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Extracellular Nucleotide Regulation of Airway Epithelial Cell Immunological Mediator Release

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Abstract

The airway epithelial cells (AECs) lining the conducting passageways of the lung secrete a variety of immunomodulatory factors. One interesting pair of molecules produces by AECs is IL-6 and prostaglandin E2 (PGE₂). PGE₂ limits lung inflammation and promotes bronchodilation. By contrast, IL-6 drives intense airway inflammation, remodeling, and fibrosis. The signaling that differentiates the production of these opposing mediators is not understood. In this thesis, we find that the production of PGE₂ and IL-6 following stimulation of AECs by the danger associated molecule pattern (DAMP), extracellular ATP, share a common requirement for Ca²⁺ release-activated Ca2+ (CRAC) channels. ATP-mediated synthesis of PGE2 required activation of cell surface metabotropic P2Y₂ receptors and CRAC channel-mediated cPLA₂ signaling. By contrast, ATP-evoked synthesis of IL-6 occurred via activation of P2X receptors and CRAC channel-mediated calcineurin/NFAT signaling. In contrast to ATP, which elicited the production of both PGE₂ and IL-6, the uridine nucleotide, UTP, stimulated PGE₂ but not IL-6 production. These results reveal that AECs employ unique receptor-specific signaling mechanisms with CRAC channels as a signaling nexus to regulate release of opposing immunomodulatory mediators. Collectively, our results identify P2Y₂ receptors, CRAC channels, and P2X receptors as potential intervention targets for airway diseases.

The airway epithelial cells (AECs) lining the conducting airways of the lung form the first line of defense against a variety of inhaled pathogens, allergens and environmental irritants. When a respiratory virus infects cells within the airway epithelium, it provokes the release of numerous immunomodulatory mediators. One essential component of a productive antiviral response is the production of interferons, a family of cytokines known to exhibit powerful antiviral influences. Cells derived from asthmatic patients are known to exhibit diminished interferon release. However, the cellular basis of this phenomenon is not well understood. In this thesis work, we find that two mediators known to be elevated in asthmatic airways, namely extracellular nucleotides and histamine, both potently inhibit the release of interferons from airway epithelial cells. Pharmacological evidence demonstrated that activation of G-protein coupled P2Y₂ and H₁ receptors elicited this effect. Differentiation of airway epithelial cells at an air-liquid interface confirmed that this phenotype is conserved following differentiation to develop mucociliary function. Mechanistically, receptor signaling through PKC was required to exert these inhibitory effects on interferon release. Significantly, histamine and ATP inhibited interferon release from airway cells infected with live influenza A virus. These results reveal a conserved role for G-protein coupled receptor signaling restraining release of interferons from airway epithelial cells. Collectively, our results provide a potential cellular and molecular basis for the observed limited interferon responses in asthmatic cells.

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Isaac Newton is attributed with the quote, "If I have seen further it is by standing on the shoulders of giants". During my time in graduate school, I may have seen a bit further in some areas of airway cell biology, but I would be remiss to claim the credit myself. First, I will thank my scientific mentors, then I will move to more personal mentors.

One memory early in my scientific training occurred in Mr. Betzler's 8th grade science class. The homework was simple: jump rope for a set series of time and then measure your heart rate. Prior to the experiment, I had the unconscious hypothesis that as I jumped rope for longer periods of time, my heart rate would naturally increase. However, much to my dismay, the raw data did not precisely follow this trend and my heart rate slowed at the longest interval of jump roping. Without reflecting too much on the raw data, I altered the data to match my unconscious hypothesis. As I entered the classroom the next day to turn in the assignment, Mr. Betzler announced that he would know who had fabricated the experiment because he had asked us to take our pulse for 15 seconds and then multiple by four. Thus, all pulse values that were not multiples of four would be revealed to be fabricated. I was immediately dismayed. After class, I confessed my falsification of data to Mr. Betzler and he warned me that falsification of data was a serious offense and that I should steer clear of all such activity from that point on. Needless to say, the event had a long-term affect scientific outlook. Thank you Mr. Betzler for teaching me the importance of scientific integrity.

I had many great scientific teachers in high school, but time and space demands I focus on the major influencers. I came into college at the University of Washington intending to follow the pre-medicine route. At the end of my sophomore year, out of a desire to strength my CV for medical school, I began volunteering in the laboratory of Dr. Chris Hague in the Pharmacology Department. Dr. Kyung-Soon Lee patiently trained me in lab techniques and Chris was an enthusiastic mentor. Chris has a deep love for training scientists and we connected quickly on a personal level. He was able to persuade me that graduate school and scientific research was a potential career tract that interested me. Chris gave me much autonomy in the lab and fanned into flame my passion for biological research.

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Chapter 1: Introduction

Asthma and Respiratory Viruses

Human airway diseases are a major burden on society and individuals. Airway diseases can be characterized as either chronic or acute. One chronic airway disease is asthma. Estimates are that approximately 10% of the world population suffers from asthma [2]. Asthma is а complex airway disease with hallmarks such as airway hyperresponsiveness, smooth muscle proliferation, decreased epithelial barrier function and goblet cell metaplasia [3, 4]. Inflammation is a common component of asthma as well, with approximately 50% of patients showing elevated type 2 inflammation [5]. Prototypical type 2 inflammation is linked to cell types such as Th2 and ILC2's releasing cytokines such as IL-4, IL-5, and IL-13 [5]. Type 2 inflammation is atopic, hence allergens play an important role. Common airway allergens implicated in asthma include house dust mite (HDM), pollen, cockroach, Aspergillus fumigatus, and ragweed [2]. HDM is the most common aeroallergen in humans [2]. Although historic therapeutic modalities include chronic treatment with inhaled corticosteroids and acute treatment with β_2 -adrenergic receptor agonists, recent additions to the pharmacopoeia include modulators of interleukins and IgE [5, 6].

One genre of acute airway disease is infection with respiratory viruses. In the United States alone, estimates are that 29-59 million people are infected annually with influenza virus and approximately 36,000 die [7]. However, these numbers can significantly increase upon a pandemic such as in 1918, when estimates are that 50 million deaths occurred globally [8]. More recently, we have witnessed the emergence of the SARS-CoV-2 pandemic. Other respiratory viruses that cause the common cold,

such as human rhinovirus, also exact a significant economic burden on society [9]. Although vaccines do exist for some of these viruses, new therapies and understanding of molecular events that alter the course of infection are necessary.

Airway Epithelial Cells

In the context of human airway diseases, one essential cell type is the airway epithelial cell. The airway epithelial cells (AECs) lining the conducting airways of the lung form the first line of defense against a variety of inhaled pathogens, allergens and environmental irritants. The airway epithelium is pseudostratified and the cells are polarized [10]. In the upper airways, comprising trachea and bronchi, the dominant cell types include ciliated cells, goblet cells, club cells, and basal cells (Figure 1.1) [10]. In the lower airways and alveoli, type 1 and type 2 alveolar cells are predominant. Importantly, AECs are primary host target cells for infection by respiratory viruses [11, 12]. In the context of asthma, the epithelium contributes to disease through deficient barrier function and excessive goblet cell differentiation [3, 4]. Further, AECs not only provide a physical barrier but also actively orchestrate immune responses to inhaled substances through the production of a wide array of secreted factors that include alarmins, chemokines, cytokines, and eicosanoids [3]. The release of these immunomodulatory mediators can drive complex biological processes such as allergic sensitization [3, 4]. Additionally, AECs express many pattern recognition receptors (PRRs) that are activated by exogenous allergens or viruses [3, 4]. Activation of these receptors can then direct immune cells such as DCs and ILC2s to initiate a Th2-polarized response [4, 13].

However, many of the receptors and pathways in the epithelium orchestrating this inflammation are not well understood.



Figure 1.1 Air-liquid interface cultures of AECs. Normal human bronchial epithelial cells can be differentiated for 3 weeks at the air-liquid interface. Using this standard protocol, the bronchial epithelial cells differentiate into many of the cell types found in the upper airways such as ciliated cells, goblet cells, club cells, and basal cells. This system allows for the *in vitro* study of processes related to mucociliary clearance and mimics a more physiologically relevant system than submerged epithelial cultures, which are undifferentiated and not polarized.

One core function of the airway epithelium is mucociliary clearance (MCC). Human diseases such as cystic fibrosis and primary cilia dyskinesia are caused by mutations in genes essential for proper MCC, demonstrating the functional significance of MCC [14]. MCC is an indispensible innate host defense mechanism that comprises three components: 1) the cilia on ciliated cells 2) the airway surface liquid 3) the mucus layer [14]. The process begins when pathogens and particles become trapped in the mucus layer. Then, the mucus containing pathogen is shuttled up the respiratory tract through cilia beating, culminating in either swallowing or expectoration. One *in vitro* model that replicates many of the functional features of the intact airways is the airliquid interface (ALI) model (Figure 1.1). Using this system, AECs can differentiate into ciliated and goblet cells and aspects of MCC biology can be investigated [15]. A deeper understanding of cilia and mucus may lead to helpful interventions in airway diseases.

Purinergic Signaling in the Airways

The airways harbor a plethora of small molecules and proteins that can interact with cellular receptors to drive dynamic responses. One small molecule in the airways that regulates physiology is adenosine triphosphate (ATP). Extracellular ATP in the airways is of growing interest due to its ability to drive airway inflammation [16-18]. Extracellular ATP is a damage- or danger-associated molecular pattern (DAMP) [16, 18]. Importantly, elevated ATP in the bronchoalveolar lavage (BAL) fluid is a key characteristic of many lung disorders including asthma, acute respiratory distress syndrome (ARDS), and chronic obstructive pulmonary disease (COPD) [16, 19-22]. Upon allergen challenge in the lungs, ATP levels in the bronchoalveolar lavage fluid increase dramatically [16, 18].

In the airways, ATP stimulates cytokine release, activates the inflammasome, and recruits immune cells [13, 16-18]. This extracellular ATP regulates allergic sensitization and inflammation through purinergic P2 receptors [16, 18]. However, the molecular identity of the purinergic receptors that drive the release of immunomodulatory mediators in the airways is unclear.

In contrast to its role in driving proinflammatory processes, ATP can also elicit protective responses. For instance, ATP signaling is linked to protective physiological processes in the lungs such as wound healing, rejection of tumors, killing of bacterial pathogens, and mucociliary clearance (MCC) [17, 23-27]. In addition to ATP, UTP is also released in the airways and increases MCC [28]. UTP can also stimulate numerous other physiologically important airway functions such as ion transport and mucin secretion [28]. However, how these nucleotides elicit both proinflammatory and protective effects on airway function is not well understood.

P2 receptors are a class of 15 purinergic receptors that are either P2Y metabotropic G-protein couple receptors (GPCRs) or P2X ionotropic ion channels (Figure 1.2) [29-31]. There are eight P2Y receptors including *P2RY1, 2, 4, 6, 11-14* [29]. P2Y ligands are diverse and include ATP, ADP, UTP, UDP, and UDP-glucose [29]. P2X channels comprise seven subtypes including *P2RX1-7* with ATP as the primary physiological agonist [31]. Another class of purinergic receptors are the four adenosine receptors termed P1 receptors [32]. P2 receptors have well known roles in inflammation. One well-described role is that ATP-evoked opening of P2X7 receptors drives inflammasome activation [17]. P2 receptors can also drive nuclease and cytokine release in eosinophils and dendritic cells [33, 34]. Many cell types express multiple P2

receptors. In some circumstances, cross talk can occur between receptors culminating in either synergy or antagonism at downstream endpoints such as cytokine release [35]. In AECs, P2 receptor activation evokes IL-6 secretion [36]. Collectively, purinergic receptors have diverse roles in the regulation of inflammatory processes.



Figure 1.2 Purinergic Signaling. First, nucleotides are released from cells into the extracellular space. These extracellular nucleotides can then be degraded from ATP-ADP-AMP-Adenosine. A similar degradation process exists for uridine nucleotides. Three main classes of purinergic receptors exist. P2RX receptors are ion channels with ATP are the dominant physiological agonist. P2RY receptors are GPCRs with agonists that range from ATP, ADP, UTP, UDP, and UDP-glucose. P1 receptors are GPCRs with adenosine as their physiological agonist. Enzymes that degrade ATP/ADP into AMP are termed ecto-nucleoside triphosphate diphosphohydrolases (E-NTPDases), such as CD39. Enzymes that degrade AMP into Adenosine are termed ecto-5'-nucleotidase, such as CD73. Enzymes that degrade AMP into adenosine are termed purine nucleoside phosphorylase (PNP) [1]. Apyrase will degrade ATP/ADP into AMP. ARL 67156 prevents the degradation of ATP.

Nucleotides can be release from cells via lytic or non-lytic mechanisms. In general, there are three mechanisms whereby cells release nucleotides in a non-lytic fashion. The first is constitutive release through the ER-Golgi pathway. The second is a Ca²⁺ dependent exocytotic release. The third is pannexin- or connexin-mediated release of nucleotides [37]. AECs are known to release ATP via all three of these mechanisms [37]. Interestingly, goblet cell metaplasia, a phenomenon whereby the abundance of goblet cells in the epithelium increases, is linked to a greater release of ATP from AECs [38]. This release of ATP also contained other nucleotides such as ADP, AMP, and adenosine [38]. In AECs derived from cystic fibrosis patients, the inflammatory state of the cells has been linked to increased nucleotide release [39]. Respiratory virus infection of AECs can also increase nucleotide release [38, 40-42]. Toll-like receptor 3, a sensor for dsRNA, has been implicated in this virus-induced release of nucleotides [40, 42]. Airway allergens, such as Alternaria and cockroach also drive the release of nucleotides from AECs [13]. A further mechanism that elicits nucleotide release from AECs is cyclic compressive stress [43]. This cyclic compressive stress has been proposed to be a model for normal tidal breathing in humans suggesting that normal breathing rhythm may induce low levels of nucleotide release [43]. Importantly, the release of nucleotides from AECs is not limited to adenine derivatives but includes uridine nucleotides as well [44, 45]. Direct quantification suggests that ATP concentrations in cellular supernatants are approximately 3-5 fold higher than UTP concentrations, correlating strongly with intracellular nucleotide ratios [46, 47]. Collectively, an abundance of stimuli have been reported to induce the release of nucleotides from AECs implying that AEC purinergic signaling may occur after a host of different physiological insults.

The two most well described purinergic receptors expressed in AECs are P2Y₂ receptors and A_{2B} receptors [48]. AECs are polarized cells and P2Y₂ receptors are reported to be expressed on both apical and basolateral surfaces [49, 50]. Agonists for P2Y₂ receptors include ATP and UTP while adenosine is the physiological agonist for A_{2B} receptors. Thus, when AECs release extracellular ATP, which is subsequently degraded into adenosine, both of these receptors may be simultaneously activated. Both of these purinergic receptors have essential roles in the regulation of mucociliary clearance (MCC). Specifically, P2Y₂ receptor activation can drive the rapid release of mucin proteins from goblet cells [51-53]. Further, both P2Y₂ receptor and A_{2B} receptor activation can elicit the opening of Cl⁻ channels on the apical surface of AECs [48]. This Cl⁻ channel activation is essential for proper hydration of the mucus. However, the underlying mechanisms for how these receptors induce this response are divergent. Activation of P2Y₂ receptors evokes Ca²⁺ signaling and leads to opening of the Ca²⁺ activated Cl⁻ channels (CACCs) [48]. On the other hand, activation of A_{2B} receptors evokes cAMP signaling and leads to opening of the cystic fibrosis transmembrane conductance regulator (CFTR), the Cl⁻ channel mutated in cystic fibrosis [48]. Another mechanism whereby these two receptors increase MCC is that they can induce an increase in cilia beat frequency [48]. Interestingly, a feedback mechanism exists between MCC and nucleotide release. Cilia can sense the viscosity of the mucus layer in the airways and when it is too viscous, cilia cause the release of ATP [24]. This ATP and subsequently adenosine then drives hydration of mucus through P2Y₂ receptor and

 A_{2B} receptor activation of Cl⁻ channels [24]. Because P2Y₂ receptors drive activation of CACCs and not CFTR, activation of these receptors was proposed as a means to restore Cl⁻ channel function in cystic fibrosis patients [54]. Unfortunately, stable agonists of P2Y₂ receptors were ultimately abandoned in CF clinical trials due to low efficacy [55]. Altogether, P2Y₂ receptors and A_{2B} receptors are essential regulators of MCC in AECs. However, the role of P2 receptors in AEC release of immunological mediators is less clear.

There are some reports suggesting that ionotropic P2X receptors are expressed on AECs [56]. Activation of AEC P2X channels can enhance Ca^{2+} signaling [57]. Although not as dominant as P2Y₂ receptors, ATP gated P2X channels have been implicated in increasing both cilia beat frequency and mucin secretion in AECs [58, 59]. The biophysical properties of P2X channels in AECs suggest that both P2X7 and P2X4 channels are functional [60]. Further, P2X channel activation has been implicated in the release of IL-8 from AECs [61]. Interestingly, *P2rx4* knockout mice are protected in models of allergic lung inflammation [62]. Collectively, the roles of AEC P2X receptors are less well understood than P2Y receptors.

Histamine Signaling in AECs

Another important mediator in the airways is histamine. Histamine was the first mediator causally linked to allergic disease as it recapitulated many of the symptoms of allergy. Histamine is typically released from mast cells and basophils upon degranulation [63]. In the airways, histamine evokes vasodilation, smooth muscle contraction, and pruritus [63]. In airway epithelial cells, histamine induces a strong Ca²⁺ response [64]. Although

H₁ receptors are thought to be the dominant histamine receptor subtype in AECs, some reports suggest H₂₋₃ may also be expressed [64, 65]. Histamine can drive the release of cytokines from AECs [64]. It can also drive ROS signaling in AECs [66]. In polarized AECs, histamine receptors are predominantly expressed on the basolateral surfaces [67]. Decreased AEC barrier function is a hallmark of asthmatic disease and histamine receptor activation can transiently decrease AEC barrier function [68]. Altogether, histamine receptors are a classic regulator of allergic lung inflammation but how histamine modulates AEC immune responses are not clear.

Ca²⁺ signaling and CRAC Channels in AECs

One key-signaling mechanism in AECs is Ca^{2+} -dependent pathways. Ca^{2+} is a ubiquitous second messenger that drives numerous biological phenomena including transcription, exocytosis, and enzyme regulation [69-71]. Resting Ca^{2+} concentrations are approximately 100 nM in the cytosol, 300-400 μ M in the ER, and 2 mM in the extracellular space thereby setting the stage for steep concentration gradients. One primary mechanism for Ca^{2+} entry into the cytosol is described as store-operated Ca^{2+} entry (SOCE). This occurs when the intracellular Ca^{2+} stores, such as the $[Ca^{2+}]_{ER}$ decrease, leading to Ca^{2+} entry across the plasma membrane from the extracellular space. The prototypic channel that is operated in a store-dependent manner is the Ca^{2+} release-activated Ca^{2+} (CRAC) channel.

CRAC channels are formed by the ORAI proteins, which comprise the pore subunits, and are activated by the ER Ca²⁺ sensing STIM proteins. STIM1 and STIM2 are single pass transmembrane proteins localized to the ER. The ER luminal portion of

STIM1 and STIM2 contains a Ca^{2+} -binding domain called an EF hand that acts as a $[Ca^{2+}]_{ER}$ sensor. When the $[Ca^{2+}]_{ER}$ decreases, Ca^{2+} is released from STIM1-2 causing oligomerization and the unveiling of a binding domain for ORAI proteins on the cytosolic portion of STIM. Activated STIM1-2 localize to the ER-PM junction and binding ORAI proteins, they cause ORAI pore opening and Ca^{2+} influx into the cytosol (Figure 1.3). Following channel opening, inactivation occurs through Ca^{2+} -dependent mechanisms and also the refilling of ER Ca^{2+} stores through the SERCA pump [70]. Interestingly, STIM1 binding to ORAI1 channels increases the Ca^{2+} selectively of ORAI1 channels [72]. The best understood ORAI and STIM proteins are ORAI1 and STIM1.



Figure 1.3 CRAC Channel Activation. Store-operated calcium entry through The CRAC channel occurs when $[Ca^{2+}]_{ER}$ decreases causing STIM1 to oligomerize. STIM1 then relocates to PM-ER junctions binding ORAI1 and causing pore opening. Image adapted from, *Yeung, P.S., M. Yamashita, and M. Prakriya, Molecular basis of allosteric Orai1 channel activation by STIM1. J Physiol, 2019.*

The CRAC channel is most well studied in immune cells, although the components ORAI1 and STIM1 are widely expressed in other tissues [70]. In T cells, CRAC channels regulate processes such as IL-2 production and proliferation [70, 73, 74]. The molecular identity of the channel was elucidated when ORAI1 was discovered because of a human missense mutation, R91W, which leads to a severe combined immune deficiency (SCID) phenotype [74]. ORAI1 deficient patients are not only immunodeficient, but experience myopathy and ectodermal dysplasia as well [75]. ORAI1 deficient patients also have defects in dental enamel formation [76]. The list of clinical syndromes described for STIM1 deficient patients includes immunodeficiency, hepatosplenomegaly, autoimmune hemolytic anemia, thrombocytopenia, muscular hypotonia, and defective enamel formation [77]. However, CRAC channels are increasingly tied to diverse physiological processes. In T cells, Orai1 deficiency in mice has been linked to mitochondrial metabolic defects [78]. In neutrophils, both Stim1 and Stim2 are necessary for full stimulus-evoked cytokine production [79]. In mast cells, CRAC channel function is essential for cysteinyl leukotriene production and degranulation [80-83]. In the nervous system, Orai1 channels have been linked to longterm potentiation, astrocyte gliotransmitter and cytokine release [84-86]. Altogether, CRAC channels have established roles in immunity and a host of other physiological processes.

In recent years, CRAC channels have been linked to regulated exocytosis in secretory epithelium [87]. In lacrimal glands, loss of *Orai1* leads to less fluid and protein secretion in response to muscarinic receptor activation [88]. Within pancreatic acinar cells, loss of *Orai1* leads to decreased secretion of digestive enzymes and antimicrobial

peptides [89]. Similarly, in sweat glands, loss of *Orai1* leads to decreased chloride and fluid secretion [90]. Thus, CRAC channels are known regulators of exocytosis in secretory epithelial cells.

In airway epithelial cells (AECs), Ca²⁺ is known to regulate a host of biological processes. Mucociliary clearance is dynamically regulated by Ca²⁺ signaling. Specifically, Ca²⁺ can increase cilia beat frequency, enhance Cl⁻ channel activation, and induce mucin secretion [14, 48, 91, 92]. Ca²⁺ signaling in AECs can also drive the release of nucleotides into the extracellular space [44, 45]. Receptor-mediated Ca²⁺ signaling in AECs can also drive the release of immunomodulatory lipids such as PGE₂ [93, 94]. Finally, the synthesis and release of cytokines such as IL-6 and IL-33 is Ca²⁺ dependent [13, 36]. However, which of these Ca²⁺-dependent processes are also CRAC channel dependent is unclear.

We have recently identified CRAC channels as a major route of calcium entry in airway epithelial cells [95]. In AECs, direct activation CRAC channels causes cytokine induction that is largely NFAT dependent [95]. These cytokines include TNF- α , IL-6, IL-8, GM-CSF, and TSLP [95]. Other genes reportedly regulated through direct CRAC channel activation include c-Fos and EGF [96]. Furthermore, PAR2 agonists have been shown to activate CRAC channels in AECs [95]. Indeed, CRAC channel activation is necessary for the production of IL-6, IL-8 and GM-CSF downstream of PAR2 activation (Figure 1.4) [95]. Allergens have also been shown to activate CRAC channels in AECs and drive IL-6 and IL-8 production [97]. In summary, CRAC channels in AECs have primarily been investigated for their role in the production of proinflammatory cytokines. However, a scarcity of information exists on how these channels regulate enzymes and

exocytosis. Additionally, how CRAC channel activation may contribute to the diverse functions of purinergic receptors in AECs is unknown.



Figure 1.4 PAR2 activation in AECs evokes CRAC channel dependent production of proinflammatory cytokines, chemokines and eicosanoids. PAR2 activation leads to phospholipase C signaling and IP3 generation. IP₃ elicits opening of IP₃Rs in the endoplasmic reticulum. A decrease in ER Ca²⁺ levels drives STIM1 activation and subsequent opening of plasma membrane ORAI1 channels. Ca2+ activates a host of Ca^{2+} dependent enzymes including calcineurin. The production of PGE₂ is CRAC channel dependent in this system but the mechanism for CRAC channel-mediated PGE₂ production is unclear. GM-CSF is also produced in a CRAC channel dependent manner. Calcineurin activation leads to NFAT transcription of IL-6 and IL-8. Thus, PAR2 activation leads to CRAC channels as a signaling nexus provoking the release of PGE₂, GM-CSF, IL-6, IL-8 from AECs.

Release of AEC Immunomodulatory mediators

Airway epithelial cells release a host of mediators that direct subsequent immune responses. These include lipid mediators such as prostaglandins as well as protein products such as cytokines, chemokines, mucin proteins, and antimicrobial peptides that direct immune responses in the context of allergic responses or antiviral responses. Thus, understanding the mechanisms that drive the synthesis and release of these mediators are essential for a deeper understanding of immunological responses in the lungs.

One prominent mediator released by AECs in PGE₂. [94, 98-100]. PGE₂ stimulates dilation of the lung airways thereby protecting the lung against severe bronchoconstriction that is a hallmark of diseases such as asthma [101, 102]. PGE₂ also inhibits several inflammatory processes, including the Membrane Phospholipids Phospholipase A2 release of histamine and cysteinyl leukotrienes from mast **Arachidonic Acid** cells [101], T-cell migration [103], ILC2 function [104], and COX-1/COX-2 PGG₂ the production of proinflammatory TNF- α and IL-12 β by COX-1/COX-2 dendritic cells [105]. In addition to inhibiting proinflammatory PGH₂ signaling in the lungs, it also enhances the synthesis of the PGE Synthase PGE₂ anti-inflammatory cytokine IL-10 [105] and promotes Figure 1.5 The biosynthetic pathway that culminates in the wound healing [106]. Further, growing evidence suggests production of prostaglandin E2. that PGE₂ can drive reverse migration and removal of

neutrophils from sites of inflammation to dissipate inflammation *in vivo [107]*. Failure of resolution of inflammation can lead to inflammatory diseases such as chronic obstructive pulmonary disease (COPD) and acute respiratory distress syndrome

(ARDS). Altogether, within the lung, PGE₂ exerts predominantly bronchoprotective and anti-inflammatory effects [108].

The synthesis of PGE₂ is well studied (Figure 1.5). The process begins when arachidonic acid (AA) is liberated from phospholipids in membranes via phospholipase activity. Cyclooxygenase (COX) enzymes then process AA in a two-step reaction into PGH₂ [109]. Prostaglandin E synthase enzymes then convert PGH₂ into PGE₂, which is subsequently transported out of cells via passive diffusion or the transporter MRP4 [110-112]. This enzyme cascade is tightly regulated and therapeutics to inhibit this pathway are a hallmark of modern medicine. The enzymes COX-2 and mPGES-1 are primarily regulated through increases in protein expression [109-111]. In contrast, regulation of cPLA₂ occurs posttranslationally through direct ERK1/2 phosphorylation of Ser505 and Ca²⁺-dependent membrane translocation [98, 113]. Ca²⁺ binding to the Ca²⁺-dependent phospholipid-binding domain of cPLA₂ is both necessary and sufficient for PGE₂ synthesis. However, the ion channels responsible for this influx of Ca²⁺ into the cytosol in AECs remain enigmatic. *The first hypothesis of my thesis dissertation is to determine how CRAC channel activation may be involved in PGE₂ synthesis.*

Mucin proteins, along with water and ions are an important component of mucus [114]. In the airways, mucus is used in the mucociliary escalator, a process in which ciliated cells pump mucus up and out of the airways to be either swallowed or expectorated [114]. Although this physiology is important for host pathogen protection, mucus hypersecretion and goblet cell metaplasia are hallmarks of both asthma and chronic obstructive pulmonary disease (COPD) [114-116]. Importantly, the most common cause of death in asthmatic patients is excessive mucus plugs [114]. Thus,

therapies that can attenuate mucin hypersecretion have vast potential to improve modern asthma treatment. In human airways, club (Clara) and goblet cells synthesize and secrete mucin proteins [114, 115]. The major secreted mucins of the airways are MUC5AC and MUC5B. These large glycoproteins are packaged into secretory granules [114]. Although some basal exocytosis of these granules occurs, secretion can rapidly increase in a receptor dependent manner [115, 117, 118]. These receptors are numerous but include P2Y, PAR2, and EGFR [53, 118-120]. One conserved mechanism for inducing mucin secretion is Ca²⁺ signaling [116]. Although it is understood that IP₃Rs are involved in mucin secretion from AECs, it remains unclear if Ca²⁺ influx from the extracellular space is also required. If so, inhibiting these Ca²⁺ channels may prove a novel mechanism to selectively reduce mucus plugs in airway diseases. *The second hypothesis of my thesis dissertation is to investigate the role of CRAC channels in goblet cell exocytosis and the secretion of mucin proteins.*

A key cytokine released from AECs is IL-6. IL-6 is a potent inflammatory cytokine that elicits a wide-range of inflammatory effects including T-cell expansion, pulmonary neutrophil infiltration, airway mucus secretion, lung fibrosis, and the hyperplasia and hypertrophy of airway smooth muscle cells [121-124]. Further, IL-6 is linked to numerous airway diseases from asthma to COPD [121-124]. Investigations with patients suffering from severe COVID-19 have revealed massive increases in IL-6 in the lung airways, a feature thought to contribute to microvascular thrombosis in the lung and multiple organ dysfunction in these patients [125]. Importantly, blockade of IL-6 signaling in mouse models of asthma protects against airway inflammation [122, 126], and early reports indicate that targeting IL-6 may be a viable therapy to decrease

mortality in severe COVID-19 patients [127]. In AECs, P2 receptor activation induces IL-6 secretion [36]. Understanding the mechanisms that provoke IL-6 release from AECs may uncover novel therapeutic modalities for use in both allergic inflammation and severe COVID-19. The third hypothesis of my thesis dissertation is to determine the role of CRAC channels in purinergic receptor-driven IL-6 production.

When a respiratory virus infects AECs, one essential class of antiviral cytokines that is produced is interferons (Figure 1.6) [12, 128, 129]. Interferons (IFNs) are classified as type 1 (IFN- α/β), 2 (IFN- γ), or 3 (IFN- λ). Respiratory virus-infected AECs produce predominantly type 1 and type 3 IFN [130]. While both of these cytokines have antiviral activity, important distinctions exist. Type 3 IFN receptors are restricted to mucosal surfaces while type 1 IFN receptors are considered ubiquitous [12, 128]. Thus, IFN- λ is a mucosal specific mechanism for antiviral defense. Although, AECs generally make higher quantities of type 3 IFN than type 1 IFN following infection [130], type 1 is more potent at inducing an antiviral state in cells [131]. Both type 1 and type 3 IFN signaling induces the expression of interferon-stimulated genes (ISGs) that enhance antiviral defense of cells [12, 128].



Figure 1.6 Respiratory Virus infection of AECs drives Interferon release.

Respiratory viruses in the airways are most often RNA viruses. The virus infects AECs and as the virus replicates, dsRNA is synthesized and dsRNA sensors such as TLR3 and RLRs are activated. Activation of these sensors then drives activation of transcription factors such as NF-kB and IRF family members. One of the key mediators that is released is the antiviral cytokines termed interferons. AECs release both type 1 and type 3 IFN. IFNs signal through IFN receptors to induce the transcription of interferon stimulated genes (ISGs) that induce an antiviral state in the neighboring cells.

IFN production can be regulated in a host of manners. Respiratory viruses themselves often exhibit a capacity to inhibit IFN production or downstream IFN signaling [128]. This capacity to dampen host IFN responses is often critical for successful viral infection and replication. However, many host receptors and signaling pathways can also enhance or inhibit interferon pathways. In macrophages, CCL2 has been shown to dampen IFN- α release [132]. In plasmacytoid dendritic cells (pDCs), ligands such as histamine and nucleotides have been shown to inhibit IFN-α release [133, 134]. In AECs, EGFR activation can decrease IFN- λ production thereby enhancing viral infection [135, 136]. The cytokines IL-4,13, and IL-17 have also been shown to dampen IFN production from AECs [137-139]. Cigarette smoke can also dampen AEC IFN production [140, 141]. Interestingly, allergens such as aspergillus, alternaria, and house dust mite, have further been shown to inhibit IFN production from AECs [142-144]. This reduction of IFN production has been proposed to be a potential mechanism whereby the airway milieu is skewed towards a Th2 phenotype upon exposure to these allergens [143, 145]. Mechanistically, both aspergillus and alternaria have been shown to activate proteinase-activated receptor 2 (PAR2) on AECs and signaling from this receptor limits the release of Th1 chemokines and IFNs [143, 146]. Altogether, understanding the signaling mechanisms that regulate AEC IFN production may enable the development of novel antiviral therapies.

Acute respiratory viral infections can also aggravate underlying chronic airway diseases and visa versa. For example, asthma may be a risk factor for severe influenza A virus (IAV) infection during IAV pandemics [11]. Furthermore, there is a strong correlation between children experiencing rhinovirus (RV) or respiratory syncytial virus
(RSV) induced wheezing episodes early in life with later development of asthma [147]. Although the exact mechanisms remain unclear, this may be related to a viral interaction with allergic sensitization [148]. Importantly, acute RV or RSV infections are responsible for most exacerbations of asthma [9, 147, 149, 150]. While asthmatics are not prone to greater incidence of respiratory tract infections, they are prone to more severe and longer lasting lower respiratory tract symptoms during the course of infection compared to healthy controls [151]. There are also correlations between asthma and the production of the key antiviral cytokines interferons. On a cellular level, most [137, 149, 152-157], but not all [158], studies have suggested that cells or tissue derived from patients with asthma or chronic obstructive pulmonary disease (COPD) have an intrinsic defect in IFN production following viral infections. Mechanisms to explain how asthmatics may come to have deficient IFN production are not clear.

Two mediators present in the airways during asthma are histamine and extracellular nucleotides [16, 63]. However, whether there may be a causative relationship between nucleotides, histamine and deficient IFN production is unclear. It is also important to note that nucleotides are released following viral infection of AECs [38, 40-42]. Thus, nucleotide signaling may regulate not only allergic sensitization [16] but also antiviral responses in the airways. Dissecting these hypotheses using cellular models may be of the upmost importance for understanding the clinical observations regarding asthmatics and IFN production. *The fourth hypothesis of my thesis dissertation is that nucleotides and histamine regulate AEC IFN production.*

Summary

Understanding how airway epithelial cells produce immunomodulatory factors such as cytokines and eicosanoids will lead to a better understanding of host immune responses against allergens and viruses. In Chapter 2, I focus on investigating receptors that elicit the activation of Ca²⁺ signaling and CRAC channels in AECs. Chapter 3 and 4 are devoted to interrogating mechanisms AECs employ to produce PGE₂ or IL-6. Chapter 5 and 6 are an investigation of mechanisms whereby nucleotides and histamine suppress the release of interferons from AECs. Chapter 7 is devoted to studying AEC function at the air-liquid interface, particularly with a focus on validating previous findings in submerged NHBEs and testing the CRAC channel dependence of mucin secretion. Chapter 8 is a short pilot study using the CRAC channel inhibitor CM4620 in an animal model of allergic lung disease. Chapter 9 is a brief conclusion followed by materials and methods in chapter 10. Overall, this thesis work uncovers novel mechanisms whereby AECs may orchestrate downstream immune responses in the lungs through mediator release.

Chapter 2: G-protein Coupled Receptor Activation elicits Ca²⁺ signaling and Store-Operated Ca²⁺ Entry in Human Airway Epithelial Cells

Introduction

Calcium is a ubiquitous second messenger that encodes for numerous biological phenomena including transcription, exocytosis, and enzyme regulation [69, 70]. One critical set of proteins for cellular calcium signaling are ORAI and STIM [70, 159]. These two proteins comprise the Calcium Release-Activated Calcium (CRAC) channel, the prototypic store-operated calcium channel [70, 159]. The CRAC channel component STIM functions as a sensor for ER calcium levels such that when $[Ca^{2+}]_{ER}$ decreases, STIM binds to ORAI in the plasma membrane. STIM thereby acts as a ligand for ORAI, the pore subunit, ultimately leading to sustained calcium entry into the cytosol from the extracellular space. Many receptors and pathways lead to a decrease in $[Ca^{2+}]_{ER}$ and subsequent CRAC channel opening. The most well studied role for ORAI is in T cells where loss of function mutations leads to defective T cell function and ultimately severe combined immunodeficiency (SCID) syndrome [74].

In human airway epithelial cells, G-protein coupled receptors (GPCRs) and allergens elicit the activation of CRAC channels [95, 97]. CRAC channel activation in AECs has been shown to evoke the release of numerous immunomodulatory mediators [95, 97]. Although the proteinase-activated receptor 2 (PAR2) has been demonstrated to drive CRAC channel dependent release of mediators [95], the other receptor subtypes that induce CRAC channel activation in AECs remain unclear. Here we set out to investigate the scope of GPCRs that evoke Ca²⁺ signaling and CRAC channel

activation. Purinergic ligands such as ATP and UTP have previously been demonstrated to activate CRAC channels, yet the subtype responsible was unknown [95]. Histamine is also a biologically relevant ligand in the context of allergic airway diseases [63]. We tested purinergic ligands and histamine for their ability to drive CRAC channel activation in AECs. Both sets of ligands substantially evoked Ca^{2+} signaling and CRAC channel activation, albeit purinergic ligands consistently elicited stronger responses. Purinergic ligands ATP and UTP elicited the activation of P2Y₂ receptors while histamine activated H₁ receptors in AECs. This data suggests that purinergic ligands and histamine may induce the release of inflammatory mediators from human AECs through their harnessing of CRAC channel dependent Ca^{2+} signaling.

Results

The P2Y₂ receptor mediates ATP- and UTP-induced Ca²⁺ signals in AECs

ATP acts on numerous membrane receptors including metabotropic P2Y receptors along with ionotropic P2X receptors [31, 160]. Previous literature suggests AECs express P2Y₂, P2Y₆ and P2X receptors [48, 60, 61, 161]. All of these receptors then elicit Ca²⁺ signaling. Thus, we sought to identify the receptor subtypes that drive ATPinduced Ca²⁺ elevations. We used primary human airway epithelial cells and the ratiometric dye, Fura-2 as previously described [95] to interrogate the receptor identity. Our experiments revealed that a saturating dose of ATP (100µM) evoked a rapid increase in [Ca²⁺]_i followed by a sustained phase (Figure 2.1A). When extracellular Ca²⁺ was removed, the rapid rise in [Ca²⁺]_i was preserved while the sustained phase was lost (Figure 2.1B). This data was highly suggestive that the initial rise in [Ca²⁺]_i was driven by Ca²⁺ store-release while the sustained phase required Ca²⁺ entry across the plasma membrane.

Next, we utilized the selective metabotropic P2Y receptor agonist, uridine triphosphate (UTP) [28]. When primary AECs were stimulated with ATP and UTP the Ca²⁺ signals elicited were nearly identical (Figure 2.1C). This is highly reminiscent of the pharmacological footprint of the P2Y₂ receptor [29, 160]. Thus, we tested the selective P2Y₂ antagonist AR-C 118925XX (hereby "AR-C") [53]. AR-C pretreatment abolished both ATP- and UTP- evoked Ca²⁺ signals (Figure 2.1D-F). The PAR2 activating peptide SLIGKV was still capable of mounting a Ca²⁺ response in the presence of AR-C suggesting that AR-C is indeed selective for P2Y₂ receptors (Figure 2.1D-E). These results indicate that the nucleotides ATP and UTP evoke Ca²⁺ signals in AECs primarily through the activation of metabotropic P2Y₂ receptors.



Figure 2.1 The P2Y₂ receptor mediates ATP- and UTP-induced Ca²⁺ elevations in AECs. A) ATP (100 μ M) stimulates a bi-phasic [Ca²⁺]_i rise in primary human AECs consisting of an initial rapid, transient Ca²⁺ peak followed by a sustained [Ca²⁺]_i elevation in the presence of extracellular Ca²⁺ (2 mM). [Ca²⁺]_i was measured using Fura-

2 AM as previously described [95]. Each trace shows response of single cells in the imaging field. **B**) The removal of extracellular Ca²⁺ abolishes the sustained phase of the ATP-induced [Ca²⁺]_i elevation without affecting the initial transient [Ca²⁺]_i rise. **C**) The uridine nucleotide UTP (100 μ M) evokes a Ca²⁺ rise that is similar in amplitude and kinetics to the ATP-evoked signal. Data are mean ± SEM of n = 35-37 cells. **D**) The selective P2Y₂ receptor antagonist, AR-C 118925XX (10 μ M), completely abrogates ATP (100 μ M)-induced Ca²⁺ rise but does not affect the ability of the PAR2 peptide, SLIGKV, to induce Ca²⁺ signaling. Data are mean ± SEM of n = 21 cells. **E**) Likewise, AR-C 118925XX (10 μ M) abrogates UTP (100 μ M)-induced Ca²⁺ rises but does not affect the Ca²⁺ rises the does not affect the Ca²⁺ rises but does not affect the Ca²⁺ rises the does not affect the Ca²⁺ rises but does not affect the Ca²⁺ rises the does not affect the Ca²⁺ rises the does not affect the Ca²⁺ rises but does not affect the Ca²⁺ rises the doe

CRAC channel inhibitors block the P2Y₂-evoked Ca²⁺ elevations

The sustained [Ca²⁺]_i phase elicited upon P2Y₂ receptor activation lead us to probe whether CRAC channels are activated in this signal. We employed the ORAI1 inhibitor, CM4620 [162], and measured ATP-induced Ca²⁺ signals. Pretreatment of cells with CM4620 strongly abrogated the ATP-induced sustained [Ca²⁺]_i phase but left intact the rapid [Ca²⁺]_i rise (Figure 2.2A and Figure 2.2C). Next, we used the well-studied CRAC channel inhibitor BTP2 [163-165]. BTP2 also inhibited the UTP-induced sustained [Ca²⁺]_i phase but left intact the rapid [Ca²⁺]_i rise (Figure 2.2B-C). To confirm this finding, we performed a Ca²⁺ add-back experiment where intracellular Ca²⁺ stores are first depleted in the absence of extracellular Ca²⁺, and then extracellular Ca²⁺ is reintroduced allowing for more accurate measurement of Ca²⁺ entry across the plasma membrane. Pretreatment of cells with CM4620 stifled the Ca²⁺ entry following reintroduction without altering intracellular Ca²⁺ store release (Figure 2.2D-E). Collectively, this data suggests that P2Y₂ receptor activation elicits activation of CRAC channel mediated Ca²⁺ signals in AECs.



Figure 2.2 CRAC channel inhibitors block the P2Y₂-evoked Ca²⁺ elevations.

A) Pretreatment of NHBE cells with the CRAC channel inhibitor, CM4620 (1 μ M, 2 hrs) abolishes the sustained entry evoked by 100 μ M ATP. Data are mean ± SEM of n = 18-27 cells per trace. **B)** Likewise, pretreatment of cells with BTP2 (1 μ M, 2 hrs) abolished the sustained entry elicited by 100 μ M UTP. Data are mean ± SEM of n = 23-31 cells per trace. **C)** Quantification of $[Ca^{2+}]_i$ from A-B taken 5 minutes after agonist addition. Each data point is the mean $[Ca^{2+}]_i$ (averaged over 20-30 cells) for a given experiment (one dish) and the bar graph is mean ± SEM of n = 3-6 independent experiments. **D)** ATP-induced Ca²⁺ influx is inhibited by pretreatment (2hrs) with the ORAI1 inhibitor CM4620 (1 μ M). Cells were treated with ATP (50 μ M) in Ca²⁺ free Ringers solution to allow for store release followed by perfusion of Ringers contained 2mM Ca²⁺. Data are mean ± SEM of n = 14-21 cells. **E)** Quantification of the rate of Ca²⁺ influx in D. Rate of

influx was calculated for the 24 seconds immediately following extracellular Ca^{2+} addition. Each data point is the mean Ca^{2+} influx rate for a given experiment (one dish) and the graph is the mean \pm SEM of n = 3 independent tests *p<0.05, ***p<0.001

ORAI1 and STIM1 are the molecular components of P2Y₂ activated CRAC channels

Multiple ORAI and STIM isoforms exist that have the potential to form CRAC channels [70, 166]. Thus, we set out to identify the molecular identity of P2Y₂ receptor activated CRAC channels. ORAI1 and STIM1 were selectively knocked down using siRNA. Knockdown of either ORAI1 or STIM1 abrogated the ATP-induced sustained $[Ca^{2+}]_i$ phase but left intact the rapid $[Ca^{2+}]_i$ rise (Figure 2.3A-B). These results strongly suggest ORAI1 and STIM1 are predominant CRAC channel protein isoforms involved in P2Y₂ receptor signaling.



Figure 2.3 ORAI1 and STIM1 are the molecular components of P2Y₂ activated CRAC channels. A) siRNA constructs targeting ORAI1 (10 nM) or STIM1 (10 nM) block the sustained Ca²⁺ entry stimulated by ATP without affecting the initial Ca²⁺ release from intracellular stores. Data are mean \pm SEM of n = 21-31 cells per trace. B) Quantification of $[Ca^{2+}]_i$ from A. $[Ca^{2+}]_i$ was measured 5 minutes after agonist addition. Each data point is the mean $[Ca^{2+}]_i$ (averaged over 20-30 cells) for a given experiment (one dish) and the bar graph is the mean \pm SEM of n = 3-4 independent experiments.

Histamine activates CRAC channels in AECs

Previous data had implicated PAR2 receptors in CRAC channel mediated Ca^{2+} signaling [95]. Histamine is another inflammatory mediator in the airways and we tested whether histamine could elicit Ca^{2+} signals in primary human AECs. Histamine evoked a similar initial Ca^{2+} rise as UTP and the PAR2 activator SLIGKV (Figure 2.4A-B). However, the sustained Ca^{2+} elevations were much more substantial for UTP than for either histamine or the PAR2 activator SLIGKV (Figure 2.4C). Next, we employed the ORAI1 inhibitor CM4620 to test whether histamine activates CRAC channels. CM4620 strongly inhibited the histamine-induced sustained $[Ca^{2+}]_i$ phase but left intact the rapid $[Ca^{2+}]_i$ rise (Figure 2.4D). Altogether, these findings suggest that while AECs express P2Y₂ receptors, histamine receptors, and PAR2 receptors, P2Y₂ receptor activation elicits the strongest Ca^{2+} signals. Furthermore, all three of these receptors have the capacity to activate CRAC channels in AECs.



Figure 2.4 Histamine activates CRAC channels in AECs. A) The GPCR agonists UTP, histamine, and the PAR2 activator SLIGKV all elicit a $[Ca^{2+}]_i$ elevation. $[Ca^{2+}]_i$ was measured using Fura-2 AM as previously described [162]. Data are mean ± SEM of n = 40-50 cells. **B)** Summary of peak Ca^{2+} signal following agonist addition. Each data point is the mean peak Ca^{2+} signal (averaged over approximately 30-50 cells) for a given experiment (one dish) and the bar graph is mean ± SEM of n = 3-5 independent experiments. **C)** Quantification of $[Ca^{2+}]_i$ measured 5 minutes after agonist addition. Each data point (one dish) and the bar graph is the mean ± SEM of n = 3-5 independent experiment (one dish) and the bar graph is the mean ± SEM of n = 3-5 independent experiment (one dish) and the bar graph is the mean ± SEM of n = 3-5 independent experiment (one dish) and the bar graph is the mean ± SEM of n = 3-5 independent experiment (one dish) and the bar graph is the mean ± SEM of n = 3-5 independent experiment (one dish) and the bar graph is the mean ± SEM of n = 3-5 independent experiments. **D)** Pretreatment of NHBE cells with the CRAC channel inhibitor, CM4620 (1 µM, 2 hrs) abolishes the sustained entry evoked by 100 µM histamine. Data are mean ± SEM of n = 27-32 cells per trace.

Discussion

Extracellular ATP is a damage-associated molecular pattern [18]. Upon allergen challenge in the lungs, ATP levels in the bronchoalveolar lavage fluid increase dramatically [16, 18]. This extracellular ATP regulates allergic sensitization and inflammation through purinergic P2 receptors [16, 18]. Histamine is also linked to airway inflammation [63]. However, it was unknown if nucleotides or histamine drive CRAC channel activation in AECs. Here we demonstrate that the nucleotides ATP and UTP both activate P2Y₂ receptors in AECs, eliciting Ca²⁺ signaling and CRAC channel activation through ORAI1 and STIM1. Likewise, histamine also activates CRAC channels in AECs through H₁ receptors. However, P2Y₂ receptor activation elicits more sustained Ca²⁺ signaling than H₁ receptor activation. The discovery that both ligands activate AEC CRAC channels leads us to speculate that CRAC channels may be a signaling nexus driving airway inflammation. Nonetheless, the function ramifications of nucleotide or histamine signaling and subsequent CRAC channel activation in AECs remain to be elucidated.

Chapter 3: Nucleotides evoke PGE₂ synthesis through P2Y₂ receptors, CRAC

channels, MEK1/2-ERK1/2, and ultimately cPLA₂ signaling

Introduction

One of the most prominent mediators produced by AECs is Prostaglandin E2 (PGE₂). PGE₂ is synthesized through an enzymatic cascade tied to the activities of phospholipase A2, the COX-1 and COX-2 enzymes, and a terminal PGE synthase [109]. PGE₂ stimulates dilation of the lung airways thereby protecting the lung against severe bronchoconstriction that is a hallmark of diseases such as asthma [101, 102]. PGE₂ also inhibits several inflammatory processes, including the release of histamine and cysteinyl leukotrienes from mast cells [101], T-cell migration [103], ILC2 function [104], and the production of proinflammatory TNF- α and IL-12 β by dendritic cells [105], while also enhancing the synthesis of the anti-inflammatory cytokine IL-10 [105] and promoting wound healing [106]. Further, growing evidence suggests that PGE₂ can drive reverse migration and removal of neutrophils from sites of inflammation to dissipate inflammation *in vivo* [107]. Failure of resolution of inflammation can lead to inflammatory diseases such as COPD and ARDS. Thus, within the lung, PGE₂ exerts predominantly bronchoprotective and anti-inflammatory effects [108].

The mechanism(s) by which ATP and UTP signaling engages the synthesis of PGE₂ in AECs is largely unclear. There is compelling evidence, however, that CRAC channel dependent cytosolic Ca²⁺ elevations are necessary [95]. As a multifunctional second messenger, Ca²⁺ activates distinct genetic programs to regulate many cellular functions including gene transcription, cytokine production and activation of numerous enzymes [167]. Other important signaling pathways such as the MEK1/2-ERK1/2

pathway and reactive oxygen species (ROS) have also been implicated in PGE₂ synthesis [93, 113, 168-170]. Here we find that nucleotides activate P2Y₂ receptors in AECs, initiating signaling culminating in CRAC channel dependent activation of cPLA₂ and subsequent PGE₂ release. Both the MEK1/2-ERK1/2 pathway and ROS from NADPH oxidases appear necessary for full production of PGE₂. These findings reveal the key nucleotide signaling checkpoints that mediate the synthesis of PGE₂ involving Ca²⁺ signals through CRAC channels as a key signaling nexus. We speculate that engaging these pathways may elicit bronchoprotective responses in the human airways.

Results

P2Y₂ receptor stimulation evokes PGE₂ synthesis

Prostaglandin E2 (PGE₂) is a major mediator released from AECs eliciting antiinflammatory effects and limiting bronchoconstriction in the lungs [101, 102]. Nucleotides are known to elicit PGE₂ synthesis from AECs, but the receptors and signaling pathways responsible for this are largely unknown. Thus, we set out to identify the molecular mediators driving PGE₂ synthesis in AECs. To begin, we performed a time course analysis of PGE₂ in the supernatant following ATP stimulation. ATP-evoked a rapid increase in PGE₂ within 1 hour, which was sustained for several hours (Figure 3.1A). Next, we performed a dose-response analysis for ATP-mediated PGE₂ synthesis. Our analysis revealed an ATP-induced PGE₂ response with an EC₅₀ of approximately 7 μ M (Figure 3.1B). When we tested ATP and UTP in parallel, both caused release of PGE₂ to a similar degree (Figure 3.1C). This was highly suggestive of a common nucleotide membrane receptor driving the PGE₂ response. Therefore, we tested the P2Y₂ receptor antagonist, AR-C 118925XX (hereby termed, "AR-C"), for its ability to inhibit the nucleotide driven PGE₂ response [53]. AR-C strongly abrogated the ATP- and UTP-mediated PGE₂ response (Figure 3.1C). To verify the involvement of P2Y₂ receptors using an RNAi-based method, we utilized siRNA to knockdown *P2RY2* mRNA. siRNA targeting *P2RY2* strongly decreased the mRNA levels (Figure 3.1D). *P2RY2* siRNA also abrogated the ATP-induced PGE₂ response, confirming the involvement of P2Y₂ receptors (Figure 3.1E). Interestingly, AR-C and siRNA targeting *P2RY2* both effectively inhibited the basal PGE₂ release, suggesting that P2Y₂ receptors exhibit a low-level, basal activation (Figure 3.1F-G). Collectively, these findings demonstrate that nucleotides drive PGE₂ release through the activation of AEC P2Y₂ receptors.



Figure 3.1 P2Y₂ receptor stimulation evokes PGE₂ synthesis. A) Time course of PGE₂ induction elicited by 250 μ M ATP. Data are mean ± SEM of n = 6 samples/time

point. **B)** Dose-response of PGE₂ synthesis by ATP. PGE₂ was measured in the cell culture supernatant 2 hrs following agonist addition. The solid line is a four-parameter nonlinear regression fit of the Hill equation (*response*= $1/(1 + (EC_{50}/[agonist])^n]$) with EC₅₀ = 7.4 µM and Hill Slope = 1.35. Baseline PGE₂ was set to 0% and maximal agonist-evoked response was set at 100% for the fitting procedure. Data are mean ± SEM of n = 5-17 samples from 3 independent experiments. **C)** The selective P2Y₂ antagonist, AR-C 118925XX (10 µM), abrogates nucleotide (50 µM)-induced PGE₂ synthesis. Cells were pretreated with the antagonist for 1 hr prior to agonist stimulation (2 hr). Data are mean ± SEM of n = 4 samples. **D)** *siP2RY2* decreases *P2RY2* mRNA expression. Expression was normalized to the housekeeping gene *RPLP0*. Data are mean ± SEM of n = 1-3 samples. **E)** siRNA knockdown of *P2RY2* blocks ATP (100 µM)-induced PGE₂ synthesis. Data are mean ± SEM of n = 5-6 samples. **F)** The P2Y₂ antagonist AR-C 118925XX (10µM) inhibits basal PGE₂ synthesis. Data are mean ± SEM of n = 5 samples. **C** siRNA against *P2RY2* lowers basal PGE₂ synthesis. Data are mean ± SEM of n = 5 samples. **C** siRNA against *P2RY2* lowers basal PGE₂ synthesis. Data are mean ± SEM of n = 5 samples. **C** siRNA against *P2RY2* lowers basal PGE₂ synthesis. Data are mean ± SEM of n = 5 samples. **C** siRNA against *P2RY2* lowers basal PGE₂ synthesis. Data are mean ± SEM of n = 5 samples. **C** siRNA against *P2RY2* lowers basal PGE₂ synthesis. Data are mean ± SEM of n = 5 samples. **C** siRNA against *P2RY2* lowers basal PGE₂ synthesis. Data are mean ± SEM of n = 5 samples. **C** siRNA against *P2RY2* lowers basal PGE₂ synthesis. Data are mean ± SEM of n = 5 samples. **C** siRNA against *P2RY2* lowers basal PGE₂ synthesis. Data are mean ± SEM of n = 5 samples. **C** siRNA against *P2RY2* lowers basal PGE₂ synthesis. Data are mean ± SEM of n = 5 samples. **C** siRNA against *P2RY2* lowers basal PGE₂ synthesis. Data are mea

Media change induces transient ATP release into the supernatant

Reports suggest mechanical strain can cause ATP release from cells in vitro [46, 47].

We tested whether a media change could evoke the release of ATP in NHBEs. ATP

levels were very low in the supernatant of undisturbed cells whereas a media change

provoked a rapid increase in extracellular ATP levels that decreased over time (Figure

3.2).



Figure 3.2 Media change evoked ATP release from NHBEs. A) Media was changed and ATP concentrations were measured in the supernatant at the indicated time points. Data are mean \pm SEM of n = 4 samples/time point.

CRAC channel activation is essential for receptor-evoked PGE₂ synthesis

CRAC channels are activated upon P2Y₂ receptors activation (Figure 2.2). CRAC channels have also been implicated in other cell types in the production of prostaglandins and leukotrienes [80, 171]. Thus, we tested whether CRAC channels composed of ORAI1 and STIM1 were necessary for P2Y₂ receptor-evoked PGE₂ synthesis. Indeed, knockdown of either ORAI1 or STIM1 via siRNA inhibited the ATP-induced PGE₂ response (Figure 3.3A). To confirm the involvement of CRAC channels using an alternative method, we utilized the CRAC channel inhibitors CM4620 and BTP2. Both CRAC channel inhibitors strongly repressed the nucleotide-induced PGE₂ release (Figure 3.3B-C). This data implicates AEC CRAC channels are necessary for nucleotide-mediated PGE₂ responses.

Local Ca²⁺ signaling in the immediate proximity of the Ca²⁺ channel pore drives many Ca²⁺ dependent processes [84, 172]. Therefore, we tested whether CRAC channel-mediated PGE₂ synthesis exhibits this phenomenon of local Ca²⁺ signaling. We employed the Ca²⁺ chelators EGTA and BAPTA to assess this endpoint. Interestingly, BAPTA, which binds Ca²⁺ with much faster kinetics than EGTA [173], was much more effective at inhibiting the ATP-induced PGE₂ response (Figure 3.3D). BAPTA also inhibited the basal PGE₂ release while EGTA did not (Figure 3.3E). Altogether, this observed difference between BAPTA and EGTA is highly suggestive that the Ca²⁺ dependent machinery driving PGE₂ synthesis is spatially coupled to CRAC channels.



Figure 3.3 CRAC channels activation is essential for receptor-evoked PGE₂ synthesis. A) siRNA knockdown of ORAI1 and STIM1 blocks ATP (100 μ M)-induced PGE₂ synthesis. Data are mean ± SEM of n = 4-5 samples. B) The ORAI1-selective CRAC channel inhibitor, CM4620, (1 μ M pretreated for 2 hrs; referred in the figure as "CM") abolishes ATP (100 μ M) induced PGE₂ synthesis. Data are mean ± SEM of n = 4 samples. C) CM4620 (1 μ M) and the CRAC channel inhibitor, BTP2 (1 μ M), inhibit UTP (50 μ M)-induced PGE₂ synthesis. Data are mean ± SEM of n = 4 samples. C) CM4620 (1 μ M) and the CRAC channel inhibitor, BTP2 (1 μ M), inhibit UTP (50 μ M)-induced PGE₂ synthesis. Data are mean ± SEM of n = 4 samples. D) PGE₂ synthesis induced by ATP (50 μ M) persists in cells loaded with EGTA-AM (25 μ M) but not in cells loaded with BAPTA-AM (25 μ M). Cells were loaded with EGTA-AM or BAPTA-AM for 50 min prior to agonist stimulation. Data are mean ± SEM of n = 5-6 samples. E) Likewise, the baseline PGE₂ synthesis persists in cells loaded with the slow Ca²⁺ chelator, EGTA, but is abolished by the rapid Ca²⁺ chelator, BAPTA. Cells were loaded with EGTA-AM (25 μ M) or BAPTA-AM (25 μ M) for 50 min prior to 2 hr basal measurement. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

The MEK1/2-ERK1/2 kinase pathway is essential for PGE₂ synthesis

The MEK1/2-ERK1/2 pathway has been implicated downstream of receptor activation and in the production of PGE₂. Therefore, we examined whether P2Y₂ receptor activation could elicit ERK1/2 activation. ATP-induced a transient increase in ERK1/2 activation, which was blocked by the P2Y₂ receptor antagonist AR-C (Figure 3.4A-B). In contrast, CRAC channel inhibition did not prevent this ATP-mediated increase in ERK1/2 activation (Figure 3.4C). Next, we used the selective MEK1/2 inhibitor, U0126 [174], to block ERK1/2 activation. As expected, U0126 completely blocked the phosphorylation of ERK1/2, indicative of decreased ERK1/2 activity (Figure 3.4D). U0126 also strongly abrogated nucleotide-mediated increases in PGE₂ (Figure 3.4E-F). Collectively, these results implicate P2Y₂ receptor-mediated activation of the MEK1/2-ERK1/2 pathway as an essential step for PGE₂ synthesis.



Figure 3.4 The MEK1/2-ERK1/2 kinase pathway is essential for PGE₂ **synthesis. A)** Western blot illustrating ATP (100 µM)-mediated induction of ERK1/2 phosphorylation in NHBE cells (15 min following agonist treatment). This is abolished by the selective P2Y₂ receptor antagonist AR-C 118925XX (10 µM). Cells were pretreated with AR-C 118925XX for 1 hour. (P-ERK: phospho-ERK; T-ERK: Total ERK). **B)** Densitometry analysis of the Western blot data from A. Data are mean ± SEM of n = 3-4 samples. **C)** CRAC channel inhibitors CM4620 (1µM) and BTP2 (1µM) do not alter ATP induced ERK1/2 activation (100 µM, 15min stimulation). Data are mean ± SEM of n = 3 samples and densitometry was performed for quantification. **D)** Pretreatment of cells with the MEK1/2 inhibitor U0126 (20µM) inhibits ATP (100µM) induced ERK1/2 phosphorylation. **E)** The MEK1/2 inhibitor, U0126 (20 µM), abolishes ATP (50 µM)-induced PGE₂ synthesis. Data are mean ± SEM of n = 4-5 samples. **F)** Likewise, UTP (50 µM)-induced PGE₂ synthesis is abolished by U0126 (20 µM). Cells were pretreated with U0126 for 1 hour. Data are mean ± SEM of n = 4-5 samples. *p<0.05, **p<0.01, ***p<0.001,

$\ensuremath{\mathsf{P2Y}}_2$ receptor-mediated $\ensuremath{\mathsf{PGE}}_2$ synthesis requires COX-2 activity but not COX-2 induction

One set of enzymes essential for PGE₂ synthesis is the COX-1/2 enzymes. Therefore, we tested whether COX-1 or COX-2 enzyme activity was necessary for AEC PGE₂ synthesis. The COX-1 inhibitor, FR122047, as well as the COX-2 inhibitor, Celecoxib, abolished AEC PGE₂ synthesis (Figure 3.5A). Previous work in a lung cancer cell line revealed that nucleotides could increase COX-2 protein levels [169]. Therefore, we measured COX-2 protein levels following ATP stimulation of AECs. ATP-induced a transient and modest increase in COX-2 protein levels that quickly returned to baseline (Figure 3.5B). We examined whether this modest increase in COX-2 protein levels was dependent on P2Y₂ receptor activation. The P2Y₂ receptor antagonist AR-C trended towards limiting this COX-2 induction (Figure 3.5C-D). The CRAC channel inhibitors CM and BTP2 did not inhibit this increase in COX-2 levels (Figure 3.5E). We also examined whether MEK1/2-ERK1/2 signaling was involved in this transient increase in COX-2 protein. The MEK1/2 inhibitor U0126 failed to inhibit the small increase in COX-2 protein levels (Figure 3.5F-G). Collectively, these findings suggest that the increase in COX-2 protein levels following nucleotide treatment is minimal whereas COX-2 activity is essential for AEC PGE₂ synthesis.



Figure 3.5 P2Y₂ receptor-mediated PGE₂ synthesis requires COX-2 activity but not COX-2 induction. A) PGE_2 synthesis induced by ATP (100 µM) is abolished with the COX-1 inhibitor FR122047 (1µM) and by the COX-2 inhibitor Celecoxib (1µM). Cells were pretreated for 1 hr prior to agonist stimulation. Data are mean ± SEM of n = 4-5 samples. B) Time course for ATP (100µM)-mediated COX-2 upregulation. Data are mean ± SEM of n = 2-14 samples. C) ATP (100µM, 2hrs) induces only a small extent of COX-2 upregulation, which is inhibited by AR-C 118925XX (10µM). D) Summary of COX-2 upregulation using densitometry analysis. Data are mean ± SEM of n = 7 samples. E) CRAC channel inhibitors CM4620 (1µM) and BTP2 (1µM) do not alter ATP (100µM) induced COX-2 upregulation (2hr stimulation duration). Data are mean ± SEM of n = 7-9 samples and densitometry was performed for quantification. F) ATP (100 µM, 2hrs) induces a low level of COX-2 upregulation, which is not inhibited by MEK1/2 inhibitor, U0126 (20µM). G) Densitometry analysis of the Western blot data illustrated in *F*. Data are mean ± SEM of n = 7 samples. ****p<0.0001

Inhibition of NADPH oxidase occludes ATP- and UTP- induced synthesis of PGE₂

Reactive oxidation species (ROS) has also been implicated in PGE₂ synthesis. The two

primary sources of ROS in cells are plasma membrane associated NADPH oxidase

enzymes and the mitochondria [175]. Therefore, we employed the NADPH oxidase

inhibitor, apocynin, and the mitochondrial ROS inhibitor S3QEL-2 [176], to interrogate whether ROS from either of these sources is involved in PGE₂ synthesis. Interestingly, apocynin strongly inhibited nucleotide-mediated PGE₂ release while S3QEL-2 was completely ineffective (Figure 3.6A-B). ROS has been linked to activation of the MEK1/2-ERK1/2 pathway. Thus, we investigated whether apocynin blocks ATP-induced ERK1/2 activation. Apocynin had no effect on ATP-mediated ERK1/2 activation (Figure 3.6C-D). Altogether, these results suggest that NADPH oxidase derived ROS is necessary for nucleotide-evoked PGE₂ synthesis in AECs.



Figure 3.6 Inhibition of NADPH oxidase occludes ATP- and UTP- induced synthesis of PGE₂. A) Apocynin (200 μ M), an inhibitor of NADPH oxidase, abrogates UTP (50 μ M) induced PGE₂ synthesis. By contrast, the mitochondrial complex III inhibitor S3QEL-2 (20 μ M) does not affect the UTP (50 μ M)- induced PGE₂ response. Data are mean ± SEM of n = 4-6 samples. B) Likewise, apocynin (200 μ M) abrogates ATP (50 μ M)-induced PGE₂ synthesis. Data are mean ± SEM of n = 4 samples. C) Pretreatment of cells with the apocynin (200 μ M) does not inhibit ATP (100 μ M)-induced ERK1/2 phosphorylation (15min stimulation). D) Densitometry to quantify experiments shown in *C*. Data are mean ± SEM of n = 4 samples. **p<0.01, ***p<0.001, *****p<0.0001.

P2Y₂ receptor activation of CRAC channels elicits cPLA₂ activation

We next investigated the role of Ca^{2+} -dependent enzymes in the production of PGE_2 . One key Ca²⁺-dependent enzyme implicated in agonist-evoked responses is calcineurin. Therefore, we tested the calcineurin inhibitor, FK-506, for its role in the synthesis of PGE₂. FK-506 had no effect on ATP-induced PGE₂ release (Figure 3.7A). Another Ca²⁺-dependent enzyme downstream of the COX enzymes and linked to PGE₂ synthesis is cPLA₂ [98]. Thus, we tested the cPLA₂ inhibitor, AACOCF₃, for its role in PGE₂ release. AACOCF₃ significantly inhibited ATP-evoked PGE₂ production (Figure 3.7B). Activation of cPLA₂ prompts its accumulation at intracellular membranes, where it liberates arachidonic acid from the phospholipid membrane [98, 177]. To interrogate this step more closely, we performed a nuclear versus cytosolic fractionation protocol followed by western blotting to assess cPLA₂ activation [80]. ATP-induced a rapid enrichment of cPLA₂ in the nuclear fraction (Figure 3.7C). The selective P2Y₂ receptor antagonist, AR-C, completely blocked cPLA₂ recruitment to the nuclear fraction (Figure 3.7C-D). Next, we investigated whether CRAC channel activation was required for cPLA₂ enrichment in the nuclear fraction. The CRAC channel inhibitors CM4620 and BTP2 both inhibited nucleotide-stimulated cPLA2 recruitment to the nuclear fraction (Figure 3.7E-H). Collectively, these findings demonstrate that P2Y₂ receptor activation elicits CRAC channel-induced activation of cPLA₂.



Figure 3.7 P2Y₂ receptor activation of CRAC channels elicits cPLA₂ activation. A) FK-506 (1 μ M) does not inhibit ATP (100 μ M)-induced PGE₂ synthesis. Data are mean ± SEM of n = 5-6 samples. B) ATP (100 μ M)-induced PGE₂ synthesis is inhibited with pretreatment of cells with cPLA₂ inhibitor AACOCF₃ (5 μ M). Data are mean ± SEM of n = 5 samples. C) The P2Y₂ receptor antagonist AR-C 118925XX (10 μ M) blocks ATPinduced enrichment of cPLA₂ in the nuclear fraction. D) Densitometry analysis of the Western blot data illustrated in C. Data are mean ± SEM of n = 4 samples. E,F) The CRAC channel inhibitors, CM4620/CM-EX-128 (1 μ M referred as "CM") and BTP2 (1 μ M), block ATP (100 μ M)-induced enrichment of cPLA₂ in the nuclear fraction. Data are mean ± SEM of n = 4-5 samples. G) Likewise, CM4620 (1 μ M) also blocks UTP (100 μ M)-induced enrichment of cPLA₂ in the nuclear fraction. H) Densitometry to quantify experiments shown in G. Data are mean ± SEM of n = 3 samples. *p<0.05, **p<0.01, ***p<0.001

Airway Epithelial Cell passage number regulates PGE₂ production

Throughout our experiments examining PGE_2 release from AECs, we observed significant variability in the basal PGE_2 depending on the experiment. Thus, we pooled data from many experiments to compare the basal PGE_2 release levels. Our data was highly suggestive that higher passage number of cells leads to higher levels of basal PGE_2 release (Figure 3.8).



Figure 3.8 NHBE passage number correlates with basal PGE₂ **production.** Basal PGE₂ production of NHBEs sorted by passage number. Data are mean \pm SEM of n = 6-25 samples.

Discussion

PGE₂ is a protective mediator in the airways. Specifically, it can protect against bronchoconstriction, a hallmark of diseases such as asthma [101, 102]. PGE₂ also

inhibits several inflammatory processes, such as the release of inflammatory mediators from mast cells [101], T-cell migration [103], ILC2 function [104], and the production of proinflammatory TNF- α and IL-12 β by dendritic cells [105]. Moreover, PGE₂ can also promote the production of the anti-inflammatory cytokine IL-10 [105]. Understanding mechanisms that contribute to PGE₂ production in the airways may unveil pathways that can be harnessed in the context of lung inflammation.

Here we discover a multistep signaling pathway that culminates in PGE₂ release from AECs. The pathway begins with extracellular nucleotides activating the P2Y₂ receptor on AECs. P2Y₂ receptor activation elicits CRAC channel activation leading to rapid cPLA₂ recruitment to intracellular membranes, the liberation of arachidonic acid, and COX-2 dependent synthesis of PGE₂. The MEK1/2-ERK1/2 pathway is also activated by P2Y₂ receptors and is necessary for PGE₂ release. ROS from NADPH oxidases is also a necessary component for receptor-mediated production of PGE₂. Interestingly, we observed an increase in basal PGE₂ release with increasing passage number of NHBEs. This suggests that cellular senescence may lead to higher basal PGE₂ production.

An interesting feature of PGE_2 synthesis is that it's exquisite sensitivity to blockade by the rapid Ca^{2+} buffer BAPTA but not the slower buffer EGTA (Figure 3.3D-E). This result suggests that PGE_2 synthesis relies on local Ca^{2+} signaling likely through Ca^{2+} microdomains near CRAC channels that are functionally linked to cPLA₂ activation. Previous studies have shown that Ca^{2+} microdomains arising from CRAC channels can stimulate arachidonic acid release and leukotriene production in mast cells [80]. Ca^{2+} microdomains around CRAC channels are also linked to NFAT-dependent gene transcription and exocytosis in neuronal stem cells and astrocytes [172, 178]. Thus, the finding that local Ca^{2+} signals around CRAC channels are essential for cPLA₂-mediated synthesis of PGE₂ broadens the role of Ca^{2+} microdomains linked to enzyme activation in different cell types.

Nucleotides are well known to be a danger-associated molecular pattern (DAMP) and are present in the context of asthma and COPD [16, 18, 21]. This suggests that the purinergic pathway culminating in PGE₂ release may be active in the context of ongoing lung inflammation. However, it may be therapeutically beneficial to enhance pathway activation even further with a selective P2Y₂ receptor agonist. Indeed, airway P2Y₂ receptors have attracted significant interest for therapeutics in recent years. A stable P2Y₂ receptor agonist (denufosol) was rigorously investigated in cystic fibrosis patients based on its ability to stimulate mucociliary clearance (MCC) [54]. Unfortunately, long-term treatment with denufosol showed no improvement of lung function in cystic fibrosis patients [55]. More studies may be warranted to test denufosol in the context of ongoing lung inflammation in patients with asthma or COPD.

Chapter 4: ATP evokes IL-6 release through P2X receptors and CRAC channel dependent Calcineurin-NFAT pathways

Introduction

Airway epithelial cells (AECs) can be induced to release interleukin-6 (IL-6). IL-6 is a proinflammatory cytokine that elicits a wide-range of inflammatory effects including T-cell expansion, pulmonary neutrophil infiltration, airway mucus secretion, lung fibrosis, and the hyperplasia and hypertrophy of airway smooth muscle cells [121-124]. Recent studies have linked IL-6 to numerous airway diseases such as asthma to COPD [121-124]. Importantly, patients with severe COVID-19 have revealed massive increases in IL-6 in the lung airways, a feature thought to contribute to microvascular thrombosis in the lung and multiple organ dysfunction in these patients [125]. Conversely, blockade of IL-6 signaling in mouse models of asthma protects against airway inflammation [122, 126], and early reports indicate that targeting IL-6 may be a viable therapy to decrease mortality in severe COVID-19 patients [127]. Collectively, understanding the signaling mechanisms orchestrating AEC release of IL-6 may prove beneficial for a host of human airway diseases.

One stimulus that is reported to elicit the release of IL-6 from AECs is extracellular nucleotides [36]. Recent discoveries in our lab have also highlighted AEC CRAC channels as essential for IL-6 production [95, 97]. Ca^{2+} is a multifaceted second messenger that coordinates distinct genetic programs to regulate many cellular functions including gene transcription, cytokine production and enzyme activation [167]. How nucleotides and Ca^{2+} signals combine to evoke the release of IL-6 from AECs

remains unclear. Here we discover that extracellular ATP activates ionotropic P2X receptors to provoke IL-6 release from AECs. In contrast to ATP, the uridine nucleotide UTP showed no efficacy for IL-6 release. CRAC channel activation and subsequent calcineurin/NFAT signaling was necessary for ATP-mediated IL-6 production. Similar to PGE₂ synthesis, the MEK1/2-ERK1/2 pathway was also necessary for full IL-6 release. Altogether, these findings highlight CRAC channels as a key signaling hub employed by purinergic receptor signaling.

Results

ATP drives IL-6 release through a pathway distinct from P2Y₂ receptors

ATP is known to elicit IL-6 release from AECs yet the receptor signaling mechanisms are largely unknown. To begin, we performed a time course analysis of ATP-induced IL-6 release. The majority of the IL-6 was released at overnight time points (Figure 4.1A). Next, we performed a dose-response analysis, which revealed that ATP-elicited release of IL-6 with an EC₅₀ of approximately 16 μ M (Figure 4.1B). Notably, this was significantly higher than the EC₅₀ of approximately 7 μ M for PGE₂ release (Figure 4.1B). To verify that ATP, and not a downstream metabolite of ATP, was increasing IL-6 secretion, we utilized the ATP variant, ATPγS, which is resistant to ecto-ATPase degradation. ATPγS evoked IL-6 release at similar doses seen for ATP (Figure 4.1C). As a complementary method to elucidate the active nucleotide driving IL-6 release, we employed the enzyme apyrase, which degrades ATP and ADP into AMP. When ATP was pretreated with apyrase prior to cellular stimulation, the IL-6 release was significantly decreased (Figure 4.1D). These findings strongly implicate ATP is the bona fide ligand that elicits IL-6 release. Furthermore, we tested whether the P2Y₂ receptor antagonist, AR-C, blocked ATP-induced IL-6 release. AR-C showed no effect on ATPmediated IL-6 release (Figure 4.1E). In agreement with this data, the P2Y₂ receptor agonist UTP did not elicit IL-6 release (Figure 4.1E). Altogether, these results imply that ATP drives IL-6 release through a pathway distinct from P2Y₂ receptors.



Figure 4.1 ATP drives IL-6 release through a pathway distinct from P2Y₂ receptors. A) Time course of ATP-induced IL-6 secretion from NHBE cells. Cells were stimulated with 250 μ M ATP for the indicated times. Data are mean ± SEM of n = 6 samples/time point. B) Dose-response of IL-6 induction by ATP. IL-6 was measured in the cell culture supernatant 20 hrs following addition of ATP (red). The dose-response of ATP-induced PGE₂ (grey) from Figure 3.1B is shown for comparison. The data was fit with the Hill equation with $EC_{50} = 16.5 \mu M$ and Hill Slope = 1.2. The extra sum-ofsquares F-Test used to statistically compare the two dose-response curves. IL-6 data are mean \pm SEM of n = 6-12 samples from two independent experiments. C) ATPyS stimulates IL-6 secretion. NHBE cells were treated with the indicated concentrations of ATPyS, and IL-6 was measured 16 hours following stimulation. Data are mean ± SEM of n = 3-6 samples. **D)** Pretreating ATP with apyrase (5U/mL) inhibits the ATP (250 μ M)induced IL-6 induction. Data are mean ± SEM of n = 4-6 samples. E) The ATP-induced IL-6 induction is not mediated by P2Y₂ receptors. The P2Y₂ receptor antagonist, AR-C 118925XX (10 µM), does not affect ATP (250 µM)-induced IL-6 secretion. Importantly, the P2Y receptor agonist, UTP (250 μ M), fails to induce IL-6 secretion. Data are mean ± SEM of n = 5-6 samples.

P2Y receptors do not drive IL-6 release

To test whether an alternative P2Y receptor may elicit IL-6 release, we compared the efficacy of ATP γ S and ADP β S in IL-6 secretion. ATP γ S was much more effective at eliciting IL-6 secretion than ADP β S, ruling out ADP receptor involvement (Figure 4.2A). Next, we tested whether the P2Y₆ agonist UDP and the P2Y₁₁ agonist NF546 caused IL-6 release. Neither UDP nor NF546 induced IL-6 release (Figure 4.2B-C). In agreement with this, the P2Y₁₁ antagonist, NF157, did not inhibit IL-6 secretion (Figure 4.2D). Collectively, this data excludes all known subtypes of P2Y receptors in the ATP-

induced IL-6 release.



Figure 4.2 P2Y receptors do not drive IL-6 release. A) Dose-response for ATP γ S versus ADP β S induced IL-6 secretion measured in cell culture supernatant 16 hrs following agonist addition. Data are mean ± SEM of n = 4-6 samples. **B)** UDP (P2Y₆ receptor agonist) does not elicit IL-6 secretion. Data are mean ± SEM of n = 3 samples. **C)** NF546 (P2Y₁₁ receptor agonist) fails to elicit IL-6 secretion. Data are mean ± SEM of n = 4 samples. **D)** NF157 (an antagonists of P2Y₁₁ and P2X1 receptors) enhances low dose ATP γ S induced IL-6 secretion. Data are mean ± SEM of n = 3 samples.

P2X receptors drive IL-6 secretion

We examined primary human AECs for their expression of P2X receptors via RT-qPCR. In two independent donors, we were able to detect expression of *P2RX4,5,7* (Figure 4.3A). We employed the broad-spectrum P2X receptor antagonists PPADS and suramin. Both antagonists strongly inhibited IL-6 secretion (Figure 4.3B). Then, we tested a series of P2X subtype selective antagonists. The antagonist of P2X1, P2X3, and P2X2/3 receptors, TNP-ATP, did not block IL-6 secretion (Figure 4.3C). Likewise, the P2X4 receptor antagonist, 5-BDBD, did not block IL-6 release (Figure 4.3D). Similarly, the P2X7 receptor antagonist, A740003, also did not inhibit IL-6 secretion (Figure 4.3E). Finally, we used shRNA to knockdown *P2RX4* mRNA. The knockdown showed low efficacy and did not inhibit IL-6 secretion (Figure 4.3F-G). These findings suggest that multiple P2X receptors may simultaneously engage to evoke IL-6 release.



Figure 4.3 P2X receptors drive IL-6 secretion. A) Two independent donors (NHBE cells) were examined for P2R expression via RT-qPCR. *P2RX4,5,7* were detected while *P2RY11, P2RX1-3,6* were not detected. **B)** The broad-spectrum P2X antagonists PPADS (100 μ M) and suramin (100 μ M) abrogate ATPγS (10 μ M)-induced IL-6. Data are mean ± SEM of n = 4-6 samples. **C)** TNP-ATP, an antagonist of P2X1, P2X3, and P2X2/3 receptors does not inhibit ATPγS-induced (10 μ M) IL-6 secretion. Data are mean ± SEM of n = 5 samples. **D)** The P2X4 receptor antagonist, 5-BDBD (5 μ M), does not inhibit ATPγS-induced (10 μ M) IL-6 secretion. Data are mean ± SEM of n = 4-6 samples. **E)** The P2X7 receptor antagonist A740003 (10 μ M) also does not inhibit ATPγS-induced IL-6 secretion. Data are mean ± SEM of n = 4-6 samples. **E)** The P2X7 receptor antagonist A740003 (10 μ M) also does not inhibit ATPγS-induced IL-6 secretion. Data are mean ± SEM of n = 3-6 samples. **F)** *P2RX4* mRNA knockdown using shRNA quantified via RT-qPCR. Expression was normalized to the housekeeping gene *RPLP0*. Data are mean ± SEM of n = 3 samples. **G)** Knockdown of *P2RX4* does not affect ATPγS-evoked IL-6 synthesis. Data are mean ± SEM of n = 5-6 samples.

CRAC channels drive IL-6 release through a calcineurin-NFAT pathway

CRAC channel activation in AECs has been linked to IL-6 secretion [95, 97]. Therefore, we tested whether the CRAC channel inhibitors CM4620 and BTP2 inhibited ATP γ S-induced IL-6 secretion. Indeed, both inhibitors significantly inhibited IL-6 release (Figure 4.4A). One Ca²⁺-dependent enzyme CRAC channels activate is cPLA₂. However, the cPLA₂ inhibitor, AACOCF₃, did not inhibit IL-6 secretion (Figure 4.4B). Another enzyme downstream of CRAC channels is the Ca²⁺-dependent phosphatase calcineurin. The calcineurin inhibitor, FK-506, strongly abrogated ATP γ S-induced IL-6 secretion (Figure 4.4C). These results are strongly suggestive that CRAC channel dependent calcineurin-NFAT pathways are necessary for IL-6 release.

A host of stimuli have the capacity to elicit IL-6 release from AECs. Surprisingly, the CRAC channel inhibitor CM4620 inhibited basal IL-6 release in AECs (Figure 4.4D). This result did depend somewhat on the donor and the basal levels of IL-6 release (data not shown). For example, conditions where basal IL-6 release was high were more likely to exhibit this CRAC channel dependence on the basal release. We tested whether CRAC channels are necessary for stimulus-induced IL-6 release from an array of ligands. CM4620 inhibited house dust mite (HDM)-induced IL-6 release (Figure 4.4E). Similarly, CM4620 blocked TNF- α -driven IL-6 secretion (Figure 4.4F). Moreover, both CM4620 and BTP2 abrogated IL-1 β -driven IL-6 release (Figure 4.4G). Altogether, these discoveries highlight that AEC CRAC channel activity is broadly necessary for stimulus-evoked IL-6 secretion.


Figure 4.4 CRAC channels drive IL-6 release through a calcineurin-NFAT pathway. A) CM4620 (1 μM) and BTP2 (1 μM) block ATPγS (100μM)-induced IL-6 secretion. Due to variability in basal IL-6 release between different human donors, the data shown here are normalized to the levels found in unstimulated cells. The absolute concentrations of IL-6 in unstimulated cells ranged from 100 to 700 pg/mL. Data are mean ± SEM of n = 10-11 samples. **B)** IL-6 release induced by ATPγS (100 μM) is not affected by AACOCF₃ (5μM). Data are mean ± SEM of n = 5 samples. **C)** The calcineurin inhibitor FK-506 (1 μM) blocks ATPγS-induced IL-6 secretion. Data are mean ± SEM of n = 5-6 samples. **D)** CM4620 (2 μM) can block basal IL-6 release. **E)** CM4620 (2 μM) also blocks HDM (100μg/mL)-induced IL-6 secretion. **F)** CM4620 (2 μM) also blocks IL-1β (10ng/mL)-induced IL-6 secretion. *p<0.05, **p<0.01, ***p<0.001, ****p<0.001,

Reactive Oxygen Species are necessary for IL-6 induction

Reactive oxygen species (ROS) have been linked to IL-6 from AECs. Therefore, we set out to interrogate whether plasma membrane-associated ROS, from NADPH oxidases, or mitochondrial-associated ROS were necessary for IL-6 secretion. Interestingly, the NADPH oxidase inhibitor, apocynin, and the mitochondrial ROS inhibitor, S3QEL-2, both showed partial blockade of ATP γ S-induced IL-6 secretion (Figure 4.5). This suggests that ROS from both the plasma membrane-associated NADPH oxidases and mitochondria may regulate AEC IL-6 release.



Figure 4.5 Reactive Oxygen Species are necessary for IL-6 induction. Inhibition of NADPH oxidase with apocynin (200 μ M) or the mitochondrial complex III inhibitor S3QEL-2 (20 μ M) have only modest effects on ATP γ S (100 μ M) induced IL-6 synthesis. Data are mean ± SEM of n = 4 samples.

ROS from mitochondrial complex III does not activate NFAT in BEAS-2B cells Reports suggest that ROS from mitochondrial complex III are implicated in NFAT activation and IL-6 release in immune cells [179, 180]. We utilized the NFAT firefly luciferase plasmid to dissect NFAT signaling in BEAS-2B cells. The NFAT promoter sequence in this plasmid is taken from the human IL-2 gene [181, 182]. As expected, the calcineurin inhibitor FK-506 blocked the induction of the luciferase (Figure 4.6A) confirming the calcineurin-NFAT pathway is necessary for luciferase production. The mitochondrial complex III ROS inhibitor S3QEL-2 [176] also dramatically blocked the production of the NFAT luciferase (Figure 4.6B) suggesting a role for ROS in the synthesis the luciferase. We assayed NFAT activation directly employing a NFAT4-GFP construct. Although FK-506 strongly blocked TG-induced NFAT4 nuclear translocation, S3QEL-2 did not inhibit translocation (Figure 4.6C) indicating mitochondrial complex III ROS does not directly activate NFAT4 downstream of CRAC channels. Finally, although TG-mediated IL-6 secretion from AECs is NFAT dependent [95], S3QEL-2 had no affect on TG-evoked IL-6 secretion (Figure 4.6D). It is likely that the S3QEL-2 impact on the NFAT luciferase is a result of the IL-2 NFAT promoter sequence also containing an AP-1 site [182, 183]. Altogether, mitochondrial ROS does not appear to be necessary for CRAC channel dependent IL-6 secretion in BEAS-2B cells.



Figure 4.6 Complex III ROS does not activate NFAT downstream of CRAC channels in BEAS-2B cells. A-B) NFAT and mitochondrial complex III ROS are both required from activation of NFAT luciferase construct. BEAS-2B cells were transfected with NFAT luciferase plasmids and treated with compounds for 6 hours prior to analysis. C) S3QEL-2 does not block NFAT4-GFP translocation in BEAS-2B. Cells were treated with TG for 20 minutes prior to analysis of nuclear translocation. D) S3QEL-2 does not block TG-induced IL-6 secretion in BEAS-2Bs.

MEK1/2-ERK1/2 signaling is necessary for IL-6 induction

MEK1/2-ERK1/2 signaling has also been linked to AEC IL-6 release. Indeed, the

MEK1/2 inhibitor U0126 strongly abrogated the ATPγS-evoked IL-6 secretion (Figure

4.7). This data implicates the MEK1/2-ERK1/2 signaling pathway in ATPγS-evoked IL-6

secretion in AECs.



Figure 4.7 MEK1/2-ERK1/2 signaling is necessary for IL-6 induction.

The ATP γ S (100 μ M)-induced IL-6 secretion is abolished by the MEK1/2 inhibitor U0126 (20 μ M). Data are mean ± SEM of n = 4 samples. **p<0.01

Airway Epithelial Cell passage number regulates IL-6 production

Throughout our experiments examining IL-6 release from AECs, we observed significant variability in the basal IL-6 secretion depending on the experiment. Thus, we pooled data from many experiments to compare the basal IL-6 release levels. Our data was highly suggestive that higher passage number of cells leads to higher levels of basal IL-6 release (Figure 4.8).



Figure 4.8 NHBE passage number correlates with basal IL-6 production. Basal IL-6 production of NHBEs sorted by passage number. Data are mean ± SEM of n = 5-20 samples.

Discussion

In the airways, nucleotide signaling is linked to a wide range of immune effects. High concentrations of extracellular ATP are linked to the production of inflammatory

cvtokines leading immune cell infiltration. airway remodeling. and to hyperresponsiveness [13, 16, 18, 36]. Patients with asthma, COPD, and ARDS show increased airway ATP levels in the BAL fluid and elevated extracellular ATP is thought to contribute to disease pathology [16, 21, 22]. However, while high concentrations of extracellular ATP are considered pro-inflammatory, ATP (and UTP) can also stimulate many anti-inflammatory [184], and physiologically beneficial effects in the lung including mucociliary clearance (MCC), PGE₂ synthesis, and wound healing [23-25, 27, 94]. The differential cellular pathways mediating these potentially beneficial and harmful effects are not well understood.

Here we describe the cell signaling mechanisms underlying the purinergic IL-6 production from AECs. It is worth comparing the purinergic pathways that drive IL-6 versus PGE₂ as the first pathway is potentially proinflammatory while the second is bronchoprotective. Our results indicate that ATP/UTP signaling through P2Y₂ receptors activates CRAC channels and ERK1/2, and subsequently cPLA₂, resulting in rapid synthesis of PGE₂, which is known to evoke bronchoprotective and immune suppressive effects (Figure 4.9) [101-105, 108, 185]. To our knowledge, this is the first identification of AEC P2Y₂ receptors in stimulating protective PGE₂ synthesis. By contrast, ATP-mediated induction of IL-6, which is implicated in proinflammatory responses in the airways [121-124, 126, 127], appears to occur through stimulation of P2X receptors through a process requiring CRAC channels, ERK1/2 activation, but also distinctly involving calcineurin/NFAT activation (Figure 4.9).

Several key features both upstream and downstream of CRAC channels underscore the differences in the two pathways. First, although UTP strongly induces PGE₂, it is completely ineffective in evoking IL-6 synthesis (Figure 3.1C versus 4.1E). In contrast, ATP evokes both PGE₂ and IL-6 synthesis, albeit at different potencies (7 μ M versus ~16 μ M; Figure 4.1B) and over significantly different time courses (Figure 3.1A versus 4.1A). As noted above, this difference is related to the different receptors (P2Y₂ versus P2X receptors) involved in stimulating PGE₂ and IL-6. Second, the Ca²⁺-dependent signaling pathways downstream of receptor activation significantly differ: P2Y₂ receptor-driven PGE₂ synthesis involves Ca²⁺ activation of cPLA₂ whereas P2X-driven IL-6 secretion requires Ca²⁺-dependent transcription via the calcineurin/NFAT pathway. As well, distinct sources of ROS appear to be involved in regulating the production of these mediators.

What are the functional implications of these findings and under what conditions could these differing outcomes become apparent? Although speculative, we can envision two scenarios. First, the observation that PGE₂ synthesis by ATP occurs at lower ATP doses than that required for IL-6 suggests that the protective versus proinflammatory outcomes for ATP may be dictated in part by the concentration and duration of ATP signaling in the airways. In the healthy lung, low micromolar levels of ATP over short time scales may selectively evoke PGE₂, whereas higher levels of ATP occurring over longer durations such as those found under conditions of intense inflammation and/or cellular necrosis would be predicted to elicit robust IL-6 synthesis. Although it is worth noting that studies that have quantified purine concentrations in sputum or BALf of diseased human patients tend to find concentrations in the high nM or low µM range [21, 186]. Second, extracellular UTP secretion would be predicted to exclusively induce PGE₂. Growing evidence points to UTP as a physiologically relevant

signaling molecule linked to numerous cellular processes including ion transport, ciliary beat frequency, and mucin release [28]. Although regulated secretion of UTP is very poorly understood likely due to lack of tools to easily detect extracellular UTP [187], release of UTP *in vitro* following mechanical stress, apoptosis, and solution exchange has been demonstrated using HPLC from a number of tissues including airway epithelial cells [46, 47, 50, 188]. UTP release under these conditions would be expected to preferentially evoke bronchoprotective responses in the lung. Future *in vivo* studies using mouse models in which P2Y₂ receptors are selectively deleted in the lung epithelium could shed light on this important question.

Two important mechanistic questions raised by our study that remain to be addressed relate to the nature of the Ca²⁺ signal activated by CRAC channels that drives IL-6 induction, and the mechanism of how P2X receptor stimulation is coupled to activation of CRAC channels. The data indicate that antagonism of P2Y₂ receptors blocks both ATP- and UTP-evoked Ca²⁺ elevations to similar extents (Figure 2.1D-F). Yet, unlike ATP, UTP is completely ineffective in inducing IL-6 (Figure 4.1E). Because CRAC channel blockade strongly inhibits induction of IL-6 by ATP (Figure 4.4A), this result suggests that ATP-mediated induction of IL-6 requires Ca²⁺ influx reliant on CRAC channels that is not readily detected by Fura-2. We speculate that P2X receptor activation of CRAC channels occurs over much longer time periods than was evaluated in our experiments and may be sufficiently local so as to evade detection by the bulk Ca²⁺ indicator, Fura-2. The functional coupling between P2X receptors and CRAC channels could involve localized ryanodine receptor-mediated Ca²⁺-induced Ca²⁺ release events of the type that have been described in skeletal muscle and T-cells [189,

190]. Additional mechanistic studies using low-affinity and membrane-tethered Ca²⁺ indicators and genetic tools to manipulate specific P2X receptors are needed to help address the unknown links between P2X receptors, CRAC channels, and IL-6 induction.

Although P2X receptors have been widely investigated in many physiological contexts, their physiological roles and effector signaling mechanisms in airway epithelial cells are not well understood. One study described a key role for P2X receptor activation in inducing IL-8 production via Ca²⁺ signaling and NF-κB [61], suggesting that P2X receptors may have an important role in AECs to drive proinflammatory responses. Our finding that the P2X receptor antagonists suramin and PPADS strongly suppress ATP-evoked synthesis of IL-6 in airway epithelial cells is in agreement with this suggestion and expands the potential roles of P2X receptors in the airways to include the inflammatory cytokine IL-6.

Finally, airway CRAC channels have attracted significant interest for therapeutics in recent years. CRAC channel inhibitors have shown efficacy in preclinical models of asthma [73, 191-196]. Moreover, the CRAC channel inhibitor CM4620 is currently being tested in human patients for relieving the cytokine storm in seriously ill COVID-19 patients [197]. Our results showing that CM4620 is very effective in occluding IL-6 production may provide the mechanistic explanation for the benefits of this small molecule in improving patient survival. Although CRAC channels also play a key role in agonist-evoked PGE₂ synthesis, this may be counterbalanced under chronic inflammatory conditions *in vivo* due to its role in driving proinflammatory cytokine production, thus providing a therapeutic window to dampen chronic inflammation in the lung airways. More studies are needed to address these scenarios but the results of this study provide a framework for testing these and other models.



Figure 4.9 A model for divergent mechanisms driving PGE₂ and IL-6 synthesis in bronchial epithelial cells. The airway-derived nucleotides UTP and ATP stimulate production of PGE₂ via activation of cell surface P2Y₂ receptors, leading to activation of CRAC channels, ERK1/2, and cPLA₂. At higher doses, ATP will additionally also recruit activation of P2X receptors, leading to IL-6 induction via CRAC channels and ERK1/2 activation. In contrast to PGE₂ synthesis, the IL-6 synthesis cascade requires calcineurin-NFAT signaling.

Chapter 5: GPCR signaling inhibits IFN production in submerged AECs Introduction

Airway epithelial cells (AECs) are primary host target cells for infection by respiratory viruses [11, 12]. Although AECs were once thought to be exclusively involved in barrier function, they have increasingly been understood to orchestrate downstream immune and inflammatory responses through the production of various classes of inflammatory mediators [3]. When a respiratory virus infects AECs, one essential class of antiviral cytokines that is produced is interferons [12, 128, 129]. Interferons (IFNs) are classified as type 1 (IFN- α/β), 2 (IFN- γ), or 3 (IFN- λ). Respiratory virus-infected AECs produce predominantly type 1 and type 3 IFN [130]. While both of these cytokines have antiviral activity, important distinctions exist. Type 3 IFN receptors are restricted to mucosal surfaces while type 1 IFN receptors are considered ubiquitous [12, 128]. Thus, IFN- λ is a mucosal specific mechanism for antiviral defense. Although, AECs generally make higher quantities of type 3 IFN than type 1 IFN following infection [130], type 1 is more potent [131]. Both type 1 and type 3 IFN signaling induces the expression of interferonstimulated genes (ISGs) that enhance antiviral defense of cells [12, 128]. Altogether, understanding the signaling mechanisms that regulate AEC IFN production may enable the development of novel antiviral therapies.

Acute respiratory viral infections can aggravate underlying chronic airway diseases and visa versa. For instance, there is a strong correlation between children experiencing wheezing episodes early in life induced by rhinovirus (RV) or respiratory syncytial virus (RSV) with later development of asthma [147]. Furthermore, acute RV or RSV infections are responsible for most exacerbations of asthma [9, 147, 149, 150]. Asthma may also be a risk factor for severe IAV infections during IAV pandemics [11]. On a cellular level, most [137, 149, 152-157], but not all [158], studies have suggested that cells or tissue derived from patients with asthma or chronic obstructive pulmonary disease (COPD) have an intrinsic defect in IFN production following viral infections. Mechanisms to explain how asthmatics may come to have deficient IFN production are not clear.

IFN production can be regulated in a host of manners. Respiratory viruses themselves often exhibit a capacity to inhibit IFN production or downstream IFN signaling [128]. However, many host receptors and signaling pathways can enhance or inhibit interferon pathways. In macrophages, CCL2 has been shown to dampen IFNa release [132]. In AECs, EGFR activation can decrease IFN- λ production thereby enhancing viral infection [135, 136]. The cytokines IL-4,13, and IL-17 have also been shown to dampen IFN production from AECs [137-139]. Cigarette smoke can also dampen AEC IFN production [140, 141]. Interestingly, allergens such as aspergillus, alternaria, and house dust mite, have further been shown to inhibit IFN production from AECs [142-144]. This reduction of IFN production has been proposed to be a potential mechanism whereby the airway milieu is driven towards a Th2 phenotype upon exposure to these allergens [143, 145]. Mechanistically, both aspergillus and alternaria have been shown to activate proteinase-activated receptor 2 (PAR2) on AECs and signaling from this receptor limits the release of Th1 chemokines and IFNs [143, 146]. However, whether this also pertains to other cell surface receptors on AECs remains unknown.

Histamine and extracellular nucleotides are elevated during asthma and chronic airway diseases [16, 18, 21, 63]. In plasmacytoid dendritic cells (pDCs), ligands such as histamine and nucleotides have been shown to inhibit IFN α release [133, 134]. However, whether these ligands have the capacity to regulate IFN responses in AECs is unknown. Here we set out to screen these ligands for their ability to regulate IFN production. We identify both histamine receptors and nucleotide receptors that reduce the release of both IFN- β and IFN- λ from AECs. Pharmacological evidence demonstrated P2Y₂ and H₁ receptor activation was responsible for the inhibition by nucleotides and histamine, respectively. Our findings uncover an additional potential mechanism by which asthmatic patients manifest diminished IFN responses.

Results

Poly(I:C) drives IFN release through TLR3 signaling

AECs express multiple pattern-recognition receptors (PRRs) that can participate in the production of interferons following viral infection. One common mimic for the dsRNA produced during viral replication is poly(I:C). We began our study of interferon pathways in submerged AECs by performing a time course analysis following extracellular poly(I:C) stimulation. Poly(I:C) treatment evoked the release of both type 1 (IFN- β) and type 3 (IFN- λ 1/3) IFN (Figure 5.1A-B). Notably, type 1 IFN was released much faster than type 3 IFN, which is in accordance with known properties of type 1 IFN (ref). Extracellular poly(I:C) is thought to predominantly activate the dsRNA sensor TLR3 (Kato 2007). We tested whether shRNA-mediated knockdown of TLR3 would inhibit poly(I:C) IFN responses. Two independent shRNA sequences targeting TLR3 both had

high knockdown efficiency as measured by qPCR (Figure 5.1C). Functionally, both shRNA also strongly abrogated poly(I:C)-mediated type 1 and type 3 IFN release (Figure 5.1D-E). This strongly suggests that extracellular poly(I:C) provokes TLR3 signaling culminating in IFN release from AECs.



Figure 5.1 Poly(I:C) drives IFN release through TLR3 signaling. A) Normal human bronchial epithelial (NHBE) cells were stimulated with 10µg/mL poly(I:C) and IFN- β was measured in the supernatant at the given time points. Data are mean ± SEM of n = 4 samples/time point. **B)** Normal human bronchial epithelial (NHBE) cells were stimulated with 10µg/mL poly(I:C) and IFN- λ 1/3 was measured in the supernatant at the given time points. Data are mean ± SEM of n = 4 samples/time point. **D** and IFN- λ 1/3 was measured in the supernatant at the given time points. Data are mean ± SEM of n = 4 samples/time point. **C)** shTLR3 decreases *TLR3* mRNA expression. Expression was normalized to the housekeeping gene *RPLP0*. Data are mean ± SEM of n = 3 samples. **D)** shRNA targeting TLR3 abrogated poly(I:C)-induced (10µg/mL) IFN- β release. Data are mean ± SEM of n = 6 samples/time point. **E)** shRNA targeting TLR3 abrogated poly(I:C)-induced (10µg/mL) IFN- λ 1/3 release. Data are mean ± SEM of n = 6 samples/time point. Type 1 and 3 IFN levels were below the limit of detection in the supernatant without the presence of a stimulus such as poly(I:C). *****p<0.0001

GPCR agonists inhibit IFN release

G-protein coupled receptor (GPCR) signaling has been shown to inhibit IFN responses in a wide variety of cell types. We screened three agonists that all induce Ca²⁺ signaling in AECs: UTP, histamine and the PAR2 activator SLIGKV. All three agonists effectively inhibited the poly(I:C)-mediated release of IFN- β (Figure 5.2A). The rank order of efficacy was UTP > histamine > SLIGKV. We also interrogated the release of IFN- λ 1/3 and measured significantly less in the presence of UTP and histamine (Figure 5.2B). The PAR2 activator was ineffective at inhibiting the poly(I:C)-mediated release of IFN- λ 1/3 (Figure 5.2B). ATP also suppressed the release of type 1 IFN (Figure 5.2C). The long acting β_2 adrenergic receptor agonist, fomoterol, did not significantly inhibit type 1 or type 3 IFN release (data not shown). These results suggest that GPCR agonists that provoke Ca²⁺ signaling in AECs dampen IFN production.



Figure 5.2 GPCR agonists inhibit IFN release.

A) The GPCR agonists (100μM) UTP, histamine, and to a lesser degree SLIGKV inhibit poly(I:C)-induced (10μg/mL) IFN-β release into the supernatant (24hr time point). Data are mean ± SEM of n = 13-25 samples. **B)** The GPCR agonists (100μM) UTP and histamine inhibit poly(I:C)-induced (10μg/mL) IFN-λ1/3 release into the supernatant (24hr time point). Data are mean ± SEM of n = 5-15 samples. **(C)** ATP (10μM) inhibits poly(I:C)-induced (10μg/mL) IFN-β release into the supernatant (6-hour time point). Data are mean ± SEM of n = 11 samples. *p<0.05, ****p<0.0001

ATP and UTP show opposing effects on IFN release in submerged AECs

Two nucleotides in the airways that both elicit Ca^{2+} signaling in AECs are ATP and UTP [162]. We performed a dose-response analysis for these two nucleotides in regulation of poly(I:C)-mediated IFN release. UTP showed a classic inhibitory dose-response curve for both type 1 and type 3 IFN (Figure 5.3A-B). In contrast, ATP showed a more complex dose-response curve. For type 1 IFN, ATP showed a biphasic response with low doses of ATP (< 10µM) inhibiting IFN similarly to UTP while dose higher than 10µM began to be less effective (Figure 5.3A). For type 3 IFN, low dose of ATP (< 10µM) had no effect on IFN release, while higher doses of ATP (100µM) showed potentiation of IFN release. UTP is a selective agonist of metabotropic P2Y receptors while ATP is an agonist at metabotropic P2Y receptors and ionotropic P2X receptors [29]. Both UTP and ATP elicit the activation of P2Y₂ receptors (Figure 2.1). While many potential models immerge from this data, a likely scenario is that UTP receptors inhibit IFN release while ATP receptors can potentiate IFN release. ATP may also activate the UTP receptors leading to the biphasic response in type 1 IFN release.



Figure 5.3 ATP and UTP show opposing effects on IFN release in submerged AECs. A-B) UTP inhibits IFN release while ATP is either less effective at inhibiting (IFN- β) or potentiates (IFN- λ 1/3) release. Cells were stimulated with 10µg/mL poly(I:C) +/- ATP/UTP and supernatants were collected 16hrs later and IFN levels were measured. Data are mean ± SEM of n = 4 samples.

Pharmacological analysis of histamine and UTP responses reveals H₁ and P2Y₂

receptor activation

To begin unraveling the molecular identity of the UTP and histamine receptors driving inhibition of IFN responses, we performed a dose-response analysis of IFN release. UTP was ten times more potent than histamine in inhibiting the release of IFN- β (0.34µM versus 3.4µM) (Figure 5.4A). Regarding IFN- λ 1/3, UTP was six times more potent than histamine in inhibiting the release (1µM versus 6µM) (Figure 5.4A). Both agonists were more potent in inhibiting the release of type 1 IFN than type 3 IFN. The Hill-slope for histamine was also much more steep for both type 1 and type 3 IFN release (Figure 5.4A-B). Next, we employed the selective P2Y₂ receptor antagonist AR-C. AR-C blocked the UTP-mediated inhibition of IFN- β (Figure 5.4C). We tested the selective H₁ receptor antagonist cetirizine in reversing the histamine responses. Cetirizine effectively reversed the histamine-mediated inhibition of both type 1 and type 3 IFN release (Figure 5.4D-E). These findings strongly implicate P2Y₂ receptors and H₁ receptors in the UTP- and histamine-induced inhibition of IFN release.



Figure 5.4 Pharmacological analysis of histamine and UTP responses reveals H_1 and $P2Y_2$ receptor activation. A) Dose-response of IFN- β release inhibition by UTP and histamine. IFN- β was measured in the cell culture supernatant 24 hrs following

simultaneous addition of poly(I:C) (10µg/mL) and UTP/histamine. The solid line is a four-parameter nonlinear regression fit of the Hill equation with $IC_{50} = 0.34 \mu M$ and Hill Slope = -0.52 for UTP and IC₅₀ = 3.4 μ M and Hill Slope = -1.65 for histamine. IFN- β was undetectable without a stimulus and thus 0 pg/ml was set to 0% and maximal poly(I:C)evoked response was set at 100% for the fitting procedure. Data are mean ± SEM of n = 4-18 samples from 2 independent experiments. **B)** Dose-response of IFN- λ 1/3 release inhibition by UTP and histamine IFN- λ 1/3 was measured in the cell culture supernatant 24 hrs following simultaneous addition of poly(I:C) (10µg/mL) and UTP/histamine. The solid line is a four-parameter nonlinear regression fit of the Hill equation with $IC_{50} = 1$ μ M and Hill Slope = -0.7 for UTP and IC₅₀ = 6 μ M and Hill Slope = -4.09 for histamine. IFN- λ 1/3 was undetectable without a stimulus and thus 0 pg/ml was set to 0% and maximal poly(I:C)-evoked response was set at 100% for the fitting procedure. Data are mean \pm SEM of n = 4-18 samples from 2 independent experiments. C) The P2Y₂ antagonist AR-C 118925XX (10µM) reverses UTP-mediated (100µM) inhibition of IFN-β release. Data are mean \pm SEM of n = 9 samples. **D**) The H₁ antagonist cetirizine (10µM) reverses histamine-mediated (100 μ M) inhibition of IFN- β release. Data are mean ± SEM of n = 6 samples. **E)** The H₁ antagonist cetirizine (10 μ M) reverses histamine-mediated $(100\mu M)$ inhibition of IFN- λ 1/3 release. Data are mean ± SEM of n = 6 samples. **p<0.01, ****p<0.0001

GPCR signaling inhibits cGAS-STING-mediated IFN release

In addition to dsRNA sensors, AECs also express functional dsDNA sensors that elicit IFN synthesis [198]. One such dsDNA sensor is cGAS, which signals through the adaptor protein STING to drive IFN responses [199, 200]. We compared the kinetics of IFN- β release evoked by extracellular poly(I:C) versus transfected 2,3 cGAMP (a STING agonist). Both ligands induced IFN- β with similar kinetics and abundances (Figure 5.5A). We tested UTP and histamine for the capacity to inhibit 2,3 cGAMP-mediated IFN release. Both UTP and histamine significantly inhibited 2,3 cGAMP-mediated IFN release, with a greater degree of inhibition measured for type 1 compared to type 3 IFN (Figure 5.5B-C). To activate cGAS upstream of STING, we employed the dsDNA sequence known as interferon stimulatory DNA (ISD). UTP alone inhibited ISD-dependent type 1 IFN responses while histamine was without effect (Figure 5.5D).

Neither agonist significantly inhibited ISD-mediated type 3 IFN responses (Figure 5.5E). Altogether, these findings imply that UTP and histamine have the capacity to inhibit cGAS-STING-mediated IFN release, although the magnitude of the inhibition appears weaker than that observed for TLR3-mediated release.



Figure 5.5 GPCR signaling inhibits cGAS-STING-mediated IFN release. A) Normal human bronchial epithelial (NHBE) cells were stimulated with 10µg/mL poly(I:C) or transfected with 10µg/mL 2,3 cGAMP and IFN-β was measured in the supernatant at the given time points. Data are mean ± SEM of n = 4 samples/time point. B) The GPCR agonists (100µM) UTP and histamine inhibit 2,3 cGAMP-induced (10µg/mL) IFN-β release into the supernatant (24hr time point). Data are mean ± SEM of n = 17-19 samples. **C)** The GPCR agonists (100µM) UTP and histamine inhibit 2,3 cGAMP-induced (10µg/mL) IFN-λ1/3 release into the supernatant (24hr time point). Data are mean ± SEM of n = 13-15 samples. **D)** The GPCR agonist (100µM) UTP inhibits ISD-induced (1µg/mL) IFN-β release into the supernatant (24hr time point). Data are mean ± SEM of n = 12-14 samples. **E)** The GPCR agonists (100µM) do not significantly inhibit

ISD-induced (1µg/mL) IFN- λ 1/3 release into the supernatant (24hr time point). Data are mean ± SEM of n = 8-10 samples. *p<0.05, **p<0.01, ****p<0.0001

Agonists inhibit RIG-I-dependent IFN release

TLR3 is a dsRNA sensor that resides in endosomes while RIG-I-like receptors (RLRs) reside in the cytosol similar to cGAS [201, 202]. To test if GPCR agonists inhibit RLRmediated IFN responses, we employed the RIG-I agonist 3p-hpRNA. Transfection of 3p-hpRNA evoked a powerful induction of type 1 IFN (Figure 5.6A). At the early time point of 6 hours, all three GPCR modulators, ATP, UTP, and histamine suppressed RIG-I-mediated IFN-β release (Figure 5.6B), ATP showing the strongest inhibition. UTP and histamine also suppressed the induction of IFN- β release but to a lesser extent (Figure 5.6B). However, at later time points (24 hours), ATP and histamine retained their efficacy to suppress 3p-hpRNA-mediated IFN- β , while UTP was ineffective (Figure 5.6C). These results indicate that ATP is highly effective at inhibiting RIG-I-induced IFN- β release stimulated by 3p-hpRNA while histamine and UTP exhibit lower efficacy. At the early time point, the P2Y₂ receptor antagonist AR-C partially reversed the ATPmediated inhibition of 3p-hpRNA-mediated IFN-β (Figure 5.6D). Interestingly, both ATP and adenosine suppressed 3p-hpRNA-mediated IFN release (Figure 5.6E-F), suggesting that at least part of ATP's suppression may stem from ATP metabolites like adenosine. In agreement with this interpretation, the NTPDase inhibitor, ARL 67156, which inhibits the enzymes that degrade ATP, blocked ATP-mediated IFN suppression (Figure 5.6G). However, the adenosine receptor agonist NECA did not suppress IFN release suggesting that a classical adenosine receptor may not be involved (Figure

5.6G). Collectively, these findings suggest that ATP and its metabolites strongly suppress RIG-I-induced IFN release.



Figure 5.6 Agonists inhibit RIG-I-dependent IFN release. A) Transfection of NHBEs with 3p-hpRNA elicits IFN- β release into the supernatant. Data are mean ± SEM of n = 3 samples. (B) ATP (100µM) strongly while UTP (100µM) and histamine (100µM) mildly inhibit 3p-hpRNA-induced (10ng/mL) IFN-β release into the supernatant. Supernatants were collected at a 6-hour time point. The absolute concentrations of IFN-β ranged from 12.9-321 pg/mL. Data are mean ± SEM of n = 12 samples from two independent experiments. (C) ATP (100µM) and histamine (100µM) inhibit 3p-hpRNA-induced (10 ng/mL) IFN- β release into the supernatant. Supernatants were collected at a 24-hour time point. The absolute concentrations of IFN- β ranged from 156-1552 pg/mL. Data are mean \pm SEM of n = 13-30 samples. (D) The P2Y₂ antagonist, AR-C 118925XX (10 μ M), partially reverses ATP-mediated (100µM) inhibition of 3p-hpRNA-evoked (10ng/mL) IFN- β release. Supernatants were collected 6 hours after stimulation. Data are mean \pm SEM of n = 12 samples. (E and F) ATP (100μ M) and Adenosine, labeled as ADO, (50µM) inhibits 3p-hpRNA-induced (10ng/mL) IFN- β (E) and IFN- λ 1/3 (F) release into the supernatant. Cell supernatants were collected at a 16-hour time point. Data are mean \pm SEM of n = 4 samples. (K) The NTPDase inhibitor, ARL 67156 (100 μ M), reverses ATP-mediated (100µM) inhibition of 3p-hpRNA-evoked (10ng/mL) IFN-B

release. The adenosine receptor agonist NECA (10 μ M) did not inhibit 3p-hpRNAevoked (10ng/mL) IFN- β release. Supernatants were collected at a 16-hour time point. Data are mean ± SEM of n = 4 samples. *p<0.05, **p<0.01, ****p<0.0001

Influenza A virus drives IFN responses partially through TLR3

We transitioned to a live respiratory virus, influenza A virus (IAV), to measure functional IFN responses. Infection of AECs with IAV elicited type 1 IFN release in a multiplicity of infection (MOI) dependent manner (Figure 5.7A). To interrogate if TLR3 was necessary for IAV-induced IFN responses, we again utilized shRNA lentiviral transduction. Knockdown of TLR3 partially inhibited IAV-induced release of both type 1 and type 3 IFN (Figure 5.7B-C). Thus, although TLR3 is necessary in IAV-mediated IFN responses, other dsRNA sensors such as RLRs are likely involved.



Figure 5.7 Influenza A virus drives IFN responses partially through TLR3. A) Influenza A virus strain A/WSN/33(H1N1) was used to infect NHBEs at a multiplicity of infection (MOI) of 0.1, 0.5, or 1.0 and IFN- β release into the supernatant was measured 24 hrs after infection. Data are mean ± SEM of n = 4 samples. **B)** shRNA-mediated knockdown of TLR3 partially blocks IAV-induced (MOI 0.5) IFN- β release into the supernatant. Data are mean ± SEM of n = 4 samples. **C)** shRNA-mediated knockdown of TLR3 partially blocks IAV-induced (MOI 0.5) IFN- β release into the supernatant. Data are mean ± SEM of n = 4 samples. **C)** shRNA-mediated knockdown of TLR3 partially blocks IAV-induced (MOI 0.5) IFN- λ 1/3 release into the supernatant. Data are mean ± SEM of n = 4 samples. *p<0.01

Histamine, ATP, and Adenosine inhibits respiratory virus-mediated IFN

production

We tested histamine and UTP for their ability to inhibit IFN release induced by the live respiratory virus IAV. Histamine significantly inhibited IAV-mediated release of both type 1 and type 3 IFN (Figure 5.8A-B). In contrast, UTP was completely ineffective (Figure 5.8A-B). ATP much more powerfully inhibited IAV-induced IFN release (Figure 5.8C-D). This data is highly reminiscent of the discoveries related to the RIG-I agonist 3p-hpRNA. The infections and agonists did not dramatically alter cellular cytotoxicity or cellular ATP levels (Figure 5.8E-F). In agreement with the discoveries related to the RIG-I activator, adenosine also suppressed IAV-induced IFN release (Figure 5.8G-H), suggesting ATP and its metabolites may both contribute to the inhibition of IAV-mediated IFN release.

Rhinovirus, a family of viruses that contribute to the common cold, is another important family of viruses that can contribute to asthma exacerbation [9]. Thus, we infected airway cells with rhinovirus strain 1B (RV1B) and measured IFN release. Type 1 IFN release into the supernatant was low and difficult to accurately quantify so we quantified *IFNB1* mRNA levels. Importantly, ATP strongly suppressed RV1B-induced *IFNB1* mRNA levels (Figure 5.8I). These results indicate that histamine and particularly ATP are powerful suppressors of RIG-I-, IAV-, and RV1B-induced IFN production from

AECs and suggest that these agonists may be responsible for the well-described suppression of IFN responses in asthmatics (Figure 5.8J).



Figure 5.8 Histamine, ATP, and Adenosine inhibits respiratory virus-mediated IFN production. A) Histamine (100μM) inhibits IAV-induced (MOI 1) IFN-β release into the supernatant. Data are mean ± SEM of n = 6 samples from two independent experiments. **B)** Histamine (100μM) inhibits IAV-induced (MOI 1) IFN-λ1/3 release into the supernatant. Data are mean ± SEM of n = 6 samples from two independent experiments. (**C and D)** ATP (100μM) inhibits IAV-induced (MOI 0.5) IFN-β (*C*) and IFNλ1/3 (*D*) release into the supernatant. Cell supernatants were collected at a 24-hour time point. Concentrations of IFN-β ranged from 2-81 pg/mL. Concentrations of IFNλ1/3 ranged from 68-836 pg/mL. Data are mean ± SEM of n = 8 samples from two

independent experiments. (E) IAV (MOI 0.5) and agonists (100µM) do not strongly induce cytotoxicity as measured via CellTox assay. Data are mean ± SEM of n = 4 samples. (F) IAV (MOI 0.5) and agonists (100µM) do not strongly inhibit cellular metabolism/proliferation as measured via CellTiter-Glo assay. Data are mean ± SEM of n = 8 samples. (**G and H**) Adenosine (50 μ M) inhibits IAV-induced (MOI 0.5) IFN- β (G) and IFN- λ 1/3 (H) release into the supernatant. Cell supernatants were collected at a 24hour time point. Data are mean \pm SEM of n = 4 samples. (I) ATP and histamine (both 100µM) inhibit RV1B-induced (MOI 10) IFNB1 mRNA expression. Expression was normalized to the housekeeping gene RPLP0. RNA was collected 24 hours after infection. Within a given experiment, expression was normalized to mock infection. The data are displayed as normalized between experiments with the mean RV1B-induced expression set to 100 and all other treatments scaled proportionally. Data are mean ± SEM of n = 7-11 samples from three independent experiments. (J) Summary model: poly(I:C) drives TLR3-mediated IFN release while 3p-hpRNA drives RIG-I-mediated IFN release. IAV and likely RV activate both TLR3 and RIG-I pathways to induce IFN release. Histamine dampens IFN release from both pathways. UTP strongly inhibits poly(I:C)-mediated IFN release but only inhibits early release of RIG-I-induced IFN. ATP shows modest inhibition of poly(I:C)-mediated type 1 IFN but powerfully suppresses RIG-I-, IAV-, and RV1B-induced IFN production. *p<0.05, **p<0.01, ****p<0.0001

Discussion

Interferons are powerful antiviral cytokines induced upon viral infection. One mechanism IFNs employ to evoke antiviral responses is the upregulation of interferonstimulated genes (ISGs). While not all ISGs have established roles in viral defense, many are classic antiviral genes. Type 1 IFNs are also involved in adaptive immune responses, particularly due to their role in dendritic cell-mediated T-cell activation and antibody responses [203, 204]. Airway viruses, especially RV and RSV, are also well known to induce exacerbations of asthma [9, 147, 149, 150]. In the context of chronic airway disease like asthma, both histamine and nucleotides are elevated [16, 18, 21, 63]. Yet, the crosstalk between histamine and nucleotide signaling and IFN responses in AECs is unclear.

Here we demonstrate that histamine and nucleotides are able to inhibit the stimulus-evoked release of type 1 and type 3 IFNs from AECs. Our results demonstrate

that UTP activates $P2Y_2$ receptors and thereby reduce poly(I:C) and cGAS-STINGinduced IFN release. Likewise, we show that histamine activates H₁ receptors and also limits poly(I:C) and RIG-I-induced IFN release. UTP was more potent than histamine as an inhibitor of poly(I:C)-mediated IFN release. Importantly, histamine and ATP also diminished IAV- and RV1B-induced IFN release. To our knowledge, this is the first report that P2Y₂ receptors and H₁ receptors on AECs have the capacity to dampen IFN release.

Our data illustrates how infection of AECs with respiratory viruses is a much more complex phenomenon than poly(I:C) treatment. Interestingly, while UTP inhibited poly(I:C)-mediated IFN release, it proved less capable at inhibiting RIG-I- or IAVinduced IFN release (Figure 5.2A-B, 5.6C, 5.8A-B). However, histamine had efficacy in inhibiting IFN release induced by poly(I:C), RIG-I, and IAV (Figure 5.2A-B, 5.6B-C, 5.8A-B). On the other hand, ATP powerfully inhibited both RIG-I and IAV-induced IFN secretion (Figure 5.6E-F, 5.8C-D). These differences are likely due to the fact that IAV activates multiple RNA sensors, including TLR3 and RLRs [205, 206] while extracellular poly(I:C) exclusively activates TLR3 (Figure 5.7B-C vs. Figure 5.1D-E). Another explanation for this data is found in that the ATP metabolite adenosine also suppresses RIG-I- and IAV-induced IFN release (Figure 5.6E-F, 5.8G-H). Thus, it seems likely that ATP activates two distinct pathways, the first adenosine-mediated, the second P2Y₂ receptor-mediated, both contributing to suppression of IFN. UTP on the other hand, selectively activates P2Y₂ and does not produce adenosine metabolites and is therefore insufficient to powerfully inhibit respiratory virus-induced IFN. Collectively, these discoveries suggest caution when interpreting IFN response data generated from

stimulation with the model viral agonist poly(I:C) alone without confirmation using live respiratory viruses.

Histamine is a classic allergic mediator in the context of Th2 inflammation [63]. In contrast, IFNs are known to inhibit Th2 bias and mast cell degranulation [207-209]. Thus, our discovery that histamine can inhibit IFN release by AECs may reveal a positive feedback loop in which histamine reinforces Th2 inflammation. Clinically, pediatric atopic patients often progress from atopic dermatitis (AD) towards asthma later in childhood [210]. This progression of disease has long been termed the "atopic march" [210]. Interestingly, there have been multiple reports that treatment of atopic infants with an H₁ receptor antagonist can decrease the likelihood of subsequent development of asthma [211, 212]. One of these studies showed that infants with atopy to house dust mite (HDM) or grass pollen had lower incidence of later asthma development if they were given cetirizine [213]. Our discovery that histamine can inhibit the release of IFNs from AECs, thereby potentially skewing the environment further towards a Th2 milieu, may provide some mechanistic basis for these clinical observations.

Asthmatic cells have been shown to have deficient IFN responses [137, 149, 152-155]. This impairment may contribute to the well-known ability of respiratory viruses to trigger acute asthma exacerbations. Insofar as IFNs counter-regulate allergic responses, this deficiency may also allow unchecked allergic responses in asthmatics. One report has demonstrated that treatment with omalizumab, a monoclonal antibody that inhibits IgE activation of allergic cells, can partially restore the *ex vivo* IFN response and decrease the incidence of asthma exacerbations [214]. Thus, IFN may decrease exacerbations through its antiviral activity. Another group has shown that nebulized IFN-

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β following cold symptoms could protect against worsening lung symptoms in asthmatics with poorly controlled disease [215]. This same group reported that inhaled IFN-β improves outcomes of infection with SARS-CoV2 reinforcing the antiviral effects of intrapulmonary IFN-β [216]. It is reasonable to conclude that IFN responses in asthmatics during respiratory tract infections are important for the preservation of lung function and prevention of exacerbations. Our present finding that histamine and nucleotides, which are known to be in the airways following allergen exposure [16, 18, 63], inhibit IFN release from AECs may provide a mechanism for the deficient IFN responses found in asthmatics. Finally, although data is limited suggesting that H₁ antagonists alone can improve lung function during asthma, our data suggests that H₁ antagonists should be tested for their ability to restore IFN production in asthmatics, as has been found with omalizumab, an antibody that reduces the release of histamine from mast cells and basophils [214, 217].

Recent studies have also suggested that IAV can directly provoke mast cells to release proinflammatory cytokines, chemokines and mediators such as histamine [218, 219]. Indeed, in multiple animal models of IAV infection, histamine levels were elevated in the airways during infection [220, 221]. There is also some evidence suggesting that H₁ antagonists may decrease pneumonia and inflammatory mediators in the context of IAV infection [220]. Therefore, histamine may actively inhibit the ability of IAV to induce the expression of protective IFN during *in vivo* IAV infection. However, further *in vivo* studies utilizing a conditional knockout of H₁ receptors in AECs would be necessary to test this hypothesis.

ATP is released at sites of many forms of inflammation [16, 18, 21]. IFNs can be damaging in some contexts of severe inflammation [222]. Thus, the ability of ATP to inhibit AEC IFN release may comprise a negative feedback loop preventing excessive tissue damage in the context of severe inflammation. On the other hand, ATP and purinergic receptor signaling has been identified as a driver of allergic lung inflammation [16, 18]. Given the antagonist relationship between IFN and allergic asthma, our finding that ATP powerfully inhibits IAV-induced IFN secretion may provide a cellular basis for the observation that P2 receptor antagonists reverse allergic airway inflammation [16, 18]. With regards to viral infection, multiple reports have suggested that infection of AECs can elicit nucleotide release [38, 40, 41]. Thus, our discovery that ATP strongly suppresses the virus-induced IFN release may be a novel mechanism viruses employ to dampen host IFN responses. Altogether, these findings suggest ATP may modulate the immune response during respiratory virus infection and allergic inflammation. Nevertheless, further in vivo studies utilizing a conditional knockout of P2 receptors in AECs would be necessary to test these hypotheses and investigate the physiological significance of these discoveries.

Chapter 6: Mechanisms underlying GPCR-mediated inhibition of IFN secretion Introduction

Interferons are an essential class of antiviral cytokines. The stimulus that evokes the release of IFNs is typically either dsDNA or dsRNA. Both of these chemical moieties are sensed by intracellular receptors. These sensors, such as TLR3, RLRs, cGAS-STING, then evoke a signaling response that activates transcription factors such as NF-kB or IRF3 and other IRFs [128]. The transcription factors drive the transcription of various interferon genes, culminating in their synthesis and release from the infected cells. Due to the importance of IFNs for host defense against viruses, many studies have investigated how their production is regulated. Some of these mechanisms include Ca²⁺ or cAMP signaling [223-225]. Furthermore, β -arrestin signaling has also been implicated in the inhibition of IFN responses [132, 226]. The pathway that culminates in the synthesis of IFNs includes many kinases and not surprisingly, multiple phosphatases have been shown to regulate IFN production [227, 228]. Reactive oxygen species (ROS) have also been implicated in the inhibition of IFN responses [137, 140]. PKC signaling downstream of nucleotide receptors in plasmacytoid dendritic cells has been shown to inhibit IFN responses [133]. Another family of proteins that regulate interferons are the suppressor of cytokine signaling (SOCS) proteins [139]. Altogether, a host of receptors and signaling pathways converge on IFN production to fine-tune the antiviral response.

Results

P2Y₂ receptors inhibit IFN release through Gq signaling

GPCRs that evoke Ca^{2+} signaling often do so through a heterotrimeric G-protein subunit termed Gq [229]. We tested the Gq inhibitor YM-254890 [229] (hereby termed "YM") for its ability to inhibit UTP-meditated Ca^{2+} signaling. YM completely abrogated UTPevoked Ca^{2+} signaling (Figure 6.1A). We next tested YM for its ability to reverse UTPinduced inhibition of IFN responses. YM significantly reversed UTP-mediated inhibition of both type 1 and type 3 IFN release (Figure 6.1B-C). These findings suggest that Gq signaling is necessary for P2Y₂ receptors to dampen AEC IFN responses.



Figure 6.1 P2Y₂ receptors inhibit IFN release through Gq signaling. A) The Gq inhibitor YM-254890 (1µM) abrogates UTP-induced $[Ca^{2+}]_i$ elevations. $[Ca^{2+}]_i$ was measured using Fura-2 AM as previously described [95, 97]. Data are mean ± SEM of n = 27-37 cells. B) The Gq inhibitor YM-254890 (1µM) reverses UTP-mediated (100µM) inhibition of IFN-β release. Supernatants were collected 6 hrs after stimulation. Data are mean ± SEM of n = 4 samples. C) The Gq inhibitor YM-254890 (1µM) reverses UTP-mediated (100µM) inhibition of IFN- λ 1/3 release. Supernatants were collected 20 hrs after stimulation. Data are mean ± SEM of n = 4 samples. *p<0.05, ****p<0.0001

PKC signaling is necessary for GPCR-mediated inhibition of IFN production Another signaling mediator downstream of GPCRs coupled to Gq is PKC. One report has suggested that PKC activation in pDCs can dampen type 1 IFN responses [133]. We tested the broad-spectrum PKC inhibitor, Gö 6983, for its ability to reverse GPCR responses. Gö 6983 reversed both UTP- and histamine-mediated inhibition of type 1 IFN release (Figure 6.2A). The reversal appeared stronger for histamine than UTP. Similar to UTP, ATP-mediated suppression of type 1 IFN release was inhibited by the PKC inhibitor, Gö 6983, and the Gg inhibitor, YM-254890 (Figure 6.2B). A second PKC inhibitor GF 109203X also partially reversed UTP-mediated inhibition of IFN release (Figure 6.2C). Turning to type 3 IFN, Gö 6983 reversed only the histamine-induced inhibition while the UTP-induced inhibition was left larger intact (Figure 6.2D). This data suggests that while both receptors utilize PKC signaling to inhibit type 1 IFN responses, type 3 IFN responses appear more complex. To confirm that PKC activation is sufficient to dampen type 1 IFN responses, we employed two PKC activators, the phorbol esters PDBu and PMA. Both PDBu and PMA strongly abrogated the poly(I:C)-mediated release of type 1 IFN (Figure 6.2E). Likewise, PMA strongly suppressed 3p-hpRNAmediated type 1 IFN release (Figure 6.2F). Thus, PKC activation is sufficient to inhibit type 1 IFN secretion.



Figure 6.2 PKC signaling is necessary for GPCR-mediated inhibition of IFN-β **production. A)** The PKC inhibitor Gö 6983 (2.5µM) reverses UTP and histaminemediated (100µM) inhibition of IFN-β release. Supernatants were collected 20 hrs after stimulation. Data are mean ± SEM of n = 6 samples. **(B)** The PKC inhibitor Gö 6983 (2.5µM) and the Gq inhibitor YM-254890 (1µM) reverses ATP-mediated (10µM) suppression of IFN-β release. Supernatants were collected 6 hours after cell stimulation with poly(I:C). Data are mean ± SEM of n = 6 samples. **. (C)** The PKC inhibitor GF 109203X (5µM) reverses UTP-mediated (100µM) inhibition of IFN-β release. Supernatants were collected 20 hours after stimulation. Data are mean ± SEM of n = 6 samples. **D)** The PKC inhibitor Gö 6983 (2.5µM) reverses histamine-mediated (100µM) inhibition of IFN-λ1/3 release. Supernatants were collected 20 hrs after stimulation. Data are mean ± SEM of n = 6 samples. **E)** The phorbol esters PDBu and PMA (100nM) inhibit IFN-β release. Supernatants were collected 6 hrs after stimulation. Data are mean ± SEM of n = 4 samples. **F)** PMA (100nM) blocks 3p-hpRNA (10ng/mL) evoked IFN-β release into the supernatant. Supernatants collected 6 hours after stimulation. Data are mean ± SEM of n = 4 samples. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001

GPCR signaling inhibits IFNB1 mRNA levels

We turned to examine if agonist stimulation inhibited *IFNB1* mRNA levels. Importantly, at a four hour time point, all the agonists suppressed poly(I:C)-driven *IFNB1* mRNA levels (Figure 6.3A). In contrast, the agonists were less effective at regulating the mRNA levels of the Th2 cytokine TSLP (Figure 6.3B). Collectively, this data suggests that the agonist regulation of type 1 IFN is primarily at the level of mRNA.



Figure 6.3 Agonists inhibit *IFNB1* mRNA levels but not *TSLP* mRNA levels. (A) UTP (100 μ M), histamine (100 μ M), ATP (10 μ M), PMA (100nM) suppress poly(I:C)-induced (10 μ g/mL) *IFNB1* mRNA expression. Expression was normalized to the
housekeeping gene RPLP0. RNA was collected 4 hours after stimulation. Data are mean \pm SEM of n = 4-8 samples. **(B)** UTP (100µM), histamine (100µM), ATP (10µM), PMA (100nM) do not suppress poly(I:C)-induced (10µg/mL) *TSLP* mRNA expression. Expression was normalized to the housekeeping gene RPLP0. RNA was collected 4 hours after stimulation. Data are mean \pm SEM of n = 4-8 samples. ****p<0.0001

UTP does not inhibit IFN receptor signaling

Some reports suggest that IFN signaling can drive IFN synthesis and release in a positive feedback loop [139]. We therefore tested whether UTP can directly inhibit IFN signaling. We first utilized the JAK inhibitor ruxolitinib to abrogate IFN signaling and measured IFN release. While ruxolitinib did modestly inhibit IFN release at longer time points (24hrs), UTP inhibited IFN release at earlier time points (6hrs) as well, suggesting two distinct mechanisms of action (Figure 6.4A-B). Next, we speculated that IFN- λ 1/3 production might depend on IFN- β due to the faster release of IFN- β (Figure 6.4A-B). If this is the case, UTP induced inhibition of IFN- β may be responsible for the decrease in IFN- λ 1/3 production by UTP. To test this, we applied exogenous IFN- β to rescue the deficient production of IFN- β in the context of UTP stimulation. However, exogenous IFN- β was not able to rescue the UTP-mediated inhibition of IFN- λ 1/3 (Figure 6.4C). Finally, we pretreated cells with UTP and stimulated them with exogenous IFN- β to measure IFN signaling directly. UTP did not inhibit the phosphorylation of STAT1, or the induction of STAT1 and IRF1 (Figure 6.4D). These results suggest that UTP does not directly inhibit IFN signaling.



Figure 6.4 UTP does not inhibit IFN receptor signaling. A-B) The time course of JAK1/2 inhibitor ruxolitinib (1µM) and UTP (100µM)-mediated inhibition of IFN release does not phenocopy. Cells were stimulated with 10µg/mL poly(I:C) and supernatants were collected at 6 hrs or 24 hrs later for IFN analysis. Data are mean ± SEM of n = 4 samples. C) Exogenous IFN-β does not rescue the UTP-dependent IFN-λ1/3 release deficiency. Exogenous IFN-β (100pg/mL) was added to cells 2 hrs after simultaneous poly(I:C) (10µg/mL) and UTP (100µM) stimulation. Samples were collected at a 20 hrs time point and accessed for IFN analysis. Data are mean ± SEM of n = 4 samples. **D)** Western blot showing UTP does not inhibit exogenous IFN-β signaling. Cells were pretreated with UTP (100µM) 2 hrs prior to IFN-β stimulation (1000 IU/mL). Cells were lysed 1 or 4 hrs after IFN-β addition. (P-STAT: phospho-STAT1; T-STAT1: total-STAT1).

UTP does not inhibit activation of TBK1 or nuclear import of IRF3 and p65

Activation of TLR3 drives activation of the kinase TBK1, leading to nuclear import of the

transcription factors IRF3 and NF-κB [202]. We next tested whether UTP inhibits phosphorylation of TBK1. UTP had no effect on poly(I:C)-mediated phosphorylation of TBK1 (Figure 6.5A). We then determined whether UTP inhibited nuclear import of either IRF3 or the important NF-κB subunit p65. UTP had no clear effect on the nuclear translocation of either of these transcription factors (Figure 6.5B). These findings suggest that UTP does not inhibit the activation of TBK1, IRF3 or p65.



Figure 6.5 UTP does not inhibit activation of TBK1 or nuclear import of IRF3 and p65. A) Western blot showing UTP does not inhibit activation of TBK1. Cells were simultaneously stimulated with UTP (100 μ M) and poly(I:C) (10 μ g/mL) and lysed at the indicated time points. (P-TBK1: phospho-TBK1; T-TBK1: total-TBK1). B) Western blot showing UTP does not inhibit nuclear import of IRF3 or p65 (NF- κ B subunit). Cells were simultaneously stimulated with UTP (100 μ M) and poly(I:C) (10 μ g/mL) and cells were simultaneously stimulated with UTP (100 μ M) and poly(I:C) (10 μ g/mL) and cells were lysed for nuclear vs. cytosolic fraction 3 hrs later.

CRAC channel activation is not necessary for GPCR-mediated inhibition of IFN

release

UTP consistently inhibited IFN release more powerfully than histamine or SLIGKV with

all stimuli besides RIG-I agonists and IAV (Figure 5.2 and Figure 5.5). UTP also elicited

the most sustained Ca²⁺ signal (Figure 2.4A,C). We hypothesized that Ca²⁺ signaling

and more specifically CRAC channels may be involved in GPCR-mediated inhibition of

IFN secretion. We tested the CRAC channel inhibitor BTP2, which showed no efficacy

for reversing the UTP-mediated inhibition of 2,3 cGAMP-induced IFN- β (Figure 6.6A).

BTP2 had no effect on the 2,3 cGAMP-mediated release of IFN-β either (Figure 6.6A). We also tested the CRAC channel inhibitor, CM4620, for its role in the regulation of IFN release. Neither BTP2 nor CM4620 had any effect on the release of IFN regardless of PRR activated or nucleotide used to suppress IFN (Figure 6.6B-G). Thus, we conclude that CRAC channel activation is not necessary for PRR-mediated IFN release or nucleotide-mediated suppression of IFN release.



Figure 6.6 CRAC channel activation is not necessary for agonist-mediated inhibition of IFN release. A) The CRAC channel inhibitor BTP2 (1µM) does not reverse UTP-mediated (100µM) inhibition of 2,3 cGAMP-driven (10µg/mL) IFN- β release into the supernatant (24hr time point). Data are mean ± SEM of n = 4 samples. (B-G) The CRAC channel inhibitors CM4620 (1µM) and BTP2 (1µM) do not reverse UTP-mediated (100µM) inhibition of poly(I:C)-driven (10µg/mL) IFN release into the supernatant (24hr time point) (*B*-*C*) or ATP-mediated (100µM) inhibition of 3p-hpRNAdriven (10ng/mL) IFN release into the supernatant (24hr time point) (*D*-*E*) or IAV-driven (MOI 1) IFN release into the supernatant (24hr time point) (*F*-*G*). Data are mean \pm SEM of n = 4 samples.

EGF inhibits IFN release from airway epithelial cells

Multiple reports suggest a role for EGFR signaling in the suppression of IFN release from AECs [135, 136]. Purinergic receptor signaling has also been linked to transactivation of EGFR in AECs [230]. We first replicated the prior findings, demonstrating that EGF powerfully inhibits the release of both type 1 and type 3 IFN induced by poly(I:C) from AECs (Figure 6.7A-B). The strength of the inhibition was similar to a saturating dose of UTP (Figure 6.7A-B). Then, we utilized the EGFR kinase inhibitor AG 1478 [231]. AG 1478 partially reversed the UTP-mediated inhibition of type 1 IFN, but showed little effect on UTP-mediated suppression of type 3 IFN (Figure 6.7C-D). This result was similar to the broad spectrum PKC inhibitors that were tested prior (Figure 6.2A,D) and suggests that EGFR signaling downstream of P2Y₂ receptors may be partially involved in the suppression of type 1 IFN but are unlikely to contribute to the suppression of type 3 IFN.



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Discussion

Numerous studies have demonstrated that G-protein coupled receptor signaling inhibits IFN secretion [133, 134]. Here we demonstrate that Gq signaling is necessary for the inhibition of IFN release by P2Y₂ receptors. We interrogated poly(I:C)-dependent activation of TBK1, as well as nuclear import of the transcription factors IRF3 and the NF-kB subunit p65. However, we found no clear inhibition of any of these endpoints by UTP (Figure 6.5). However, when we quantified the synthesis of *IFNB1* mRNA directly all agonist suppressed type 1 IFN (Figure 6.3A). This suggests a model where the agonist-directed inhibition occurs downstream of transcription factor import into the nucleus. This is likely at the point of transcriptional activation of the relevant transcription factors. We measured *IFNB1* mRNA half-life in the presence of UTP and saw no differences (data not shown). We also investigating whether UTP disrupted IFN receptor signaling and no clear inhibition was observed (Figure 6.4). Collectively, the agonist-mediated suppression appears to be at a transcriptional level, although the precise mechanism remains to be determined.

One study in pDCs has demonstrated that strong PKC activation can inhibit type 1 interferon production [133]. Here we demonstrate that in AECs, PKC activation was necessary for agonist-mediated suppression of type 1 IFN (Figure 6.3A-C). Additionally, phorbol esters directly inhibited IFN- β release (Figure 6.2D-E). This suggests that PKC is both necessary and sufficient to drive the suppression of type 1 IFN, likely at the level of transcription (Figure 6.3A). Further studies will be required to uncover the complex mechanisms behind PKC regulation of type 1 IFN production in AECs.

Chapter 7: GPCR and CRAC channel function in AECs following mucociliary differentiation

Introduction

Submerged cultures of primary human airway cells lack many of the features of the differentiated airways such as motile cilia and goblet cells producing mucus [115, 117]. Following differentiation, many of the receptors that activate CRAC channels, such as $P2Y_2$ receptors, H_1 receptors, PAR2 are also functional [49, 67, 232, 233]. These receptors have functions such as the activation of the Ca²⁺ activated Cl⁻ channel (CACC), increasing cilia beat frequency, mucin secretion, barrier function, and cytokine release [26, 48, 51-53, 94, 115, 118]. Interestingly, GPCR expression in differentiated AECs is reported to be polarized such that $P2Y_2$ receptors are often found on the apical and basolateral surfaces while H_1 receptors and PAR2 receptors are restricted to basolateral surfaces [49, 67, 232-234].

Mucin proteins, along with water and ions are an important component of mucus [114]. In the airways, mucus is used in the mucociliary escalator, a process in which ciliated cells pump mucus up and out of the airways to be either swallowed or coughed up [114]. Although this physiology is important for host pathogen protection, mucus hypersecretion and goblet cell metaplasia are hallmarks of both asthma and chronic obstructive pulmonary disease (COPD) [114-116]. The most common cause of death in asthmatic patients is excessive mucus plugs [114]. Thus, therapies that can attenuate mucin hypersecretion have vast potential to improve modern asthma treatment. In human airways, club (Clara) and goblet cells synthesize and secrete mucin proteins [114, 115]. The major mucins of the airways are MUC5AC and MUC5B. These large

glycoproteins are packaged into secretory granules [114]. Although some basal exocytosis of these granules occurs, secretion can rapidly increase in a receptor dependent manner [115, 117, 118]. These receptors are numerous but include P2Y, PAR2, and EGFR [53, 118-120]. One conserved mechanism for inducing mucin secretion is Ca²⁺ signaling [116].

Ca²⁺ signaling is also known to be elevated in cells derived from cystic fibrosis patients [234]. Although Ca²⁺ signaling is essential for differentiated AEC function, which of these may be attributed to CRAC channel activation is unknown. To dissect the signaling pathways and CRAC channel function in AECs following differentiation, we utilized an air-liquid interface system. To our surprise, we found that ATP-evoked PGE₂ synthesis became CRAC channel independent in AECs following mucociliary differentiation. Similarly, ATP-evoked MUC5AC release was not inhibited with the CRAC channel inhibitor CM4620. This could be explained in part by a diminished sustained phase of Ca²⁺ entry following GPCR activation in AECs that have been differentiated. However, GPCR agonists largely retained their ability to suppress interferon release in ALI cultures. This further validates that the mechanism of interferon suppression is CRAC channel independent. Collectively, we see large scale rewiring of Ca²⁺ signaling in AECs following mucociliary differentiation.

Results

ATP evoked PGE₂ synthesis is independent of extracellular Ca²⁺ entry following mucociliary differentiation

We tested whether agonists and activators of CRAC channels evoke PGE₂ synthesis in AECs following mucociliary differentiation. Both ATPyS and TG evoked release of PGE2 to both the apical and basolateral compartments (Figure 7.1A). When ATP and ATPvS were compared directly, ATP seemed less effective than ATPyS at inducing release to the apical surface (Figure 7.1B). Higher doses of ATP (500µM) replicated ATPvS. This suggests that the apical surface may have high expression of ecto-ATPases that degrade ATP. Next, we tested whether the CRAC channel inhibitors CM4620 and BTP2 inhibited ATP-mediated PGE₂ synthesis. Surprisingly, both inhibitors had no effect (Figure 7.1C). This is in contrast to the results in submerged NHBE cultures (Figure 3.2). However, in agreement with the submerged cultures, the ATP-mediated PGE₂ release was abrogated in the presence of AR-C (Figure 7.1C). This suggests that P2Y₂ receptors drive PGE₂ synthesis in ALI cultures as well as submerged cultures. Finally, we tested whether extracellular Ca^{2+} was required for ATP-mediated PGE₂ synthesis. Chelation of all extracellular Ca²⁺ did not inhibit ATP-evoked PGE₂ synthesis (Figure 7.1D). This data strongly suggests that extracellular Ca²⁺ entry is not required for ATPdriven PGE₂ synthesis following mucociliary differentiation. Altogether, this data suggests that the Ca²⁺ dependence of PGE₂ synthesis alters following AEC differentiation likely switching from Ca²⁺ entry through CRAC channels to Ca²⁺ release from intracellular stores.



Figure 7.1 ATP evoked PGE₂ synthesis is independent of extracellular Ca²⁺ entry following mucociliary differentiation. A-D) NHBEs were differentiated using LifeLine ALI media. The day before stimulation, basolateral ALI media was replaced with 2 Ca BEBM media to remove hydrocortisone. All drugs were added to both apical and basolateral compartments and PGE₂ levels were measured independently for both compartments. A) ATPγS (100µM) and TG (500nM) evoke PGE₂ synthesis (2 hrs) in ALI cultures. Data are mean \pm SEM of n = 4 samples. B) ATPγS (100µM) and ATP (100 or 500µM) evoke PGE₂ synthesis (2 hrs) in ALI cultures. Data are mean \pm SEM of n = 3 samples. C) CRAC channel inhibitors do not block ATP (500µM) evoked PGE₂ synthesis (2 hrs) in ALI cultures. Cells were pretreated with CM4620 (1µM), BTP2 (5µM), or AR-C (10µM) for 2 hrs prior to ATP stimulation. Data are mean \pm SEM of n = 4-5 samples. **D)** Ca²⁺_{ext} is not necessary for ATP (500µM) evoked PGE₂ synthesis (2 hrs) in ALI cultures. BEBM media with 2mM Ca²⁺ or 0mM Ca²⁺ (adjusted using EGTA) was used for stimulation phase. Data are mean \pm SEM of n = 4-5 samples.

Agonists evoke mild IL-6 release into the basolateral compartment

We tested whether agonists such as the PAR2 activator, SLIGKV, histamine, or ATP induce an increase in IL-6 release in the ALI cultures. When cultures were stimulated with agonists, an apical wash showed no induction of IL-6 by the PAR2 activator (Figure 7.2A). However, the basolateral compartment showed small increases in IL-6 levels upon treatment with the PAR2 activator and high doses of ATP (Figure 7.2B). When ALI cultures were differentiated using the StemCell Technologies media, IL-6 in the basolateral compartment was not detectable (data not shown). This suggests that ALI cultures produce much less IL-6 than submerged cultures, similar to the results comparing PGE₂ production in these two models.



Figure 7.2 Agonists evoke mild IL-6 release into the basolateral compartment. NHBEs were differentiated using LifeLine ALI media. The day before stimulation, basolateral ALI media was replaced with 2 Ca BEBM media to remove hydrocortisone. All drugs were added to both apical and basolateral compartments and IL-6 levels were measured independently for both compartments. **A-B)** Agonists evoke modest IL-6 secretion to basolateral compartment but not to the apical compartment. IL-6 was quantified via ELISA from either an apical wash or the basolateral media 20 hours following stimulation. Concentrations for compounds were SLIGKV (100µM), BTP2 (5µM), Histamine (100µM), and ATP (500µM). Data are mean \pm SEM of n = 3-4 samples.

Store-operated Ca²⁺ entry is diminished following mucociliary differentiation

This alteration in the Ca²⁺ dependence of PGE₂ synthesis following differentiation led us

to test whether Ca²⁺ signaling itself alters. In ALI cultures, ATP evoked a rapid Ca²⁺ rise

followed by a swift decay back to baseline (Figure 7.3A). Importantly, neither CRAC

channel inhibitor CM4620 (also known as CM-EX-128) or BTP2 dramatically decreased

the ATP-mediated Ca²⁺ signal (Figure 7.3A). To test if cytokines or house dust mite

(HDM) could restore the sustained Ca²⁺ signal, we treated cells overnight with IL-1 β , IL-13, or HDM. However, none of these molecules had any effect on the ATP-mediated Ca²⁺ signal (Figure 7.3B). Therefore, we conclude that during the process of mucociliary differentiation, a rewiring of Ca²⁺ signaling occurs causing the sustained Ca²⁺ signal attributed to CRAC channels in submerged cultures (Figure 2.2) to diminish.



Figure 7.3 Store-operated Ca²⁺ entry is diminished following mucociliary differentiation. A-B) NHBEs were differentiated using LifeLine ALI media. The day before stimulation, basolateral ALI media was replaced with 2 Ca BEBM media to remove hydrocortisone. Cells were loaded with 5µM Fluo-4 for 1 hr on the apical compartment and Ca²⁺ signaling was measured from the apical side. A) CRAC channel inhibitors (CM4620 = CM-EX-128 used at 1µM and BTP used at 5µM) do not inhibit ATP-mediated Ca²⁺ signaling in ALI cultures. B) Cytokines and house dust mite (HDM) do not restore SOCE in ALI cultures. Treated cells basolaterally with cytokines or HDM 24 hrs prior to experiment. 72 hr pretreatment showed the same lack of effect. Bovine Serum Albumin (0.1%) was used as a control for the cytokines. IL-1β (10ng/mL), IL-13 (10ng/mL), HDM (100µg/mL) were used.

Histamine evokes Ca²⁺ signaling on basolateral cells exclusively following mucociliary differentiation

Polarized GPCR expression has been reported following AEC differentiation [49, 232-234]. To test if this occurred with histamine receptors, we measured Ca²⁺ signals in ALI cultures when histamine was perfused over either the basolateral or apical cells. Strikingly, histamine evoked a rapid Ca²⁺ signal when perfused over the basolateral cells but was incompetent when perfused over the apical cells (Figure 7.4A-B). This finding strongly suggests that histamine receptors are exclusively functional on the basolateral surface of ALI cultures.



Figure 7.4 Histamine evokes Ca^{2^+} signaling on basolateral cells exclusively following mucociliary differentiation. A-B) NHBEs were differentiated using LifeLine ALI media. The day before stimulation, basolateral ALI media was replaced with 2 Ca BEBM media to remove hydrocortisone. Cells were loaded with 5µM Fluo-4 for 1 hr on the apical compartment and Ca^{2^+} signaling was measured from the basolateral side (A) or apical side (B). A) Histamine (100µM) induces a rapid Ca^{2^+} signal when applied on the basolateral compartment. B) Histamine (100µM) induces no Ca^{2^+} signal when applied on the apical compartment.

The CRAC channel inhibitor CM4620 does not inhibit nucleotide-evoked MUC5AC release following mucociliary differentiation

Ca²⁺ signaling has been implicated in the release of mucins from goblet cells [53]. To test if CRAC channels were involved in ATP-mediated MUC5AC release in goblet cells, we first optimized a protocol for the measurement of MUC5AC. MUC5AC measurements have historically been difficult, as no validated commercial kits exist. Successive washing of the apical surface is necessary to measure nucleotide-evoked MUC5AC release. In agreement with prior reports [53, 115, 235, 236], the protocol demonstrated the majority of the MUC5AC is removed during the wash steps, while ATPγS induced a 2.5 fold increase in release during the stimulation phase (Figure 7.5A). We tested the ORAI1 inhibitor CM4620 for its ability to regulated ATPγS-mediated MUC5AC release. CM4620 did not inhibit MUC5AC release when MUC5AC was measured via an ELISA or via a Dot Blot (Figure 7.5B-C). This data suggests that CRAC channel function is dispensable for nucleotide-induced MUC5AC secretion from goblet cells.



Figure 7.5 The CRAC channel inhibitor CM4620 does not inhibit nucleotideevoked MUC5AC release following mucociliary differentiation. A-C) NHBEs were differentiated using LifeLine ALI media. A) ATPyS (100µM) evokes MUC5AC secretion. ALI cultures were apically washed five times to remove excess mucins. During the stimulation phase, ATPyS was added to some transwells and MUC5AC levels were measured via ELISA. Data are mean ± SEM of n = 5 samples. B) CM4620 (5µM) does not inhibit ATPyS (100µM) evoked MUC5AC secretion. ALI cultures were apically washed five times to remove excess mucins. During the stimulation phase, ATPyS was added to some transwells and MUC5AC levels were measured via ELISA. Cells were pretreated with CM 2 hrs prior to stimulation phase. Data are mean \pm SEM of n = 4-5 samples. C) CM4620 (5µM) does not inhibit ATPyS (100µM) evoked MUC5AC secretion. ALI cultures were apically washed five times to remove excess mucins. During the stimulation phase, ATPvS was added to some transwells and MUC5AC levels were measured via Dot Blot. Cells were pretreated with CM 2 hrs prior to stimulation phase. Samples are from same experiment as (B). Data are mean ± SEM of n = 4-5 samples.

Polarized release of Interferons following mucociliary differentiation

We transitioned to test how GPCR-mediated inhibition of IFN release may alter following mucociliary differentiation. We performed a time course analysis of poly(I:C)dependent IFN secretion in ALI cultures. Interestingly, IFN release was consistently higher to the basolateral compartment than the apical compartment (Figure 7.6A-B). This may be attributed to type 1 IFN receptors being exclusively expressed on the basolateral surface [237]. Another possible explanation was that the apical surface was pulsed with poly(I:C) for 2 hours, while the basolateral compartment was left in poly(I:C) for the length of the experiment. This difference in treatment was performed to limit squamous de-differentiation of the cells that has been shown to occur during the presence of long-term liquid in the apical compartment [232]. It is also interesting to note that the type 1 IFN release to the apical compartment was very rapid (peaking within 6 hrs). This suggests that upon viral infection, AECs may release type 1 IFN into the apical compartment rapidly to limit the spread of virus within the lumen of the airways. It is also striking that following differentiation. AECs produce significantly more type 3 IFN than type 1 IFN (approximately 1,000 fold more). Collectively, this data suggests that following differentiation, AECs maintain sensors for poly(I:C) that elicit type 1 and type 3 IFN release.



Figure 7.6 Polarized Release of Interferons following mucociliary differentiation. A-B) NHBEs were differentiated at the air-liquid interface (ALI) for 4 weeks and then stimulated with 10µg/mL poly(I:C) on both apical and basolateral sides. StemCell Technologies ALI media was used for this experiment. **A)** ALI cultures were stimulated with poly(I:C), then apical and basolateral supernatant samples were collected at the indicated time points and measured for IFN- β release via ELISA. To normalize for the difference in volumes collected from apical and basolateral compartments, basolateral concentrations were multiplied by 3.2. Data are mean ± SEM of n = 4-5 samples. **B)** ALI cultures were stimulated time points and measured for IFN- λ 1/3 release via ELISA. To normalize for the difference in volumes collected time points and measured for IFN- λ 1/3 release via ELISA. To normalize for the difference in volumes collected time points and measured for IFN- λ 1/3 release via ELISA. To normalize for the difference in volumes collected time points and measured for IFN- λ 1/3 release via ELISA. To normalize for the difference in volumes collected from apical and basolateral supernatant samples were collected at the indicated time points and measured for IFN- λ 1/3 release via ELISA. To normalize for the difference in volumes collected from apical and basolateral compartments, basolateral concentrations were multiplied by 3.2. Data are mean ± SEM

GPCR agonists inhibit Interferon release following mucociliary differentiation

We tested whether the agonists regulated poly(I:C)-mediated IFN release following

differentiation. All the agonists (ATP, UTP, histamine, SLIGKV) inhibited the release of

type 1 and type 3 IFN to the basolateral compartment (Figure 7.7B, 7.7D). In contrast,

only ATP and UTP suppressed the release of type 1 IFN to the apical compartment

(Figure 7.7C). None of the agonists dampened type 3 IFN release to the apical compartment (Figure 7.7E). Collectively, these results show that GPCR-mediated signaling can inhibit interferon release from AECs that have undergone mucociliary differentiation, although the phenotypes are much more complex (Figure 7.7F).



Figure 7.7 GPCR agonists inhibit Interferon release following mucociliary differentiation. A) NHBEs were differentiated at the air-liquid interface (ALI) for 4 weeks and then stimulated with 10µg/mL poly(I:C) +/- 100µM GPCR agonists on both apical and basolateral sides. StemCell Technologies ALI media was used for this experiment. **B-E)** GPCR agonists inhibit IFN release from dsRNA-stimulated ALI cultures. ALI cultures were stimulated with simultaneously with 10µg/mL poly(I:C) and 100µM GPCR agonist on both apical and basolateral sides. Apical and basolateral supernatant samples were collected 20 hrs later and measured for IFN-β (B-C) or IFN- λ 1/3 (D-E) release via ELISA. Apical cytokine levels are shown in C,E while basolateral levels are shown in B,D. Data are mean ± SEM of n = 11-21 samples. **F)** The nucleotides ATP and UTP inhibit the release of IFN-β to both apical and basolateral compartments while histamine and SLIGKV exclusively inhibit basolateral IFN-β. In contrast, all agonists effectively inhibit basolateral release of IFN- λ 1/3 but do not inhibit apical IFN- λ 1/3 release. *p<0.05, **p<0.01, ***p<0.001, ****p<0.001

The P2Y₂ receptor antagonist AR-C reverses ATP-mediated inhibition of IFN

release following mucociliary differentiation

ATP shows divergent effects on IFN release depending on the dose and differentiation

state of the AECs. We tested the P2Y₂ receptor antagonist AR-C for its ability to

modulate the ATP-mediated inhibition of IFN in ALI cultures. AR-C significantly reversed

the ATP-driven inhibition of both type 1 and type 3 IFN (Figure 7.8A-B). This finding

suggests that P2Y₂ receptor activation inhibits IFN secretion following mucociliary

differentiation.



Figure 7.8 The P2Y₂ receptor antagonist AR-C reverses ATP-mediated inhibition of IFN release following mucociliary differentiation. A-B) NHBEs were differentiated at the air-liquid interface (ALI) for 4 weeks and then stimulated with 10µg/mL poly(I:C) +/- 100µM GPCR agonists on both apical and basolateral sides. StemCell Technologies ALI media was used for this experiment. **A)** The P2Y₂ antagonist AR-C 118925XX (10µM) reverses ATP-mediated (100µM) inhibition of IFN-β release. ALI cultures were stimulated simultaneously with 10µg/mL poly(I:C) and 100µM ATP on both apical and basolateral sides. Apical supernatant samples were collected 7 hrs later and measured for IFN-β. Data are mean ± SEM of n = 8 samples. **B)** The P2Y₂ antagonist AR-C 118925XX (10µM) reverses ATP-mediated (100µM) inhibition of IFN-λ1/3 release. ALI cultures were stimulated simultaneously with 10µg/mL poly(I:C) and 100µM ATP on both apical and basolateral sides. Basolateral supernatant samples were collected 2 hrs later and measured for IFN-λ1/3. Data are mean ± SEM of n = 6-8 samples. *p<0.05, **p<0.01

GPCR agonists are incapable of inhibiting STING-mediated IFN release following

mucociliary differentiation

Little is known about the cGAS-STING pathway in AECs following mucociliary

differentiation. Lipofectamine did not enhance 2,3 cGAMP-mediated type 1 IFN release

in ALI cultures (Figure 7.9A) This indicates that ALI cultures are resistant to transfection by lipids. The cGAS ligand interferon stimulatory DNA (ISD) did not elicit IFN release in ALI cultures (data not shown). This is likely due to the inability of lipofectamine to transfect the dsDNA across the plasma membrane into the cytosol in AECs that have been differentiated. We tested the GPCR agonists for their ability to modulate STINGevoked IFN release following mucociliary differentiation. None of the agonists tested showed significant inhibitory ability on type 1 IFN release (Figure 7.9B-C). Altogether, these findings imply that while STING is functional in AECs following differentiation, the GPCR-mediated inhibitory effects disappear (Figure 5.5 vs. Figure 7.9).



Figure 7.9 GPCR agonists are incapable of inhibiting STING-mediated IFN release following mucociliary differentiation. A-C) NHBEs were differentiated at the air-liquid interface (ALI) for 4 weeks and then stimulated with $40\mu g/mL 2.3 \text{ cGAMP} +/- 100\mu M$ GPCR agonists on both apical and basolateral sides. StemCell Technologies ALI media was used for this experiment. A) Lipofectamine does not enhance 2.3 cGAMP-mediated

IFN- β release. Data are mean ± SEM of n = 3-4 samples. **B-C)** GPCR agonists do not inhibit 2,3 cGAMP-mediated IFN- β release. Basolateral IFN- β release (B) and apical IFN- β release (C) were measured via ELISA. Data are mean ± SEM of n = 8-10 samples.

Discussion

CRAC channel activity appears to be significantly diminished in AECs following mucociliary differentiation. This is demonstrated in the weak sustained Ca²⁺ entry following agonist stimulation (Figure 7.3) and the data demonstrating ATP-evoked PGE₂ synthesis is recalcitrant to CRAC channel inhibitors (Figure 7.1). However, this data is not conclusive that CRAC channel function is inherently decreased in differentiated cultures. It is possible that GPCR signaling itself is weaker in differentiated cultures and hence store depletion is not sufficient to elicit CRAC channel activation. It is also possible that ORAI1 and STIM1 possess polarized expression such that activation is only seen in particular stimulation contexts. However, available expression data suggests that upon ALI differentiation of submerged cultures, ORAI1 expression decreases while ORAI2 expression increases [238]. Bulk RNA-Seq data from Assel Biyasheva in the Schleimer lab corroborates these changes in ORAI1 and ORAI2 expression (data not shown). Hence, the most likely scenario is that as AECs differentiate, ORAI1 expression decreases and ORAI2 expression increases, radically restructuring the subunit composition of CRAC channels. It will be interesting future work to decipher what is the function of ORAI2 dominant CRAC channels in differentiated AECs.

One interesting discovery was the divergent effects of extracellular ATP in the

context of submerged, highly proliferative primary cell cultures versus an ALI culture that has undergone mucociliary differentiation. In the submerged cultures, ATP induced mild inhibition of IFN-B release regardless of concentration, yet high concentrations of ATP (100 μ M) potentiated IFN- λ 1/3 release (Figure 5.3). However, in the ALI cultures, ATP and UTP showed identical pharmacological effects at 100µM (Figure 7.7). There are multiple potential explanations for this discrepancy. The first is that the purinergic receptor repertoire may change upon mucociliary differentiation, such that the ATP (or ATP metabolite) receptor driving the potentiation in the submerged cultures is lost upon differentiation. It is also possible that differentiation decreases expression of a downstream component of the signaling processes that is necessary for potentiation. An alternative explanation is that nucleotide metabolism may be altered by differentiation, leading to stronger activation of P2Y₂ receptors that override the other ATP (or ATP metabolite) receptors that seem to be driving the potentiation we have observed. Further investigation will be necessary to determine the mechanism responsible for this divergent effect and which response predominates in intact human airways.

In ALI differentiated primary cells, ATP, UTP, histamine, and SLIGKV all effectively inhibited the release of both type 1 and type 3 IFN to the basolateral compartment (Figure 7.7B, 7.6D). However, only nucleotides were able to inhibit the apical release of IFN- β while both histamine and the PAR2 activator SLIGKV were incompetent (Figure 7.7C). While many possible explanations exist, it is worth mentioning that this correlates well with the polarized localization of the respective receptors. P2Y₂ receptors are expressed on both apical and basolateral surfaces of differentiated cultures while both H₁ and PAR2 receptors typically reside exclusively on basolateral surfaces [49, 67, 232-234]. However, recent data suggests that in the context of inflammation, such as after exposure to IL-13 or cigarette smoke, PAR2 can lose its restricted localization and gain access to the apical membrane [239]. Thus, in the context of chronic airway diseases where IL-13 is elevated or cigarette smoke is present, AEC PAR2 may gain the capacity to inhibit apical IFN- β release. It remains unclear whether a similar insult may induce the H₁ receptor to lose its polarized localization.

Chapter 8: Preclinical studies utilizing CM4620 in a murine HDM model of allergic disease

Introduction

CRAC channels are essential for proper immune responses [70, 74]. Specifically, both mast cells and T cells are known to heavily rely on CRAC channels for processes such as degranulation, cysteinyl leukotriene synthesis, IL-2 production and proliferation of T cells [70, 73, 74, 80, 82, 83]. Furthermore, Orai1 knockdown in murine airways can protect against allergic rhinitis [240]. However, the role of CRAC channels in airway epithelial cell biology remains enigmatic. The airway epithelium regulates and orchestrates lung immune responses, especially in the context of asthma [3]. Recently, we have discovered that airway epithelial cells express CRAC channels [95, 97]. These CRAC channels are activated downstream of PAR2, HDM, Cockroach, and chitinase [95, 97]. They are responsible for the production of proinflammatory cytokines such as IL-6, IL-8, TNF-α, GM-CSF [95, 97]. However, the role of AEC CRAC channels in the development and chronic inflammation in asthma is unknown. To begin this investigation, we induced airway inflammation in C57BL/6 mice using HDM. We recently obtained CM4620, also known in our lab as CM-EX-128, a potent CRAC channel inhibitor currently in clinical trials for acute pancreatitis, courtesy of CalciMedica [241]. At the challenge phase of the protocol, mice were treated intranasally with either placebo or CM-EX-128 prior to HDM. We collected serum and BALf and performed Th2 cytokine arrays. Although the induction of these cytokines was modest, intranasal CM4620 abolished the cytokine induction both in the BALf and the serum. This data provides further evidence that AEC CRAC channels may coordinate immune responses.

Results

We performed a standard house dust mite (HDM) sensitization protocol to model allergic airway disease in mice (Figure 8.1A-B). A few specific elements of the protocol are worth highlighting. First, only a small cohort of mice was used so the data is all very preliminary. Second, the CM4620 (also known as CM-EX-128) was a lipid emulsion and the placebo was that same lipid emulsion from CalciMedica. The volumes of placebo and CM4620 were limited to prevent excessive accumulation of liquid in the lungs. This protocol induced strong allergic inflammation in the airways as demonstrated by accumulation of eosinophils in the BALf (Figure 8.2), strong cellular infiltration (Figure 8.3), and mucin staining (Figure 8.3). However, CM4620 treatment did not influence any of these endpoints (data not shown). We measured cytokine and chemokine levels in either BALf or the serum via an array. Remarkably, CM4620 did reduce many cytokine and chemokines that were measured in both the BALf and the serum (Figure 8.4). This data is highly suggestive that intranasal CM4620 treatment may dampen cytokine and chemokine production in the airways. Altogether, more sustained treatment with CM4620 may be necessary to see more global decreases in inflammation as seen in BALf analysis and lung histology.



В

Day 0: HDM or Saline (50ul) Day 6: HDM or Saline (50ul) Day 7: HDM or Saline (50ul) Day 7: HDM or Saline (50ul) Day 10: CM-EX-128 or Placebo (50ul i.n.); CM-EX-128 i.p. (200ul) Day 11: HDM or Saline (50ul) Day 12: CM-EX-128 or Placebo (25ul i.n.), CM-EX-128 i.p. (200ul) at 9am; HDM or Saline (40ul) at 6pm Day 13: CM-EX-128 or Placebo (25ul i.n.), CM-EX-128 i.p. (200ul) at 9am; HDM or Saline (40ul) at 5pm Day 14: Harvest

Figure 8.1 HDM Protocol. A) Three month old C57BL/6 mice were treated intranasally (i.n.) with either house dust mite (HDM) or PBS. At later time points, mice were also treated with either CM-EX-128 (also known as CM4620) or placebo. **B)** Volumes and kinetics for the treatments are given. HDM was used at a concentration of 50 μ g / 50 μ l. CM-EX-128 was received from CalciMedica at a stock concentration of 1.6 mg/mL.



Figure 8.2 BALf Analysis. A-C) Bronchoalveolar lavage fluid (BALf) was collected on day 14 and cytospins were performed. Mice treated with HDM had a much greater percentage of Lymphocytes, Eosinophils and Neutrophils in the BALf than Saline treated mice.



Figure 8.3 Histological Analysis. A-B) Lung sections were stained at the mouse phenotyping core with either H &E staining or PAS staining. HDM treated mice showed greater cellular infiltration via H & E and greater mucins via PAS.



Figure 8.4 CM4620 reduces chemokine and cytokine expression. A) CM4620 (also known as CM-EX-128) reduced cytokine and chemokine expression in the BALf of male mice. Data are one mouse per group. **B)** CM4620 (also known as CM-EX-128) reduced cytokine and chemokine expression in the serum of female mice. Data are one mouse per group.

Discussion

Here we demonstrate that intranasal treatment of the novel ORAI1 inhibitor CM4620 reduces the chemokine and cytokine induction in a HDM model of allergic inflammation. However, we did not see marked differences in either BALf cellular analysis or lung histology. This may be due to the relatively brief treatment with CM4620. It should be noted that many reports have highlighted CRAC channel function is necessary for allergic asthma in murine models [73, 191-196, 240]. However, the advantage of our study was the local administration of the CRAC channel inhibitor while most of the previous studies introduced the pharmacological agent systemically. Since CRAC channel function is so essential to proper immune responses, we hypothesize that local inhibition of airway CRAC channels may allow systemic CRAC channel function to

persist, leading to a greater therapeutic index. Nonetheless, further studies are necessary to confirm this hypothesis.

Chapter 9: Conclusions and Future Directions

Within this thesis dissertation, we have thoroughly characterized the interaction between AEC purinergic signaling and CRAC channel function in the release of immunomodulatory mediators. These findings provide further novel targets for airway disease such as activation of P2Y₂ receptors to elicit production of PGE₂, inhibition of P2X and CRAC channels to block IL-6 secretion from AECs as well as inhibition of purinergic signaling to enhance IFN production.

It is worth noting that all of these studies were performed in cells derived from healthy adults from both sexes and multiple ethnic backgrounds. Increasingly, complexities driven by sex, disease state, ethnicity, and age are being linked to metabolic and airway epithelial function [242, 243]. Therefore, future studies to interrogate how AEC CRAC channel or IFN production varies dependent on these characteristics would be important advances for the field.

One further line of investigation involves cGAS-STING signaling in AECs. Our data suggests that STING is functional in AECs differentiated at the ALI (Figure 7.8). Recent data suggests that the endogenous STING agonist 2,3 cGAMP can be released and imported from cells via LRCC8 channels [244, 245]. It would be interesting to

interrogate if LRCC8 channels are functional in AECs differentiated at the ALI and allow for this transport of 2,3 cGAMP into the cells. Our preliminary data suggests that lipofectamine did not enhance type 1 IFN production suggesting active transport of 2,3 cGAMP across cell membranes. Another possible set of experiments would be to test if mice with *Sting* selectively knocked out in AECs exhibit phenotypes in models of respiratory virus infection. It may be that intranasal 2,3 cGAMP would prove to be a useful antiviral therapy.

Another interesting further line of experiments is whether inflammatory insults can restore SOCE function in ALI cultures. SOCE was markedly diminished in ALI cultures (Figure 7.2A) and decreased ORAI1 expression and increased ORAI2 expression has been reported in ALI cultures [238]. Bulk RNA-Seq data from Assel Biyasheva in the Schleimer lab corroborates these changes in ORAI1 and ORAI2 expression (data not shown). However, this is all indicative of the healthy, unperturbed state of ALI cultures. In a disease context, ORAI1 and ORAI2 expression may very well revert back to levels more closely resembling submerged NHBE cultures. When IL-13, IL-1 β , and HDM were tested none of these inflammatory insults were capable of restoring SOCE in ALI cultures (Figure 7.2B). However, other inflammatory insults for longer treatment times may restore SOCE function in ALI cultures.

Numerous reports demonstrate that CRAC channel inhibition protects in models of allergic lung inflammation [73, 191, 193-196]. These studies administered the CRAC channel inhibitors in routes leading to systemic delivery. Therefore, the contribution of AEC CRAC channel inhibition to this disease protection remains uncertain. Indeed, we have recently shown that AEC CRAC channels cause GM-CSF production, a cytokine essential for dendritic cell maturation and Th2 polarization [4, 95]. If deletion of AEC CRAC channels protects in murine models of asthma, this will provide further rationale for the use of CRAC channel inhibitors in asthma. A useful Cre line to induce this would be SPC-Cre, a line that we have recently generated in the lab [246]. Although it is worth mentioning that undesirable side effects have been noted in this Cre line [247]. Systemic inhibition of the CRAC channel is likely to cause unacceptable side effects such as global immunosuppression. Therefore, local delivery of CRAC channel inhibitors through an inhaler may prove a route with a greater therapeutic index. This route would also lead to more efficient inhibition of AEC CRAC channels in allergic inflammation and whether local delivery of CRAC channel inhibitors may alleviate local inflammation while leaving host immunity intact are essential hypotheses to test.

Chapter 10: Materials and Methods

<u>Cells, media and solutions</u>: Normal human bronchial epithelial (NHBE) cells were purchased from Lonza (CC-2540) and were grown in bronchial epithelial growth media (BEGM, CC-3170). All experiments that used media for the stimulation phase utilized Lonza BEBM (CC-3171) media supplemented with Ca²⁺ to bring the total concentration up to 2mM. Cells were grown in 37°C and 5% CO₂. Ringers solutions were as follows: 2mM Ca²⁺ Ringers solution: 155mM NaCl, 4.5mM KCl, 10mM D-glucose, 5mM HEPES, 2mM CaCl₂, 1mM MgCl₂. 0mM Ca²⁺ Ringers solution: 155mM NaCl, 4.5mM KCl, 10mM D-glucose, 5mM HEPES, 1mM EGTA, 3mM MgCl₂.

Antibodies and Pharmacological Tools: Primary antibodies were as follows: COX-2 (CST 12282), β-actin (CST 3700), P-ERK (CST 4370), T-ERK (CST 9102), cPLA₂ (CST 2832), STIM1 (Feske Lab #3917), α-Tubulin (Abcam ab52866), P-STAT1 (CST 7649), β-actin (CST 3700), T-STAT1 (CST 9172), IRF1 (CST 8478), P-TBK1 (CST 5483), IRF3 (CST 11904), p65 (CST 8242), LaminA/C (CST 4777), T-TBK1 (Abcam ab40676). Pharmacological tools were as follows: UTP (Sigma U6875), SLIGKV-NH2 (Tocris 4153), FK-506 (Tocris 3631), BTP2 (Sigma 203890), ATP (Sigma A6419), Diclofenac (Tocris 4454), Apocynin (Tocris 4663), NAC (Sigma 106425), U0126 (Tocris 1144), ATPyS (Tocris 4080), AACOCF3 (Tocris 1462), AR-C 118925XX (Tocris 4890), NF546 (Tocris 3892), S3QEL 2 (Tocris 5735), ADPβS (Sigma A8016), UDP (Sigma U4125), NF157 (Tocris 2450), Apyrase (Sigma A6410 Grade VI, High ATPase/ADPase activity), TNP-ATP (Tocris 2464), 5-BDBD (Tocris 3579), A740003 (Tocris 3701), Suramin (ACROS Organics-Fisher AC328540500), PPADS (Tocris 0625), SLIGKV-NH2 (Tocris 4153), histamine (Tocris 3545), cetirizine (Tocris 2577), YM-254890 (Cayman Chemical 29735), Gö 6983 (Tocris 2285), PDBu (Tocris 4153), PMA (Tocris 1201), ruxolitinib (Tocris 7054), AG 1478 (Tocris 1276), IFN-β (R & D systems 8499-IF), EGF (R & D systems 236-EG), poly(I:C) (Invivogen tlrl-picw), 2,3 cGAMP (Invivogen tlrl-nacga23), ISD (Invivogen tlrl-isdn), 3p-hpRNA (Invivogen tlrl-hprna), CM4620 (also known as CM-EX-128) was a kind gift from CalciMedica.

<u>siRNA or shRNA Knockdowns:</u> On day 0, NHBE cells were plated onto 24 well plates in the morning in BEGM media lacking antibiotics. In the afternoon, cells were transfected

using RNAi Max and siRNA at final concentrations of 10nM. On day 1, cells were given fresh BEGM media lacking antibiotics and re-transfected using identical conditions as day 0. On day 2, cells were given fresh BEGM media lacking antibiotics and lacking hydrocortisone and retransfected using identical conditions as day 0. On day 3 (72 hrs after initial transfection), cells were either collected for analysis of protein levels, mRNA levels, or were stimulated with ATP for 2hrs for PGE₂ analysis according to the standard PGE₂ stimulation protocol (see PGE₂ measurement section). siRNA used included "siRNA Universal Negative Control #1" SICOO1 (Sigma) hereby termed "siCon", siSTIM1: SASI Hs01 00107803 (Sigma), siORAI1: 4392420 assay ID s228396 (Thermofisher). On day 0, NHBE cells were thawed into T-25 flasks at approximately 25,000 cells/flask. On day 1, cells were infected with lentivirus harboring control or gene targeting sequences at MOI of 10. On day 2, fresh BEGM media was given to each flask. On day 3, puromycin was added to the culture media at a final dose of 4µg/ml and selection was allowed to occur for 3 days. Nontransduced cells were always handled in parallel to confirm puromycin's ability to induce selection. On day 6 or 7, cells were then plated for experiments and maintained in 1µg/ml puromycin until the time of stimulation when puromycin was removed from the culture media and cells were stimulated in BEBM without growth factors. Lentiviral particles expressing shRNA were purchased shCon (SHC202V), shTLR3 1 (TRCN0000056851), from Sigma: shTLR3 2 (TRCN0000358585), shP2RX4 (TRCN0000044962).

<u>Intracellular Ca²⁺ measurements</u>: NHBE cells were grown on poly-L-lysine coated glassbottom dishes purchased from MatTek. Cells were loaded with 2µM Fura-2-AM (Thermofisher F1221) in BEGM with 5% FBS added to increase loading. Cells were

loaded for 40 min at room temperature in the dark. Cells were washed 3X with 2mM Ca²⁺ Ringers solution and then incubated for an additional 15 min in the dark before initiating Ca²⁺ imaging. Experiments were performed at room temperature. Dishes were mounted on the stage of an Olympus IX71 inverted microscope. Images were acquired every 6 seconds at excitation wavelengths of 340nm and 380nm and an emission wavelength of 510nm. Image acquisition and analysis were performed using SlideBook software. For data analysis, regions of interest were drawn around individual cells, background fluorescence was subtracted, and the F₃₄₀/F₃₈₀ ratios were calculated for each timepoint. An increase in the ratio of F_{340}/F_{380} indicates a rise in $[Ca^{2+}]_i$. The F_{340}/F_{380} ratios were then converted to an estimate of $[Ca^{2+}]_i$ through the equation: $[Ca^{2+}]_i = \beta^* K_d^* (R-R_{min})/(R_{max}-R)$, where R is the F_{340}/F_{380} ratio and the values of β , R_{min} . R_{max} were determined from an *in vitro* calibration with Fura-2 pentapotassium salt. β is determined from the F_{min}/F_{max} ratio at 380nm and K_d is the dissociation constant of Fura-2 binding to Ca²⁺ (135nM). The determined values were β = 23.152, R_{min}=0.2092, R_{max}=6.954.

<u>ATP release assays</u>: On day 0, NHBE cells were plated onto 24 well plates. On day 1, BEGM media was replaced with BEGM media lacking hydrocortisone. On day 2, media changes were performed and supernatants were collected at the indicated time points. ATP concentrations were quantified using Sigma Catalogue Number FLAA (FLAAM and FLAAB). Product FLAAM was diluted 25-fold with FLAAB prior to use. An ATP standard curve was used to determine absolute concentrations.

<u>NFAT Dual Luciferase Assays</u>: On day 0, BEAS-2B cells were plated onto 96 well plates (costar 3610) to allow analysis within plates. On day 1, cells were transfected
with 190 ng of NFAT plasmid and 10 ng of Renilla plasmid. Transfection allowed for 150 μ l of media and 50 μ l of optimum/lipofectamine/plasmid cocktail. On day 2, cells were stimulated in 2mM Ca²⁺ BEAS-2B media using the relevant compounds and Promega E1910 kits were used for analysis of luciferase levels. Data are displayed as firefly luciferase signal divided by renilla luciferase signal. Firefly luciferase is driven by the NFAT:AP-1 promoter sequence and renilla luciferase is driven by a thymidine kinase promoter.

<u>NFAT4-GFP Nuclear Translocation Assays</u>: On day 0, BEAS-2B cells were plated onto 3.5mM glass coverslips. On day 1, BEAS-2B cells were transfected with 200 ng/plate of NFAT4-GFP plasmid for 6 hours, then optimum/lipofectamine/plasmid cocktail was removed and fresh media was given to cells. Twenty four to forty eight hours later, experiments were performed. Images were taken of NFAT4-GFP localization prior to TG addition and 20 minutes following TG addition and analysis was done in a binary manner (either translocation did occur or translocation did not occur).

<u>ALI PGE₂ stimulation experiments</u>: NHBEs were differentiated using LifeLine ALI media (LM-0050). The day before stimulation, basolateral ALI media was replaced with 2 Ca BEBM media to remove hydrocortisone. Through my time working with ALI cultures, I transitioned to Promocell ALI media because it had better performed. The Promocell media also allows for the remove of hydrocortisone. See "Air-liquid interface (ALI) differentiation and stimulation" section for a fuller description of the Promocell ALI method. Washed apical side 2X prior to stimulation phase to remove excess mucus. All drugs were added to both apical and basolateral compartments and PGE₂ levels were measured independently for both compartments. *Fluo-4 ALI Ca*²⁺ *experiments*: NHBEs were differentiated using LifeLine ALI media (LM-0050). The day before stimulation, basolateral ALI media was replaced with 2 Ca BEBM media to remove hydrocortisone. On the day of experiment, wash apical side 3X with 300 μ l of 2 Ca BEBM. Load apical side only with 5 μ M Fluo-4. Load for 1 hour at 37C. At time of loading, give fresh 2 Ca BEBM to basolateral side with DMSO, BTP2, or CM4620. Included DMOS, BTP2, or CM4620 in apical side. After loading wash apical side 2X with fresh 2 Ca BEBM. Remove the membrane with a 22-gauge syringe and forceps and gently place in 2 Ca Ringers (with DMSO, BTP2, 128) with apical side facing up. Imaged using confocal microscopy with a "harp" to hold the cells in position under the microscope.

MUC5AC experiments: Quantification of MUC5AC secretion is notoriously difficult.

Thus, the methods from Dr. William Davis's group were followed closely [236]. NHBEs

were differentiated using LifeLine ALI media (LM-0050). The day before stimulation,

basolateral ALI media was replaced with 2 Ca BEBM media to remove hydrocortisone.

On the day of experiment, wash apical side 5X with 300 µl of 2 Ca BEBM.

To analyze MUC5AC via ELISA, the follow method was performed.

1. Plated 100ul of sample diluted in PBS in 96 well plate (Costar 3590), incubate overnight at 4C on shaker

2. Wash 4X in PBST (0.1% tween) using 200ul

3. Block with 5% NFDM in PBST for 1hr at 37 C in the humidified chamber using 200ul

4. Incubate with 45M1 (Invitrogen MA5-12178) primary (dissolved 1:500 in 1% NFDM in PBST) using 100ul/well for 2hr at 37 C in humidified chamber

5. Wash 4X in PBST (0.1% tween) using 200ul

6. Incubate with anti-mouse biotinylated secondary (dissolved 1:1000 in PBST) using 100ul/well for 1hr at 37 C in humidified chamber

7. Wash 4X in PBST (0.1% tween) using 200ul

8. Incubate with streptavidin-HRP tertiary antibody (Thermofisher N100) (dissolved 1:1000 in PBST) using 100ul/well for 1hr at 37 C in humidified

chamber

9. Wash 4X in PBST (0.1% tween) using 200ul 10. Develop with 150ul/well OPD substrate (1mg/mL in 1X Stable Peroxide Substrate Buffer) for 10-15 min at RT in dark, stop reaction with 50ul/well of 4M H_2SO_4

11. Determine OD at 490nM

To measure MUC5AC via Dot Blot technique, the following protocol was followed:

1. Make grid on nitrocellulose membrane using pencil and pipette on indicated amounts of cell culture supernatant

2. Let membrane dry completely at RT (approx. 1 hr)

- 3. Block for 1hr at RT in 5% BSA dissolved in TBST
- 4. Incubate with primary antibody overnight at 4C (Used Thermofisher 45M1 MA5-12178 at 1:500 dilution)

5. Wash 3X with TBST 5-10min each

6. Incubate with secondary antibody for anti-mouse biotin labeling (same one using for MUC5AC ELISA, 1:1000) for 4hrs at 4C

7. Wash 3X with TBST 5-10min each

8.Incubate with tertiary antibody (HRP-Strept from LiCor, 1:5000) for 1hr at RT

9. Wash 3X with TBST 5-10min each

10. Image

HDM model of allergic inflammation: HDM was from Greer item number XPB70D3A25

and lot number 343205. It was used at a final concentration of 50 μ g protein / 50 μ l. 50 μ l of either saline or HDM were given to each mouse. Stock HDM came as 37.40 mg

protein/vial and is dissolved in sterile saline at a concentration of 500 μg / 50 μl (10X

stock) and stored in glass vials from agilent technologies (5182-0714 and 5182-0717) in

the -80C. Prior to administration, 450 µl of sterile saline was added to the HDM stock to

adjust the concentration to the working concentration of 50 µg protein / 50 µl. CM-EX-

128 (CM4620) was an emulsion solution at 1.6 mg/mL concentration. Histology was

performed through the mouse phenotyping core facility. The cytokine and chemokine

screen was conducted using R & D kit ARY006.

<u>COX-2 and ERK1/2 activation assays</u>: On day 0, NHBE cells were plated onto 24 well plates. On day 1, BEGM media was replaced with BEGM media lacking hydrocortisone. On day 2, cells were stimulated. If cells were pretreated with drugs, half of the BEGM media lacking hydrocortisone was taken off the cells, the drug was added to that media at 2X final concentration, vortexed, and added back to the relevant wells. Cells were activated for either 15min. (for ERK1/2 measurements) or 2 hr. to overnight (for COX-2 upregulation measurements) as indicated in the Figure legends. Following stimulation, cells were lysed using 1X Cell Signaling Lysis Buffer (9803S) containing protease and phosphatase inhibitors (PPIs) (Thermofisher 78440). Cell lysates were incubated on ice for 30 minutes and vortexed every 10 minutes. Samples were spun at 12,000rpm for 15min at 4°C and supernatants were collected and analyzed via western blotting.

Western Blots: Following stimulation, cells were lysed using 1X Cell Signaling Lysis Buffer (9803S) containing protease and phosphatase inhibitors (PPIs) (Thermofisher 78440). Lysates were boiled for 5 min in 1X Laemmli Sample Buffer (Bio-Rad 1610747) containing 2-ME. Samples were then subjected to SDS-PAGE. Transfer occurred at 4°C for 1.5 hrs and at 100V. PVDF membranes were used for the transfer. Following transfer, membranes were washed in TBST (0.1% Tween 20), blocked for 1 hr at RT using 5% BSA dissolved in TBST, then incubated overnight at 4°C with primary antibodies. All dilutions for primary antibodies were 1:1000 besides anti-β-actin: 1:2000, anti-phospho ERK1/2: 1:2000, anti-α-Tubulin: 1:5000. The following day, membranes were washed 3X for 5 min each using TBST and incubated with secondary antibodies for 1 hr at RT in 5% BSA dissolved in TBST. Li-Cor secondary antibodies were used (IRDye 800 CW or IRDye 680 RD) at dilutions of 1:10000. Membranes were washed 3X for 5 min each using TBST and immediately imaged using an Odyssey CLx imaging system.

Nuclear and Cytosolic Fractionation assays: On day 0, NHBE cells were plated onto 6 well plates. On day 1, BEGM media was replaced with BEGM media lacking hydrocortisone. On day 2, cells were stimulated. If cells were pretreated with drugs, half of the BEGM media lacking hydrocortisone was taken off the cells, the drug was added to that media at 2X final concentration, vortexed, and added back to the relevant wells. This protocol was adapted from Chang et al. [80]. Cells were stimulated for 5 minutes in BEBM media lacking all growth factors. Media was immediately aspirated, cells were placed on ice, and cells were scrapped in hypotonic lysis buffer containing protease and phosphatase inhibitors (PPIs) (Thermofisher 78440) and collected into prechilled eppendorf tubes. Lysates from two wells were combined into one tube to ensure sufficient protein content. Samples were incubated on ice for 10min. Samples were then spun at 1,000rpm for 4min at 4°C. The supernatant was collected as the crude cytosolic fraction and the pellet was resuspended in hypertonic lysis buffer containing PPIs. Both the crude cytosolic fractions and the resuspended pellet were incubated on ice for another 30min, and periodically vortexed every 10min to ensure full lysis. Next, both crude cytosolic fraction samples and the resuspended pellet samples were centrifuged at 12,000rpm for 10min at 4°C and the supernatants were collected and termed "cytosolic fraction" and "nuclear fraction". The hypotonic buffer consisted of: 10mM Hepes pH 7.9, 10mM KCl, 1.5mM MgCl₂, 0.5mM EDTA, PPIs added fresh. The hypertonic buffer consisted of: 20mM Hepes pH 7.9, 420mM NaCl, 1.5mM MgCl₂, 0.2mM EDTA, 25% glcyerol, PPIs added fresh.

<u>PGE₂ measurements</u>: On day 0, NHBE cells were plated onto 24 well plates. On day 1, BEGM media was replaced with BEGM media lacking hydrocortisone. On day 2, cells were stimulated. If cells were pretreated with drugs, half of the BEGM media lacking hydrocortisone was taken off the cells, the drug was added to that media at 2X final concentration, vortexed, and added back to the relevant wells. At the time of stimulation, media was removed and cells were stimulated for 2 hours in BEBM media lacking all growth factors. Following this stimulation phase, the supernatants were collected, spun at 300g for 4min to remove cellular debris, and the supernatant from this sample was then collected and stored at -80°C until the time of analysis. To perform analysis of PGE₂ levels, the Cayman Chemical kit (514010) was used and the manufacturers protocols were followed. All samples were diluted at least 10-fold in ELISA buffer prior to analysis. All samples that were compared statistically had the same concentration of organic solvents (such as DMSO and ethanol) as organic solvents can interfere with the assay.

<u>IL-6 ELISAs</u>: On day 0, NHBE cells were plated onto 24 well plates. On day 1, BEGM media was replaced with BEGM media lacking hydrocortisone. On day 2, cells were stimulated. If cells were pretreated with drugs, half of the BEGM media lacking hydrocortisone was taken off the cells, the drug was added to that media at 2X final concentration, vortexed, and added back to the relevant wells. At the time of stimulation, media was removed and cells were stimulated overnight (16hrs) in BEBM media lacking all growth factors. Following this stimulation phase, the supernatants were collected, spun at 300g for 4min to remove cellular debris, and the supernatant from this sample was then collected and stored at -80°C until the time of analysis. To perform analysis of

IL-6 levels, the RayBiotech Human IL-6 ELISA kit (ELH-IL6-1) was used and the manufacturers protocols were followed. All samples were diluted typically 5-fold in ELISA buffer prior to analysis. Samples that were compared statistically had the same concentration of organic solvents (DMSO).

<u>Transfection of NHBEs</u>: NHBEs were transfected with 2,3 cGAMP, ISD, or 3p-hpRNA using Lipofectamine 2000 (Thermofisher Scientific 11668019) at a constant volume of 2.5µl Lipofectamine/well of 24 well plate. Transfection cocktails were mixed containing ligand (2,3 cGAMP, ISD, 3p-hpRNA), Lipofectamine 2000, and Opti-MEM media (Thermofisher Scientific 31985062) and were gently vortexed and allowed to sit 10 minutes prior to transfecting NHBEs. Using 24 well plates, 50µl of transfection cocktail was added to 450µl of BEBM media (containing 2mM Ca²⁺) to initiate transfection. Cells were incubated with transfection cocktail for the length of the experiment.

Influenza A virus infection of NHBEs: Influenza A virus strain A/WSN/33(H1N1) was used for all IAV experiments. NHBEs were plated onto 24 well plates and infected at MOI 0.1, 0.5 or 1.0 for 24 hours. Cells were washed with PBS prior to infection, 200µl of BEBM (containing 2mM Ca²⁺) with IAV was added to the respective wells and cells were incubated on shaker (approximately 30 rpm) inside an incubator set to 37°C and 5% CO₂. Infection was allowed to occur for 1 hour then virus was aspirated and fresh BEBM (containing 2mM Ca²⁺) was added to the respective wells. RV1B was purchased from ATCC (VR-1645) and was used at an MOI of 10 for all experiments. Cells were washed with PBS prior to infection, 200µl of BEBM (containing 2mM Ca²⁺) with and was used at an MOI of 10 for all experiments. Cells were washed with PBS prior to infection, 200µl of BEBM (containing 2mM Ca²⁺) with RV1B was added to the respective wells and cells were incubated on shaker (approximately 30 rpm) inside an incubator set to 33°C and 5% CO₂. Infection was allowed to occur for

2 hours then virus was aspirated and fresh BEBM (containing 2mM Ca^{2+}) was added to the respective wells. For treatments including UTP, ATP, or histamine, agonist (100µM) was added at the time of initial infection and fresh agonist was added following infection.

IFN ELISAs: On day 0, NHBE cells were plated onto 24 well or 48 well plates. On day 1, BEGM media was replaced with BEGM media lacking hydrocortisone. On day 2, cells were stimulated. If cells were pretreated with drugs, half of the BEGM media lacking hydrocortisone was taken off the cells, the drug was added to that media at 2X final concentration, vortexed, and added back to the relevant wells. At the time of stimulation, media was removed and cells were stimulated in BEBM media lacking all growth factors. Poly(I:C) and GPCR agonists were added simultaneously. Following this stimulation phase, the supernatants were collected and stored at -80°C until the time of analysis. To perform analysis of IFN-β levels, the PBL Assay Science kit (41435-1) was used and the manufacturers protocols were followed. To perform analysis of IFN-λ1/3 levels, the R & D systems kits (DY1598B and DY008) were used and the manufacturers protocols were followed. Samples that were compared statistically had the same concentration of organic solvents (DMSO).

<u>Air-liquid interface (ALI) differentiation and stimulation:</u> NHBEs were plated onto costar 3460 transwells (coated with 0.03 mg/mL collagen) at 110,000 cells/well in BEGM media on day 0. BEGM media was on both apical and basolateral sides from day 0 until day 2. On day 1, fresh BEGM media was given on both apical and basolateral sides. On day 2, the media was removed from the apical side and the basolateral side media was replaced with differentiation media. Two different differentiation medias were used in this thesis work. The first media was LifeLine ALI media (LM-0050) and the second was

from StemCell Technologies (05001) supplemented with hydrocortisone (07925) and heparin (07980) and Gibco gentamicin/amphotericin (R-015-10). The early studies were done using LifeLine ALI media as that was the media that the Berdnikovs lab uses. However, this media comes with hydrocortisone already dissolved in it. Hence, for the experiments done with this media, 24 hours prior to the experiment, differentiation media was replaced with 2mM Ca2+ BEBM media. Discussion with other labs about the ALI media they used led me to the StemCell Technologies media where the hydrocortisone was supplemented instead of predissolved. Overall, I noticed that the experiments done with the LifeLine media were stronger produces of cytokines and prostaglandins, but this is likely because they had the differentiation media replaced with 2mM Ca²⁺ BEBM media 24 hours prior to the experiment. I think the StemCell Technologies media is the preferred media choice. Regardless of which media was used, differentiation media was replaced Monday, Wednesday, and Friday and differentiated was allowed to occur for at least 28 days until experiments were performed. Once cells began releasing mucus around day 14, the apical surface was washed once weekly with PBS to remove excess mucus until the time of the experiment. On the day of the experiment, the apical side was washed 3X with 2mM Ca²⁺ BEBM media and cells were stimulated with all drugs on both the apical side (300µl) and the basolateral side (800µl). Two hours later, the apical side media was aspirated out to reestablish the air interface as long-term media on the apical side has been shown to cause de-differentiation [239]. At the time of collection, the apical side was washed with 2mM Ca²⁺ BEBM (250µl/well) and collected and the basolateral media

was collected as well. Supernatants were then used for downstream applications such as IFN analysis.

<u>CellTox and CellTiter-Glo assays</u>: CellTox Green Cytotoxicity Assay (G8741) and CellTiter-Glo 2.0 Assay (G9241) were purchased from Promega and manufacturers instructions were followed for experimentation. NHBEs were plated in 96 well plates (costar 3610) and infected with IAV at an MOI of 0.5 as described in the virus infection methods section. The sequential multiplexing protocol was followed such that both CellTox and CellTiter-Glo could be performed using the same plate of cells.

RT-gPCR analysis: Total RNA was extraction was performed using RNeasy Plus Mini Kit (Qiagen 74134). cDNA generation was performed using iScript Reverse Transcription Supermix for RT-gPCR (Biorad 1708841). gPCR was performed using PowerUp SYBR Green Master Mix (A25741). For qPCR, final concentration of primers was 500nM and cDNA was used at 6ng/well. Primer sequences used were as follows: RPLP0 Forward 5' AGCCCAGAACACTGGTCTC 3'. RPLP0 Reverse 5' ACTCAGGATTTCAATGGTGCC 3'. IFN-B1 5' Forward GAAACTGAAGATCTCCTAGCCT 3', 5' IFN-B1 Reverse GCCATCAGTCACTTAAACAGC 3' (IDT Assay Name Hs.PT.58.39481063.g), TLR3 (IDT Assav Name Hs.PT.58.25887499.q), ORAI1 Forward 5' GATGAGCCTCAACGAGCACT 3', ORAI1 Reverse 5' ATTGCCACCATGGCGAAGC 3', P2RY2 Forward 5' CCGCTTCAACGAGGACTTCAA 3', P2RY2 Reverse 5' GCGGGCGTAGTAATAGACCA 3', P2RX4 Forward 5' CTACCAGGAAACTGACTCCGT 3', P2RX4 Reverse 5' GGTATCACATAATCCGCCACAT 3', HPRT1 Forward 5' ACCCTTTCCAAATCCTCAGC 3', HPRT1 Reverse 5' GTTATGGCGACCCGCAG 3',

RPLP0 Forward 5' AGCCCAGAACACTGGTCTC 3'. RPLP0 Reverse 5' ACTCAGGATTTCAATGGTGCC 3', PPIA Forward 5' CCCACCGTGTTCTTCGACATT 3', PPIA Reverse 5' GGACCCGTATGCTTTAGGATGA 3', P2RY11 Forward 5' GTAGCAGACACAGGCTGA 3', P2RY11 Reverse 5' CCTGGAACCCACTGAGTTTG 3', P2RX1 Forward 5' CGTTATCTTCCGACTGATCCAG 3', P2RX1 Reverse 5' CACAGAGACACTGCTGATGAG 3', P2RX2 Forward 5' GAGGTGTTCGGCTGGTG 3', P2RX2 Reverse 5' GGTAGTGGATGCTGTTCTTGA 3', P2RX3 Forward 5' 3'. CAACATCATCCCCACCATCA P2RX3 5' Reverse CTCATTCACCTCCTCAAACTTCT 3', 5' P2RX5 Forward GGAAGCAGCAGTCAGAAGG 3', P2RX5 Reverse 5' AAAGGCATGGGATCACTGG 3', TGGCCTCACTACTCCTTCC 3'. P2RX6 5' P2RX6 Forward 5' Reverse ATGTCGAAGCGGATTCCATAG 3'. P2RX7 Forward 5' CCCTGTGTGTGGTCAACGAAT 3', Reverse 5' P2RX7 TGCAGACTTCTCCCTAGTAGC 3'.

<u>Data Analysis:</u> All bar graphs summarizing data are represented as mean \pm SEM. Individual points are always indicative of biological replicates. For a data set involving more than two groups, an initial one-way ANOVA was performed followed by Tukey's multiple comparison tests. For data sets with only two groups, a two-tailed unpaired Student t-test was performed. Dose-response curves were created using a four parameter (variable slope) nonlinear regression. Extra sum-of-squares F-Test used to statistically compare the PGE₂ and IL-6 dose-response curves. Statistical analysis and data analysis was performed using Prism 8 or 9 (GraphPad Software). *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001 when statistical comparisons are made.

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