reduce exposure of dendritic cells and other leukocytes to allergens and pathogens, and compromised barrier function can thereby reduce tolerance to allergens. Asthma is also associated with reduced barrier function, and this could be a primary defect or a result of airway inflammation [103]. Th2 inflammatory cytokines such as interleukin (IL) 4 and IL-13 can reduce the expression of tight junction constituent proteins, leading to barrier disruption. It is likely that CDHR3 is preferentially localized on the cell surface within intercellular junctions, where it may be protected from exposure to the airway lumen and contact with RV-C. This suggests the possibility that reduced airway barrier function in asthma exposes CDHR3 to the environment and increases susceptibility to RV-C infections in addition to the effects of “asthma risk” genotype (rs6967330) (Fig. 1). Studies to test this theory are now in progress.

Rhinovirus-induced signaling with regard to allergic disease

RV infection and asthma

RV infections and allergy in early life synergize to increase the risk of developing asthma [35]. Several theories have been proposed to explain this interaction, including (i) causal role of viruses in asthma due to direct damage of developing airways and modulation of immune

responses, (ii) secondary role only as an early indicator of abnormal airway physiology and/or diminished antiviral responses, and (iii) a “two-hit hypothesis” in which genetic predisposition to atopy is combined with early respiratory viral infection in promoting asthma [13]. In agreement with the causal role, it has been shown that acute RV infections both *in vivo* and *in vitro* can induce a number of cellular factors regulating airway growth, development, fibrosis, repair and associated with bronchial remodeling (IL-6, TGF- β , VEGF, MMP-9, MUC5AC, FGF2, HBEGF etc.) and increase secretion of prostaglandins and cyclooxygenase-2 [104–107]. However, RVs usually cause very mild (if any) visible cytopathic effect in intact fully differentiated epithelium [29, 108], likely because they replicate only in a small subset of cells [40, 109]. In agreement with these findings, ICAM-1 is expressed in small proportion of the ciliated cells in airway epithelium in the absence of inflammation; therefore, plasma membrane concentration of receptors appears to determine at least in part susceptibility to RV infection [110, 111]. Notably, both ICAM-1 and LDLR expression is induced by RV infection regardless of receptor type, which may promote additional viral binding and infection spread [68, 112–114].

RV infection initiates signaling events leading to the production of multiple cytokines, chemokines, interferons and growth factors in airway epithelial cells, and these responses can promote cellular inflammation. Several clinical studies reported that RV-A and RV-C are more virulent than RV-B, suggesting differences in the biology of RV species that are independent of their receptor specificity [21, 24]. In agreement with these findings, experiments in cultures of differentiated airway epithelial cells indicate that RV-B types have lower and slower replication, lower cellular cytotoxicity and cytokine and chemokine production compared with RV-A or RV-C [108]. Although no striking differences in epithelial cell responses between major and minor RVs were noted [115], differential signaling and cytokine responses were recently between the major- and minor-group RV treatments of macrophages [116].

Animal models of paramyxovirus-induced respiratory inflammation confirmed that Th1-type mediators can recruit the high affinity IgE surface receptor (Fc ϵ RI)-expressing plasmacytoid dendritic cells (pDC), eosinophils and T cells to the lower airways resulting in IgE mediated Th2-type response and mucous cell metaplasia [117, 118]. Increased expression and cross-linking of Fc ϵ RI before RV stimulation inhibits type I and type III interferon (IFN) secretion from peripheral blood mononuclear cells [119]. These findings demonstrate that respiratory viral infections can block antiviral responses and promote viral replication by inducing Th2-type allergic inflammation. Surprisingly and in contrast to previously published findings [120], the structural changes in cultured primary airway epithelial cells associated with Th2-type cytokine-induced goblet cell metaplasia decreased their susceptibility to RV-A16 infection [107]. The absence of interferon-producing immune cells and a lower number of target epithelial cells suitable for viral replication could be responsible for these effects *in vitro*.

Virus recognition in host cell

The initial responses and signaling to major group RVs, mediated upon binding to ICAM-1 receptor in a replication-independent manner, result in the expression of chemokines such as

IL-8 [80] and C-X-C motif chemokine ligand 10 (CXCL10) [121] in epithelial cells and monocytes. Syk is an early signaling molecule, rapidly recruited to activated ICAM-1 at plasma membrane. It becomes phosphorylated and mediates signaling via p38 mitogen activation protein (MAP) kinase and PI3 kinase, leading to downstream activation of Akt1 kinase and transcription factor NF- κ B, IL-8 expression and, ultimately, to tissue neutrophilia [80, 81].

Innate immune responses to viral and bacterial pathogens are mediated by pattern recognition receptors (PRR), which recognize a number of highly conserved pathogen associated molecular patterns. PRR signaling during viral infections results in activation of the two major classes of transcription factors, interferon regulatory factors (e.g. IRF-3, IRF-7) and NF- κ B family members, which induce the expression of type I IFNs and pro-inflammatory genes [122, 123]. Three major types of PRRs, toll-like receptors (TLR), NOD-like receptors (NLR) and retinoic acid-inducible gene-I-like receptors (RLR), contribute to the sensing of RV infections.

According to the current model, RV penetrates into the cytoplasm via endosomal membrane destabilization and rupture (major group) or through an ion-conducting pore in the endosomal membrane (minor group) [50]. The mechanism of how viral RNA is released during this process and enters the cytosol together with empty capsids is still poorly understood. Free viral RNA was first seen as soon as 10–12 min post infection (p.i.) in the perinuclear area of the cell, which is indicative of RNA release from late endosomes, and remained in the cytoplasm, whereas the protein signal almost completely disappeared in 2 h p.i.; the newly synthesized protein and RNA were first detected at 3.5 h p.i. [124].

Studies in cultured monolayers of airway epithelial cells *in vitro* revealed that the innate responses to RV are mediated by the endosomal transmembrane TLR3, followed by additional signals from the cytoplasmic RLR melanoma differentiation associated protein 5 (MDA5) that both recognize viral double-stranded (ds)RNA generated during replication [125, 126]. However, the mechanism by which dsRNA reaches the endosome and associated early signaling pathways remain incompletely understood. Notably, impaired TLR3 and MDA5 signaling, potentially leading to an inability to activate type I and type III IFN responses to RV infection was found in bronchial epithelial cells from asthmatic subjects [127]. The involvement of TLR7 and 8, sensing single-stranded RNA, and TLR2 recognizing viral capsid was also confirmed [128, 129]; however, the role of retinoic acid inducible gene-1 (RIG-I) that binds to the 5' triphosphate motif (which is not exposed but covalently linked to the viral protein g (VPg) in all picornaviruses) is more controversial [130, 131]. RV-induced proinflammatory cytokine response in macrophages was mainly TLR2 dependent in a mouse model and did not require viral endocytosis or replication [132].

Animal models utilizing MDA5-, TLR3- and TLR7-deficient mice have been used to explore RV recognition and innate immune signaling mechanisms leading to RV-induced airway inflammation and hyperresponsiveness *in vivo*. Interestingly, MDA5 null mice showed a delayed type I IFN and attenuated type III IFN response to RV-A1b infection and increased viral titer, whereas TLR3 null mice showed normal IFN responses and unchanged

viral titers. Both MDA5- and TLR3-deficient mice also showed reduced lung inflammatory and contractile responses suggesting that TLR3 and MDA5 initiate pro-inflammatory signaling pathways which can lead to airway inflammation and hyperresponsiveness [133]. More intriguingly and in contrast to findings in TLR3-null mice, allergic TLR7-deficient mice displayed impaired type I and type III IFN release upon RV infection, increased virus replication and exaggerated eosinophilic inflammation and airway hyperreactivity [134]. TLR7 expression in the lungs was suppressed by Th2-type allergic inflammation and by IL-5-induced eosinophilia in the absence of allergy. These data demonstrate that a lack of TLR7 signaling under conditions that model a viral asthma exacerbation or its inhibition by IL-5-induced lung eosinophilia impairs IFN production and exaggerates Th2-driven inflammatory responses. Collectively, these data suggest that suppression of TLR3 and MDA5 and induction of TLR7 and their downstream signaling pathway may be novel therapeutic targets for the prevention and treatment of RV-induced asthma exacerbations.

Less is known regarding the role of NLRs in the sensing of RV infections. It has been recently shown that the newly discovered dsRNA receptor Nod-like receptor X-1 (NLRX-1) interacts with RV RNA and disrupts the barrier function of the airway epithelium by increasing reactive oxygen species (ROS) in the mitochondria. Thus, these findings suggest that ROS, if not neutralized efficiently, may not only enhance susceptibility to secondary infections but also alter innate immune responses to subsequently inhaled pathogens and allergens [135].

Conclusions

RV-A, B and C utilize three major types of cellular membrane glycoproteins to gain entry into the host cell: ICAM-1, LDLR and CDHR3. Despite some substantial differences in their structure, subcellular localization, virus binding sites, mechanisms of endocytosis and downstream signaling, they all support efficient virus entry and replication resulting in induction of antiviral and inflammatory response. In contrast to the first two known RV receptors studied in more detail, there is relatively little information about molecular mechanisms of RV-C interaction with CDHR3. Notably, a coding SNP (rs6967330) in CDHR3 could promote RV-C wheezing illnesses in infancy, which could in turn adversely affect the developing lung to increase the risk of asthma. Airway inflammation can increase expression of ICAM-1 and suppress TLR7 signaling in the airway, which could provide a link between diseases of chronic airway inflammation and increased severity of illnesses caused by rhinoviruses using this receptor. Further studies are needed to determine whether reduced epithelial barrier function, which also contributes to pathogenesis of asthma, leads to increased accessibility of CDHR3, and in turn promotes more severe RV-C illnesses. These concepts suggest that the optimal treatment approach to control asthma exacerbation may need to target both virus infection and allergic inflammation.

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•• Of major importance

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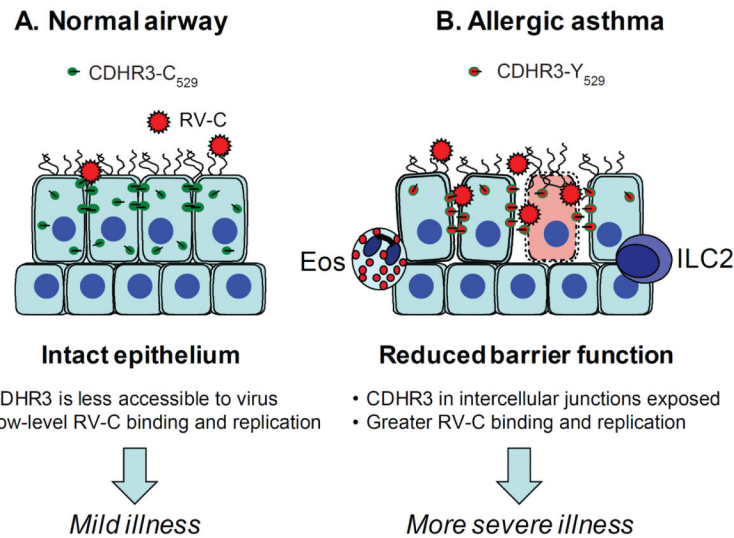
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**Fig.1.**

Potential mechanisms of RV-C infection in normal and asthmatic airway epithelium. We speculate, based on function of other cadherins, that CDHR3 could be preferentially localized on the cell surface within intercellular junctions. The CDHR3 genotype (rs6967330) that converts amino acid residue cysteine to tyrosine at position 529 (C₅₂₉→Y) leads to an increased cell surface expression of CDHR3. **a.** In a healthy intact epithelium with normal barrier function, CDHR3 is likely to be less accessible for RV-C binding resulting in a reduced infection and mild illness. **b.** Chronic allergic inflammation in asthmatic airways reduces epithelial barrier function, and this could secondarily increase accessibility of CDHR3 for RV-C binding in individuals with “asthma risk” genotype. As a result, RV-C could infect more cells, leading to more severe respiratory illness. Eos, eosinophils; ILC2, type 2 innate lymphoid cell.