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Polymicrobial respiratory tract infections in a hospital-based pediatric population, with particular emphasis on the role of human rhinoviruses

Margaret Lynn Chorazy *University of Iowa*

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POLYMICROBIAL RESPIRATORY TRACT INFECTIONS IN A HOSPITAL-BASED PEDIATRIC POPULATION, WITH PARTICULAR EMPHASIS ON THE ROLE OF HUMAN RHINOVIRUSES

by

Margaret Lynn Chorazy

An Abstract

Of a thesis submitted in partial fulfillment of the requirements for the Doctor of Philosophy degree in Epidemiology in the Graduate College of The University of Iowa

July 2010

Thesis Supervisors: Professor James C. Torner Adjunct Professor Gregory C. Gray

ABSTRACT

Pediatric acute respiratory tract infections (ARTIs) are a leading cause of morbidity and mortality. The objectives of this study were to describe the epidemiology of polymicrobial ARTI in a hospital-based pediatric population and to investigate the association of polymicrobial infection and severity of illness.

We conducted a retrospective study of 559 archived respiratory specimens from 421 children under the age of 10 years collected from March 28, 2008 through June 30, 2009 and stored by the University of Iowa Hospital and Clinics Clinical Microbiology Laboratory. Specimens were tested by direct immunofluorescent assay and/or viral culture at the time of collection (influenza A and B, parainfluenza [PIV] 1-3, respiratory syncytial virus [RSV], adenovirus [Ad]) and uniformly by RT-PCR (human metapneumovirus [hMPV], rhinovirus [HRV], human bocavirus [HBoV]) and PCR (Ad) for the current study. Demographic and clinical data were abstracted from electronic medical records.

Results from this study suggest that polymicrobial respiratory tract infections are common in this population. A virus was identified in 61.3% of 349 respiratory specimens from children with confirmed or suspected ARTI. HRV (27.5%), RSV (18.9%), HBoV (8.3%), hMPV (7.7%), and PIV (6.6%) were the most common viruses detected. A viral coinfection was identified in 21.5% of the 214 virus-positive specimens and was most often detected for Ad (53.3% of 15 Ad-positive specimens), HBoV (51.7% of 29 HBoV-positive specimens), PIV (43.5% of 23 PIV-positive specimens), HRV (35.4% of 96 HRV-positive specimens), and RSV (34.8% of 66 RSV-positive specimens). Among the 46 specimens with dual or triple viral coinfections detected, the most frequent virusvirus combination was HRV-RSV (n=12).

We hypothesized that certain host-specific risk factors were associated with the likelihood of viral coinfection. While none of the covariates in the final model were significant, the results were suggestive. Male gender (OR 1.70, 95% CI 0.83-3.46), age between 6 months to 1 year (as compared to children less than 6 months old, OR 2.15, 95% CI 0.75-6.19), and history of any chronic condition that may result in immunosuppression (OR 2.05, 95% CI 0.99-4.23) were each associated with increased odds of viral coinfection ($p > 0.05$).

We also hypothesized that children with coinfections would be more likely to have severe ARTI. Children with viral-bacterial coinfection, as compared to children with viral mono-infection, were more likely to be admitted to an intensive care unit (OR 5.58, 95% CI 1.95-15.96) even after controlling for age, history of prematurity, urban/rural residence, and leukocytosis.

This study will inform medical and public health professionals with regard to the epidemiology of mixed infections and their potential importance as a cause of severe acute respiratory tract infection in children. Furthermore, results of this study could contribute to the ongoing discussion of the importance of diagnostic ability to reliably detect multiple concurrent pathogens in a single patient.

Abstract Approved:

Thesis Supervisor

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Graduate College The University of Iowa Iowa City, Iowa

CERTIFICATE OF APPROVAL

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PH.D. THESIS

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This is to certify that the Ph.D. thesis of

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ABSTRACT

Pediatric acute respiratory tract infections (ARTIs) are a leading cause of morbidity and mortality. The objectives of this study were to describe the epidemiology of polymicrobial ARTI in a hospital-based pediatric population and to investigate the association of polymicrobial infection and severity of illness.

We conducted a retrospective study of 559 archived respiratory specimens from 421 children under the age of 10 years collected from March 28, 2008 through June 30, 2009 and stored by the University of Iowa Hospital and Clinics Clinical Microbiology Laboratory. Specimens were tested by direct immunofluorescent assay and/or viral culture at the time of collection (influenza A and B, parainfluenza [PIV] 1-3, respiratory syncytial virus [RSV], adenovirus [Ad]) and uniformly by RT-PCR (human metapneumovirus [hMPV], rhinovirus [HRV], human bocavirus [HBoV]) and PCR (Ad) for the current study. Demographic and clinical data were abstracted from electronic medical records.

Results from this study suggest that polymicrobial respiratory tract infections are common in this population. A virus was identified in 61.3% of 349 respiratory specimens from children with confirmed or suspected ARTI. HRV (27.5%), RSV (18.9%), HBoV (8.3%), hMPV (7.7%), and PIV (6.6%) were the most common viruses detected. A viral coinfection was identified in 21.5% of the 214 virus-positive specimens and was most often detected for Ad (53.3% of 15 Ad-positive specimens), HBoV (51.7% of 29 HBoV-positive specimens), PIV (43.5% of 23 PIV-positive specimens), HRV (35.4% of 96 HRV-positive specimens), and RSV (34.8% of 66 RSV-positive specimens). Among the 46 specimens with dual or triple viral coinfections detected, the most frequent virusvirus combination was HRV-RSV (n=12).

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We hypothesized that certain host-specific risk factors were associated with the likelihood of viral coinfection. While none of the covariates in the final model were significant, the results were suggestive. Male gender (OR 1.70, 95% CI 0.83-3.46), age between 6 months to 1 year (as compared to children less than 6 months old, OR 2.15, 95% CI 0.75-6.19), and history of any chronic condition that may result in immunosuppression (OR 2.05, 95% CI 0.99-4.23) were each associated with increased odds of viral coinfection ($p > 0.05$).

We also hypothesized that children with coinfections would be more likely to have severe ARTI. Children with viral-bacterial coinfection, as compared to children with viral mono-infection, were more likely to be admitted to an intensive care unit (OR 5.58, 95% CI 1.95-15.96) even after controlling for age, history of prematurity, urban/rural residence, and leukocytosis.

This study will inform medical and public health professionals with regard to the epidemiology of mixed infections and their potential importance as a cause of severe acute respiratory tract infection in children. Furthermore, results of this study could contribute to the ongoing discussion of the importance of diagnostic ability to reliably detect multiple concurrent pathogens in a single patient.

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CHAPTER 1 – INTRODUCTION

Acute respiratory tract infections (ARTIs) account for an estimated 75% of all acute morbidities and are the leading cause of hospitalization for infants and young children in developed countries [1]. Viral pathogens are the most common cause of ARTIs. A number of viruses have been identified as being causally associated with ARTIs, including influenza virus, parainfluenza virus (PIV), respiratory syncytial virus (RSV), adenovirus (Ad), and human rhinovirus (HRV). Additionally, the importance of newly recognized viruses such as human metapneumovirus (hMPV), human bocavirus (HBoV), coronaviruses (CoV), and human polyomaviruses (PyV) in the development of ARTIs is becoming increasingly evident. However, the relative importance of mixed infections, sometimes termed polymicrobial infections, has yet to be determined and constitutes an area of active research. The use of molecular detection techniques has more readily allowed for the simultaneous detection of pathogens in respiratory specimens though few studies have attempted to systematically address the clinical importance of polymicrobial infections [2-21]. Furthermore, the interpretation of the results from these studies is complicated by the numerous differences in study design including, but not limited to, the methods of pathogen detection, the composition of the respiratory pathogen panel included in analysis, and the specific population under review. However, results from recent studies suggest a role for mixed infections as a cause of severe viral ARTIs whereby multiple pathogens may act in synergy to increase the severity of illness (e.g., increased likelihood of hospitalization or more severe clinical manifestations) [3, 4, 7, 8, 11, 13, 17, 22-24].

The primary objectives of this study were to describe the epidemiology of polymicrobial ARTI in children and to investigate the association of polymicrobial infection and severity of illness, with an emphasis on mixed infections that include rhinoviruses, adenoviruses, or human bocavirus. Rhinovirus, adenovirus, and human bocavirus are pathogens for which it has been postulated that mixed infections may lead to increased severity of illness perhaps through an aggravation of symptoms caused by another virus or as helper viruses which enhance the virulence of other pathogens [18, 25-28]. Hence, the current study focused primarily on polymicrobial infections involving these three pathogens. The central hypothesis of the study was that among children with ARTI, those who were coinfected with rhinovirus, adenovirus, or human bocavirus and another pathogen were more likely to be hospitalized than those individuals with single pathogen infections. This hypothesis was addressed by the following specific aims:

Aim 1: To estimate the prevalence of polymicrobial infections associated with acute respiratory tract infection in children and to provide descriptive statistics regarding the epidemiologic and clinical significance of virusspecific mono-infection and coinfection.

Aim 2: To identify host risk factors associated with polymicrobial respiratory infections in children. We hypothesized that certain demographic and clinical covariates were associated with multiple pathogen infections.

Aim 3: To investigate the association of polymicrobial infections, particularly mixed infections involving rhinoviruses, adenoviruses, and/or human bocavirus, with severe acute respiratory tract infection in children. We hypothesized that children who were coinfected with rhinovirus, adenovirus, or human bocavirus and another pathogen were more likely to be hospitalized than those individuals with single pathogen infections.

In order to address these aims, we conducted a retrospective study of archived respiratory specimens from children under the age of 10 years collected between March 28, 2008 and June 30, 2009 and stored by the University of Iowa Hospitals and Clinics Clinical Microbiology Laboratory. The population included inpatients and outpatients. Biologic specimens were linked to the patient medical record in order to conduct in-depth analyses utilizing demographic and clinical covariates. Unlike many of its predecessors, this study was designed with an *a priori* hypothesis in mind concerning a role for coinfections in severe ARTI. A subset of the studies which detected no association between coinfection and illness severity likely were not sufficiently powered to detect an association if one truly existed. Furthermore, few studies controlled for potential confounders, and to our knowledge, none have explored the role of potential effect modifiers.

This study will inform medical and public health professionals with regard to the epidemiology of polymicrobial infections and their potential importance as a cause of severe acute respiratory tract infection in children, thus possibly contributing to the long-term goal of reduced mortality and morbidity associated with ARTI in children. Furthermore, the results of this study may contribute to the ongoing discussion of the importance of diagnostic ability to reliably detect multiple concurrent pathogens in a single patient.

CHAPTER 2 – BACKGROUND AND SIGNFICANCE

2.1 Pediatric acute respiratory tract infections

ARTIs account for an estimated 75% of all acute morbidities and are the leading cause of hospitalization for infants and young children in developed countries [1]. Furthermore, ARTIs are a major cause of death in developing nations [1]. Upper respiratory tract infections such as rhinitis and pharyngitis are among the most common childhood infections, with infants and young children becoming infected on average three to eight times per year [1]. The CDC estimates that between 12 and 32 million upper respiratory tract infections (URTIs) occur annually in children aged 1 to 2 years [29]. Furthermore, these infections can lead to complications such as acute asthma exacerbation, acute otitis media, and lower respiratory tract infections (LRTIs) like bronchitis and pneumonia [1].

Viral pathogens are the most common cause of ARTIs. A number of viruses have been identified as being causally related to ARTIs, including influenza virus, PIV, RSV, Ad, and HRV; newly identified viruses of the respiratory tract such as hMPV, CoV, PyV, and HBoV are being discovered with increasing frequency with the aid of molecular detection techniques [4]. However, the relative importance of mixed infections, sometimes termed polymicrobial infections, has been rarely studied. Results from recent studies emphasize the potential clinical importance of mixed infections as a cause of severe viral ARTIs suggesting that perhaps multiple pathogens may act in synergy to increase the severity of illness [8, 22, 23].

2.2 The importance of polymicrobial infections

The arrival of molecular methods in the biomedical sciences has given investigators the ability to detect polymicrobial infections with increasing ease. However, little is known about the clinical significance of these infections compared to single pathogen infections.

Polymicrobial infections (also known as complex infections, mixed infections, secondary infections, and coinfections) are defined as acute and chronic infections caused by various combinations of viruses, bacteria, fungi, and parasites [22]. Generally, these infections arise when one microorganism creates a niche for or predisposes the host to colonization by other pathogens [22]. More recently, an antagonistic association known as microbial interference, characterized by the generation of a niche in the host that suppresses colonization by other organisms, has been recognized as a potential mechanism of polymicrobial interaction [2].

In a review of prospective epidemiologic studies of community-acquired respiratory virus infections conducted between 1991 and 1995 at Baylor College of Medicine, Drews et al. examined charts for evidence of dual respiratory virus infection (DRVI) [8]. DRVIs were identified as the etiologic cause of 5% of acute respiratory virus infections in patients ranging from less than 1 year to 79 years of age. Of those patients with DRVIs, 42% percent were aged four years or less and 58% had underlying chronic lung disease. In this study, DRVIs were associated with upper and lower respiratory tract infections as well as exacerbations of asthma or chronic obstructive pulmonary disease (COPD). Influenza virus A and picornaviruses such as HRV were the most commonly detected pathogens in coinfections. Patients with DRVI were significantly more likely to be hospitalized than patients with a single virus infection (46.3% and

21.7%, respectively). The studies under review utilized various diagnostic tests including cell culture alone (n=2), cell culture with serology (n=4), and cell culture with serology and PCR (n=2). Not surprisingly, studies which used multiple diagnostic methods more frequently detected viral coinfections.

In a recent study, Bonzel et al. identified viral coinfection in 16.1% of children hospitalized with ARTI using real-time PCR to detect 12 respiratory viruses [4]. RSV was the most frequently detected virus (44.1%) followed by HBoV (19.3%) and HRV (6.7%). RSV-HBoV coinfection was the most frequent combination detected. Viral coinfection was found in 17% of children with bronchitis, 23% of children with bronchiolitis, and 33% of children with pneumonia. The investigators detected a weakly significant association between viral coinfection and more severe manifestation of disease.

The elucidation of the epidemiologic and clinical importance of mixed respiratory infections has become an area of active research in recent years. Coinfection rates vary widely among these studies and are estimated to account for 8.4% to 36.1% of ARTIs for which at least one virus was detected [3, 4, 6, 7, 9, 14-16, 19, 20]. Results from some studies suggest that children infected with 2 or more viruses do not have more severe clinical illness than children infected with only one virus [6, 9, 10, 12, 14]. However, results from other studies have suggested an association between respiratory coinfections and severe illness [3, 4, 7, 11, 13, 17, 20, 24]. In a study of community-acquired pneumonia in children less than 3 years of age, Cilla et al. detected at least one virus in 66.9% of specimens [7]. Of these virus-positive specimens, viral coinfections were detected in 27%. Furthermore, age and viral coinfection were shown to be independent risk factors for hospitalization. In a study of pediatric patients with LRTIs, Bharaj et al. detected at least one virus in 35.2% of specimens and mixed

infections in 18.8% of the virus-positive specimens [3]. A high proportion of children with mixed infections had severe or very severe acute LRTI. Few studies have included both viral and bacterial pathogens when assessing the presence of coinfections [11, 17, 30, 31]. Among these, studies by Jennings et al. and Templeton et al. have suggested increased severity in subjects with mixed virus-bacteria pneumonia [11, 17]. The remaining two studies detected no association.

As evidenced by the above studies, a wide range of coinfection rates have been reported in the literature. This may be due to multiple factors including differences in patient population (e.g., age range, hospital or community source, inclusion or exclusion of comorbidities), timing of the study (e.g., season), diagnostic methods used (e.g., cell culture versus PCR), and pathogens under review (e.g., viral and/or bacterial, inclusion or exclusion of newly recognized agents).

HRV, Ad, and HBoV are pathogens for which it has been postulated that mixed infections may lead to increased severity of illness perhaps through an aggravation of symptoms caused by another virus or as helper viruses which enhance the virulence of other pathogens [18, 25-28]. Each of these pathogens is frequently detected with co-pathogens in respiratory samples from children with ARTIs; however, little is known with regard to the impact of polymicrobial infections on the clinical course of disease.

2.3 Human rhinoviruses

2.3.1 Epidemiology and clinical characteristics

Discovered in the 1950s, human rhinoviruses (HRVs) have long been known for their association with mild upper respiratory disease [1]. To date, over

100 serotypes of HRV, distinguishable by serology or partial viral capsid sequencing, have been identified and grouped into two genetic clusters – HRV A and HRV B. Recently, a novel rhinovirus group (HRV C) has been identified and associated with a broader range of clinical disease than its predecessors, including lower respiratory tract infection [32-47]. Rhinoviruses are estimated to be the cause of 50% to 80% of common colds in the United States and are the most common cause of ARTIs worldwide [45, 48]. The incidence of HRV infection is higher in children than in adults, and almost all children will have experienced at least one HRV infection by the age of two years [49]. In a serological analysis of a prospective cohort of children during their first two years of life, Blomvquist et al. determined that by the age of two years, 91.3% of children in the cohort had rhinovirus-specific antibodies and 79% had confirmed rhinovirus infection as determined by virus detection (methods included observation of CPE in culture and RT-PCR) [50]. HRVs are also a leading cause of asthma and COPD exacerbations [48]. HRV infections are usually characterized by sore throat, nasal congestion, and rhinorrhea; malaise, coughing, and sneezing may also be present [51]. These symptoms are a result of the host's immune response to the virus rather than as a result of the cytopathic effects of the virus. HRVs are most prevalent in early spring and fall in temperate climates, though slight variations in seasonal peaks have been suggested for each of the HRV subgroups [33]. Little is known about the epidemiology of HRV C; however, recent studies suggest that these viruses are frequently detected in patients with other pathogens [47, 52-58], may account for up to half of all rhinovirus-associated hospitalizations [38, 43, 55, 59], and are frequently co-detected in patients with other pathogens.

2.3.2 Potential role in polymicrobial acute respiratory tract infections

Human rhinoviruses are often co-detected with other pathogens, and it has been recognized that HRV infection increases the risk of secondary bacterial infection [26]. Reported coinfection rates involving HRV and at least one additional pathogen vary widely. Recent studies report coinfection rates ranging from 17.7% to 47% [47, 52-58]. Furthermore, some studies suggest that coinfections with HRV lead to more severe disease manifestations [52, 57, 58].

HRV infects epithelial cells which leads to the release of inflammatory mediators by the host immune system such as pro-inflammatory cytokines, vasoactive peptides and chemokines resulting in the migration of leukocytes such as neutrophils, monocytes, and dendritic cells to the site of infection. HRVs have evolved mechanisms to evade the immune system's defenses. HRVs are believed to interfere with the Type I interferon (IFN) pathway, to modulate leukocyte interactions with the receptor ICAM-1, to modulate cytokine production by monocytes, and to target dendritic cells. Each of these mechanisms may result in decreased antiviral activity within the immune system, resulting in increased likelihood of secondary infection [26].

Paradoxically, a role for HRVs in microbial interference has also been postulated. A study by Greer et al. of pediatric inpatients and outpatients noted that although HRV was the most commonly detected pathogen, higher proportions of coinfections were detected for other respiratory viruses including HBoV, RSV, Ad, CoV, human enterovirus (HEV) and PyV [53]. Furthermore, detection of HRV was associated with a consistent pattern of reduced likelihood of coinfection with a number of other viruses. The authors suggest that HRV infection protects its host from infection by other viruses. Other studies have noted similar findings and suggest that the HRV-signaled production of IFNs and

other cytokines causes the cells to enter an antiviral state [60-62]. Further investigation regarding the role of HRV as facilitator and/or inhibitor of secondary infection is warranted.

2.4 Human adenoviruses

2.4.1 Epidemiology and clinical characteristics

Adenoviruses (Ads), first described in the 1950s and 1960s, are doublestranded, non-enveloped DNA viruses belonging to the family *Adenoviridae*. There are 51 recognized serotypes of human Ads which have been classified into six species (A-F) based on DNA homology among other characteristics [63]. Recently, a novel Ad serotype (Ad52, species G) has been described in a patient with gastroenteritis [64]. There is some clinical significance to the division of species as organ specificity and syndromic patterns seem to cluster within species, see Table 1 for associated respiratory syndromes [63]. Serotypes 1 through 5, 7, 14, and 21 most commonly infect the respiratory tract, resulting in a range of symptoms including but not limited to: fever, rhinitis, pharyngitis, cough, bronchiolitis, pneumonia, and acute respiratory distress syndrome. Ad serotypes 1, 2, 3, 5, and 6 are associated with endemic respiratory disease in children, including pharyngitis, bronchitis, croup, and pneumonia; Ad7 is sometimes a cause of fatal pneumonia in children [65]. By the age of two years, most children will have been infected by at least one Ad serotype [65]. The prevalence of adenoviral respiratory infection in children ranges from 2-14% [1]. It has been estimated that as much as 10% to 20% of childhood pneumonias in children under the age of 10 years can be attributed to Ads [65, 66]. The emergence of novel strains of Ad, most recently variants of Ad7, Ad3, and Ad14, have been

associated with outbreaks of respiratory disease in military and civilian populations [67-72].

2.4.2 Potential role in polymicrobial acute respiratory tract infections

As is the case with HRVs, several case reports and studies support the hypothesis that infection with Ad can facilitate secondary infection [18, 25, 27] with reported coinfection rates ranging from 0-77.8% [7, 14, 15, 53, 73-77]. However, the mechanisms by which this occurs require further elucidation. Singh et al. suggest that perhaps this is a result of direct virus-virus interactions, an effect of cohabitating viruses on host cell function, or a result of impaired host immune response [78]. Others suggest that perhaps the reports of severe pneumonia and bronchiolitis are a result of reactivation of latent adenoviral infection of the respiratory tract as a result of infection with another pathogen [79]. Replication-competent adenovirus and adenoviral DNA have been detected in human adenoidal and tonsillar tissue leading investigators to believe that the virus can remain latent in these tissues for years [80, 81]. More recently, Garnett et al. have shown that species C adenoviruses can persist in mucosal lymphocytes and can be reactivated upon stimulation resulting in RNA transcription, DNA replication, and infectious virus production [82, 83].

2.5 Human bocavirus

2.5.1 Epidemiology and clinical characteristics

Human bocavirus (HBoV) is a newly identified, single-stranded DNA virus in the family *Parvoviridae*. HBoV was first described in 2005 in nasopharyngeal aspirates of children with ARTIs and has subsequently been reported in respiratory samples from children worldwide with reported prevalence ranging

from 1.5-18.9% [28, 84]. A number of studies report that HBoV can be detected year-round with peaks in early winter [28, 85]. HBoV infection is most prevalent in children under the age of three years and is believed to be a likely cause of lower respiratory tract infections; however, causality has not been firmly established due to the few number of epidemiologic studies involving a control group without respiratory illness and inability to grow HBoV in cell culture until recently [28, 86]. However, evidence for HBoV virulence and a causal association with ARTI is increasing. Of the four case-control studies conducted to date, all but one detected HBoV more frequently in cases than asymptomatic controls [85, 87-89]. Additionally, a recent study by Don et al. concluded that HBoV is capable of inducing a specific immune response [90]. Furthermore, it was noted that an increasing antibody response was correlated with a decrease in detectable viral genomes. Clinical symptoms most frequently reported in individuals with HBoV infection include cough, rhinorrhea, and fever. The most common diagnoses associated with HBoV infection include upper respiratory tract infection, bronchitis, bronchiolitis, pneumonia, acute wheezing, and exacerbation of asthma [28]. Gastroenteric symptoms have been reported in up to 25% of HBoV-positive individuals, though the role of HBoV as an agent of gastrointestinal illness is heavily debated [91]. Two novel strains (HBoV-2 and HBoV-3) have recently been described in the literature; both strains were first isolated from stool samples and their epidemiologic and clinical importance in ARTI and gastroenteritis are unclear [92-95].

2.5.2 Potential role in polymicrobial acute respiratory tract infections

HBoV is frequently co-detected with other pathogens with co-detection rates ranging from 18% to 90% [28]. A number of hypotheses have been put

forward to explain this high rate of co-detection. One such hypothesis is that HBoV harmlessly persists and is shed for extended periods of time following symptomatic infection; some studies have noted prolonged periods of asymptomatic shedding (up to 4.5 months) following symptomatic illness in immunocompetent children [96-98]. Others believe that HBoV is more intimately associated with pathogenesis and the aggravation of respiratory symptoms caused by either an underlying condition such as asthma or infection by another respiratory pathogen. Some hypothesize that HBoV may act as a helper virus which increases the pathogenesis of other viruses or that HBoV itself requires another virus in order to infect epithelial cells. Manning et al. suggest that it is possible that HBoV increases the severity of RSV and other LRTI-associated viruses [99]. As Fry et al. note, parvoviruses such as HBoV are dependent on host cellular functions for replication and only multiply in cells that are in the process of their own DNA replication. They suggest that perhaps coviral-induced cellular damage results in increased levels of cellular division allowing for the replication of HBoV [87].

Several studies have found no significant clinical findings, such as increased severity of illness, in association with HBoV coinfection [100-103]. However, a few recent studies suggest that there may in fact be clinical significance to HBoV coinfection [13, 23, 87]. Fry et al. noted that more patients with pneumonia associated with HBoV-RSV or HBoV-PIV coinfections had wheezing than did patients with RSV and PIV alone [87]. Through a prospective study of HBoV in children with acute respiratory disease, Esposito et al. concluded that HBoV coinfections had a significantly greater clinical and socioeconomic impact on the children and their households as measured by increased association with LRTI, proportion of patients requiring laboratory tests
and radiographic examinations, and hospitalization rate as compared to children with HBoV infection alone [23].

Until recently, the direct study of HBoV coinfections has been limited by the lack of a permissive cell line [86]. Additional epidemiologic studies are necessary to further elucidate the clinical significance of HBoV coinfection.

2.6 Public health and clinical significance

ARTIs account for an estimated 75% of all acute morbidities and are the leading cause of hospitalization for infants and young children in developed countries [1]. Most ARTIs arise from a viral origin. This study will inform medical and public health professionals with regard to the epidemiology of mixed infections and their potential importance as a cause of severe acute respiratory tract infection in children, thus possibly contributing to the long-term goal of reduced mortality and morbidity associated with ARTI in children. Furthermore, results of this study could contribute to the ongoing discussion of the importance of diagnostic ability to reliably detect multiple concurrent pathogens in a single patient.

Table 1 Select respiratory clinical syndromes associated with adenovirus infections

CHAPTER 3 – RESEARCH DESIGN AND METHODS

3.1 Overview of study design

We conducted a retrospective, cross-sectional study of 559 frozen, archived respiratory specimens from 421 children under the age of 10 years collected from March 28, 2008 through June 30, 2009 and stored by the University of Iowa Hospital and Clinics (UIHC) Clinical Microbiology Laboratory. The population included outpatients and inpatients. In addition to routine testing for viral pathogens conducted by the UIHC laboratory, we (Center for Emerging Infectious Diseases, CEID) also tested these specimens for rhinoviruses, adenoviruses, human bocavirus, and human metapneumovirus by reverse transcription polymerase chain reaction (RT-PCR) or PCR methods followed by agarose gel electrophoresis. Specimens that were positive for HRV, Ad or HBoV were submitted for further analysis, specifically DNA/cDNA nucleotide sequencing to identify genotype and phylogenetic analysis to compare those strains circulating in our population to strains described in the published literature. A respiratory coinfection was defined as a sample with a positive test result for 2 or more pathogens from tests performed by UIHC and/or CEID.

All primary analyses were limited to either confirmed (physician diagnosis) or suspected (physician-documented signs and symptoms) ARTI. Secondary analyses also included a third group of children for whom a concern for ARTI existed but traditional signs and symptoms such as cough and runny nose were not present; for example, a neonate with episodes of oxygen desaturation and a child with episodes of febrile seizure unaccompanied by respiratory symptoms would be included in this latter category. Children for whom a specimen was

submitted but who were eventually diagnosed with a chronic respiratory condition (e.g., laryngomalacia) were excluded from all analyses.

We estimated the period prevalence of polymicrobial infections associated with acute respiratory tract infection in children under the age of 10 years whose samples were submitted to the UIHC Clinical Microbiology Laboratory during the study period (Aim 1).Furthermore, a review of the patient medical record was conducted to obtain relevant demographic and clinical covariates. These data were utilized in statistical analyses and modeling to identify host risk factors associated with polymicrobial respiratory tract infections in our study population (Aim 2). To investigate the association of polymicrobial infections, particularly mixed infections involving HRV, Ad, and HBoV with severe ARTI in children, we conducted additional case-control analyses of the cross-sectional data (Aim 3). Exposure was defined as a positive test result for rhinovirus, adenovirus, or human bocavirus (as performed by CEID) and at least one additional positive result from other tests performed on the specimen by UIHC and/or CEID. A case was defined as a child who was hospitalized at the UIHC between March 28, 2008 and June 30, 2009 as a result of ARTI for whom a respiratory specimen was submitted. Children for whom a respiratory specimen was submitted but who were not hospitalized during this time period as a result of ARTI served as controls. Once again, clinical and demographic data from the patient medical record were utilized in statistical analyses to identify host risk factors, control for potential confounders, and identify effect modifiers associated with severe ARTI and respiratory coinfections. Secondary analyses were conducted to identify associations between ARTI coinfection and other markers of severe infection. Among hospitalized patients, secondary outcomes of interest included intensive care unit admission, length of stay, and requirement for mechanical ventilation.

Among all patients, additional outcomes of interest included requirement for supplemental oxygen, oxygen saturation less than 90%, and use of a bronchodilator.

This study was approved by the University of Iowa Institutional Review Board and was granted a waiver of informed consent and a waiver of HIPAA authorization.

3.2 Clinical respiratory specimens

The Clinical Microbiology Laboratory at the University of Iowa Hospital and Clinics (UIHC) receives specimens for respiratory viral direct antigen assays and/or culture from various clinics, hospital wards, and intensive care units. Most often, respiratory virus specimens are obtained from nasopharyngeal washes, tracheal aspirates, and bronchoalveolar lavage procedures. Occasionally, nasal swabs and other respiratory specimens are submitted. In the year previous to the current study period, approximately 50% of all respiratory specimens submitted to the UIHC Clinical Microbiology Laboratory originated from outpatients. In order to be eligible for this study, the respiratory sample must have originated from a child under the age of 10 years at the time of specimen collection and must have been collected between November 1, 2007 and June 30, 2009. As the UIHC Clinical Microbiology Laboratory stores specimens for a period of 1 year, only specimens collected on or after March 28, 2008 were available for this study. Furthermore, specimens that were not archived were not available for the study. A complete description of eligible, included, and excluded respiratory specimens appears in Chapter 4 (Figure 1). Specimens were transported to the CEID laboratory in dry ice transport containers and stored at -80°C until thawed for nucleic acid extraction procedures.

Respiratory specimens received from the UIHC Clinical Microbiology Laboratory were labeled with patient name, patient medical record number, and laboratory accession number. Patient identifiers were removed and the specimen was blinded according to the following procedure: Upon arrival at the CEID laboratory, specimens were taken to a data coordinator. The data coordinator was not involved in the testing of the specimens. The data coordinator recorded the patient medical record number and the laboratory accession number into a password-protected database file maintained in Microsoft Access. Members of the research team who were charged with molecular testing of the specimens did not have access to this file until all laboratory testing was complete, and then only to link medical record information to the appropriate specimen. Within the database, the data coordinator assigned a 4-digit study ID number (beginning with 0001) to each specimen. The data coordinator removed the original label from the specimen, and the specimen was re-labeled using the 4-digit study ID number. Specimen labels with patient identifiers were destroyed.

3.3 Clinical data

3.3.1 Description

UIHC Clinical Microbiology Laboratory specimens were labeled with a laboratory accession number and patient medical record number. These identification numbers were retained by the investigator and were linked to patient medical record data via the Epic electronic medical record system. These data were used to generate descriptive statistics for virus-specific monoinfections and coinfections (Aim 1), for risk factor analyses (Aim 2), and for the

control of potential confounders and identification of effect modifiers in multivariate models (Aim 3).

A database containing the following demographic variables was requested from the university's Health Care Information Systems (HCIS) specialists: patient gender, date of birth, date of death if applicable, race/ethnicity, and zip code of primary residence.

Due to time constraints and a significant delay in receiving data from HCIS, the following clinical covariates were abstracted from the patient's medical record by the principal investigator: clinic source for specimen, date of specimen collection, clinical signs and symptoms, clinical diagnosis, hospital admission and discharge dates if applicable, ICU admission and discharge dates if applicable, date and cause of death if applicable, laboratory results regarding other pathogens detected in specimens collected during illness (viral, bacterial, and fungal), current or recent use of antimicrobials, vaccination history, exposure to second-hand tobacco smoke, history of chronic respiratory conditions, history of chronic medical conditions that may lead to immunosuppression, related hospital visits (inpatient or outpatient), requirement for mechanical ventilation, requirement for supplemental oxygen, bronchodilator use, vitals associated with infection of interest (e.g., oxygen saturation), white blood cell count at time of visit (if available), C-reactive protein level at time of visit (if available), and payor (insurance coverage).

The following laboratory covariates were provided by the UIHC Clinical Microbiology Laboratory: patient medical record number, specimen accession number, date specimen received, specimen source (e.g., nasopharyngeal wash), and results from viral antigen testing and/or culture.

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3.3.2 Coding of clinical data

 A complete list of clinical variables included in this study, the source of the variable, and a description of how variables were coded can be found in Table 2.

3.4 Specimen processing

3.4.1 UIHC Clinical Microbiology Laboratory procedures

The Clinical Microbiology Laboratory routine respiratory virus culture procedure involved inoculating supernatant fluid from processed specimens into two R-Mix Too shell vials (mixed cell line of A549/MDCK). These vials were then centrifuged for 1 hour and incubated for 48 hours at 37°C. The cover slip of one shell vial was fixed and stained by immunofluorescence (IF) using a pooled reagent for influenza A and B, parainfluenza 1, 2, and 3, adenovirus, and respiratory syncytial virus. A positive pooled result was followed by staining for individual respiratory viruses. Cells were stained independent of the presence of CPE. If CPE was observed, but the IF stain was negative, then the specimen was re-inoculated and evaluated for other viruses routinely cultured in the laboratory. A 1-2 ml aliquot of remaining processed specimen was diluted with an equal amount of 20% MEM and stored in cryovials at -80°C.

Direct IF antibody stains (DFAs) are performed directly on patient specimens and may be ordered for single viruses or the full respiratory virus panel. Because DFA is less sensitive than culture, specimens with negative DFA results were submitted for virus culture. If the DFA was positive, culture was not performed. Furthermore, if a specimen is submitted out of season for viral culture, DFA would not normally be completed.

3.4.2 CEID procedures

3.4.2.1 Overview of Molecular Methods. Ad PCR and HRV, HBoV and hMPV RT-PCRs were performed at the CEID laboratory. Even though a specific hypothesis regarding hMPV coinfection was not included in this study, the virus was included in molecular analyses for completeness of data regarding coinfections as hMPV is recognized as a common viral cause of ARTI in children. At the time of this study, the Clinical Microbiology Lab did not perform routine testing for hMPV.

3.4.2.2 Nucleic acid extraction. The MagMax-96 Total RNA Isolation Kit (Applied Biosystems/Ambion, Austin, TX) and Thermo KingFisher magnetic processor were used to extract viral nucleic acids (both RNA and DNA) from respiratory specimens. Briefly, a guanidinium thiocyanate-based solution rapidly releases viral RNA and DNA while simultaneously inactivating nucleases within the sample (50μl volume). Paramagnetic beads with a nucleic acid binding surface were added to bind nucleic acids. The beads and attached nucleic acids were captured on magnets while proteins, other contaminants, and residual binding solution were washed away. Nucleic acids were eluted in a small volume of elution buffer. Approximately 50μl of total nucleic acid (includes viral and cellular nucleic acid) was stored at -80°C until further processing by PCR.

 3.4.2.3 Two-step reverse transcription polymerase chain reaction (RT-PCR). A two-step RT-PCR was utilized to generate cDNA for all virus-specific RT-PCR assays (includes HRV, HBoV, and hMPV). Random decamers (4.0μl, 50μM) were added to 22.0μl of each sample or control in 0.2ml thin-walled PCR tubes. Samples were then placed in the thermocycler at 80°C for 3 minutes.

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14.0μl of RT reaction mix (containing 7.7μl Gibco UltraPure dH_2O , 4.0μl 10X RT buffer, 0.8μl 25mM dNTP, 0.5μl 40U/μl Ambion RNase inhibitor, and 1.0μl 100U/μl Ambion M-MLV-Reverse Transcriptase per sample) was added to each tube. RT was performed under the following conditions: 44°C for 1 hour, followed by 92°C for 10 minutes and a 4°C holding period.

3.4.2.4 Rhinovirus PCR. Procedures have been adapted from Kiang et al. [104] and Savolainen et al. [105, 106]. A gold standard molecular typing method for human rhinoviruses does not exist. Current classification of HRVs is based on capsid region (VP4/VP2) coding sequences. More recent interest in HRV genetic typing has focused on the 5' noncoding region (NCR) which possesses relatively conserved areas that allow for broad-spectrum primer design. Genotyping results from different regions do not always agree. Piralla et al. compared the methods of Kiang et al. (5' NCR) and Savolainen et al. (VP4/VP2) side-by-side and showed that (1) the 5' NCR method showed greater sensitivity allowing strains not typeable by the VP4/VP2 method to be typed, (2) the VP4/VP2 method classified all HRV C strains as belonging to a single homogenous group, and (3) the 5' NCR method classified new HRV C stains into four groups (including HRV A), all of which fell into the HRV C group when tested by the VP4/VP2 method. Given our interest in comparing results from this study to previous studies of HRV and HRV C and the frequency with which the methods of Savolainen et al. were used in these studies, we decided to test all clinical samples by the VP4/VP2 method first, followed by typing of all HRVpositive samples by the 5' NCR method.

The first strand cDNA generated by the RT step described above was used as the template for HRV PCR. A clinical isolate of HRV A was used as a positive control.

PCR was performed using primer pair 9895-forward (5'-GGG ACC AAC TAC TTT GGG TGT CCG TGT-3') and 9565-reverse (5'-GCA TCI GGY ARY TTC CAC CAC CAN CC-3') generating a product of 549 bp spanning the hypervariable region of the 5' NCR, the entire VP4 gene, and the 5' terminus of the VP2 gene [106]. Briefly, 5μl of the first strand cDNA produced during RT was added to 45.0μl PCR master mix (containing 37.2 μl Gibco UltraPure dH_2O , 5.0μl Invitrogen 10X PCR Buffer minus Mg, 0.4 μ l 25mM dNTP, 1.5 μ l 50mM MgCl₂, 0.2μl each of 50mM forward and reverse primers, and 0.5μl 5U/μl Invitrogen Platinum Taq DNA polymerase per sample). PCR was performed under the following conditions: 94°C for 5 minutes, followed by 40 cycles of 94°C for 15 seconds, 60°C for 15 seconds, and 72°C for 30 seconds. PCR products were visualized on an ethidium bromide-stained 1% agarose gel, and positive samples were submitted for cDNA nucleotide sequencing and phylogenetic analysis to determine genotype.

For all HRV-positive specimens, a second PCR was performed using forward primer DK001 (5'-CAA GCA CTT CTG TTT CCC-3') and reverse primer DK004 (5'-CAC GGA CAC CCA AAG TAG T-3') generating a product of 390 bp spanning approximately two-thirds of the 5' NCR [104]. Briefly, 5μl of the first strand cDNA produced during RT was added to 45.0μl PCR master mix (containing 37.2 μl Gibco UltraPure dH₂O, 5.0μl Invitrogen 10X PCR Buffer minus Mg, 0.4μl 25mM dNTP, 1.5μl 50mM MgCl₂, 0.2μl each of 50mM forward and reverse primers, and 0.5μl 5U/μl Invitrogen Platinum Taq DNA polymerase per sample). PCR was performed under the following conditions: 95°C for 5

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minutes, followed by 40 cycles of 95°C for 15 seconds, 55°C for 15 seconds, and 72°C for 30 seconds. PCR products were visualized on an ethidium bromidestained 1% agarose gel, and positive samples were submitted for cDNA nucleotide sequencing and phylogenetic analysis to determine genotype.

 3.4.2.5 Human bocavirus PCR. Procedures have been adapted from Sloots et al. [107]. The first strand cDNA generated by the RT step described above was used as the template for the HBoV PCR. A plasmid containing partial NS1 and NP-1 genes corresponding to nucleotide numbers 1394 to 2691 of HBoV strain st1 was used as a positive control (kindly provided by Dr. Dean Erdman, CDC).

PCR was performed using primer pair HBoV01.2 (5'-TAT GGC CAA GGC AAT CGT CCA AG-3') and HBoV02.2 (5'- GCC GCG TGA ACA TGA GAA ACA GA-3') generating a product of 266 bp spanning the NS1 gene. Briefly, 5μl of the first strand cDNA produced during RT was added to 45.0μl PCR master mix (containing 37.2 μl Gibco UltraPure dH₂O, 5.0μl Invitrogen 10X PCR Buffer minus Mg, 0.4 μl 25mM dNTP, 1.5μl 50mM MgCl₂, 0.2 μl each of 50mM forward and reverse primers, and 0.5μl 5U/μl Invitrogen Platinum Taq DNA polymerase per sample). PCR was performed under the following conditions: 94°C for 1 minute, followed by 45 cycles of 94°C for 20 seconds, 56°C for 20 seconds, and 72°C for 30 seconds; and a single cycle at 72°C for 5 minutes. PCR products were visualized on an ethidium bromide-stained 1% agarose gel, and positive samples were submitted for cDNA nucleotide sequencing and phylogenetic analysis.

3.4.2.6 Human metapneumovirus PCR. Procedures have been adapted from Gray et al. [108]. The first strand cDNA generated by the RT step described above was used as the template for the HBoV PCR. A clinical isolate of hMPV was used as a positive control.

PCR was performed using primer pair F2 forward (5'-GAG CAA ATT GAA AAT CCC AGA CA-3') and F2 reverse (5'-GAA AAC TGC CGC ACA ACA TTT AG-3') generating a product of 347 bp spanning the F2 gene [109]. Briefly, 5μl of the first strand cDNA produced during RT was added to 45.0μl PCR master mix (containing 37.2 μl Gibco UltraPure dH₂O, 5.0μl Invitrogen 10X PCR Buffer minus Mg, 0.4 μl 25mM dNTP, 1.5μl 50mM MgCl₂, 0.2 μl each of 50mM forward and reverse primers, and 0.5μl 5U/μl Invitrogen Platinum Taq DNA polymerase per sample). PCR was performed under the following conditions: 95°C for 2 minutes, followed by 34 cycles of 94°C for 30 seconds, 52°C for 30 seconds, and 72°C for 1 minute; and a single cycle at 72°C for 10 minutes. PCR products were visualized on an ethidium bromide-stained 1% agarose gel. hMPV-positive samples were not submitted for sequencing.

3.4.2.7 Adenovirus PCR. Procedures have been adapted from Lu et al. [110]. A clinical isolate of human Ad5 was used as a positive control. As molecular methods are considered to be more sensitive than DFA procedures for the detection of adenoviruses [1, 6], the results of the adenovirus PCR assay superseded the results of the DFA assay and viral culture performed by the UIHC Clinical Microbiology Laboratory. A comparison of the results of these methods was included in our analysis.

PCR was performed on an initial sample of 5μl using primer pair AdhexF1 (5'-TIC TTT GAC ATI CGI GGI GTI CTI GA-3') and AdhexR1 (5'-CTG TCI ACI

GCC TGR TTC CAC A-3') generating a product of 764 to 896 bp spanning the hypervariable regions 1-6 of the hexon gene [110]. Briefly, 5μl of the eluted sample was added to 45.0μl PCR master mix (containing 37.2 μl Gibco UltraPure dH2O, 5.0μl Invitrogen 10X PCR Buffer minus Mg, 0.4μl 25mM dNTP, 1.5μl 50mM MgCl₂, 0.2μl each of 50mM forward and reverse primers, and 0.5μl 5U/μl Invitrogen Platinum Taq DNA polymerase per sample). PCR was performed under the following conditions: 94°C for 2 minutes, followed by 34 cycles of 94°C for 30 seconds, 50°C for 30 seconds, and 72°C for 1 minute, followed by one cycle 72°C for 5 minutes. M13 universal priming tails (forward, 5'-TGT AAA ACG ACG GCC AGT-3'; and reverse, 5'-CAG GAA ACA GCT ATG ACC-3') have been added to the previously described primers to facilitate sequencing. PCR products were visualized on an ethidium bromide-stained 1% agarose gel, and positive samples were submitted for DNA nucleotide sequencing to determine genotype.

3.4.2.8 DNA/cDNA sequencing. The University of Iowa's DNA Core Facility houses an Applied Biosystems Model 3730xl (96-capillary) DNA sequencer and offers DNA sequencing on a fee-for-service basis to investigators. The forward and reverse sequences were combined using BioEdit software (Ibis Therapeutics) and were compared with nucleotide sequences submitted to NCBI GenBank. Specimens that yielded identity scores of ≥ 90% were considered good genotypic matches.

3.4.2.9 Phylogenetic analyses. Amplified nucleotide sequences were aligned and neighbor-joining phylogenetic trees were generated using a maximum composite likelihood method. Bootstrap analysis was completed using 1000 repetitions. Alignment and phylogenetic analyses were performed using Mega 4.0 software [111].

3.5 Power calculations

Power calculations were based upon Specific Aim 3: To investigate the association of mixed infections, particularly mixed infections involving rhinoviruses, adenoviruses, or human bocavirus, with severe acute respiratory tract infection in children.

Severity of acute respiratory tract infection was defined as a categorical variable (outpatient/control or inpatient/case). Note that the probability of coinfection was based upon virus-specific prevalence and coinfection estimates (rhinovirus – 50% prevalence, 25% coinfection rate; adenovirus – 10% prevalence, 25% coinfection rate; human bocavirus - 10% prevalence, 75% coinfection rate) and the assumption that 30% of patients with single pathogen infections were inpatients.

Although we adjusted for several covariates in many of our analyses, here we considered the theoretical power of a simple comparison of two groups. The sample size needed to have 80% power to detect an unadjusted 4.0 odds ratio of hospitalization (among subjects with mixed pathogen acute respiratory tract infection when compared to subjects with single pathogen acute respiratory tract infection) was determined to be 300-1000 subjects (varied by virus).

Under Aim 3, due to time constraints for specimen collection and processing, we were only able to achieve a sufficient sample size to address HRV coinfections.

3.6 Statistical analyses

3.6.1 Specific aim 1

To estimate the prevalence of polymicrobial infections associated with acute respiratory tract infection in children and to provide descriptive statistics regarding the epidemiologic and clinical significance of virus-specific monoinfection and coinfection.

Period prevalence and 95% binomial confidence intervals were calculated for the following: infection with HRV, HBoV, Ad, hMPV, influenza A, influenza B, PIV 1-3, and RSV and coinfection. Coinfection was defined as a sample with a positive test result for 2 or more respiratory viruses from tests performed by UIHC and/or CEID. Though other viral, bacterial, and fungal microbiology results may have been available for an included episode of ARTI, since these tests were not performed on the same specimen as was viral culture, viral antigen detection, or viral PCR, they were not included in the primary analysis for this aim. However, information regarding the frequency of these other infections was included in secondary descriptive analyses.

The prevalence of selected demographic, clinical, and laboratory variables was also determined for all samples (virus-positive or -negative), virus-specific mono-infections, and all coinfections. Similar descriptive statistics were alslo generated for HRV-positive mono-infections and coinfections stratified by HRV group.

3.6.2 Specific aim 2

To identify host risk factors associated with polymicrobial respiratory infections in children. We hypothesized that certain demographic and clinical covariates were associated with multiple pathogen infections.

This analysis was conducted for (1) all coinfections and (2) HRV-positive coinfections. Analyses were limited to either confirmed (physician diagnosis) or suspected (physician-documented signs and symptoms) ARTI and were further limited to the first specimen collected from the first ARTI episode per individual (excludes duplicates). Secondary analyses also included a third group of children for whom a concern for ARTI existed but traditional signs and symptoms such as cough and runny nose were not present. Children for whom a specimen was submitted but who were eventually diagnosed with a chronic respiratory condition (e.g., laryngomalacia) were excluded from all analyses. Furthermore, to be included in analysis, a specimen must have been positive for at least one virus. We excluded specimens from individuals for whom medical record abstraction was not possible.

Univariate descriptive statistics were calculated for categorical (frequency, percent) and continuous (mean, standard deviation, maximum and minimum values) variables. Continuous variables (i.e., age) were re-classified as categorical variables where a linear effect was not considered biologically plausible. Bivariate analyses such as Pearson's chi-square test, Fisher's exact test, and bivariate logistic regression were used to examine potential risk factor associations with the respiratory coinfection.

The following variables were included in the analysis: patient gender, age, race/ethnicity, rural or urban residence as determined by zip code, exposure to second-hand tobacco smoke (when available), history of chronic respiratory conditions, history of chronic medical conditions that may lead to immunosuppression, and payor (insurance coverage).

Beginning with a saturated model, manual backwards elimination and multivariate logistic regression modeling were used to identify the model that best

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predicted the occurrence of polymicrobial infections in this population. Variables were kept in the model if the corresponding parameter estimate was significant at p<0.2. Nested models were compared using the likelihood ratio test. If the difference in the maximum likelihood estimate was significant (p<0.05) then we concluded that the full model provided a better fit to the data than the reduced model. Otherwise, if the difference in the maximum likelihood estimate was not significant, we continued with the reduced model.

3.6.3 Specific aim 3

To investigate the association of polymicrobial infections with severe acute respiratory tract infection in children. We hypothesized that children who were coinfected with more than one pathogen were more likely to be hospitalized than those individuals with single pathogen infections. Analyses were conducted separately for all coinfections and for rhinovirus-positive coinfections.

Analyses were limited to either confirmed (physician diagnosis) or suspected (physician-documented signs and symptoms) ARTI and were further limited to the first specimen collected from the first ARTI episode per individual (excludes duplicates). Secondary analyses also included a third group of children for whom a concern for ARTI existed but traditional signs and symptoms such as cough and runny nose were not present. Children for whom a specimen was submitted but who were eventually diagnosed with a chronic respiratory condition (e.g., laryngomalacia) were excluded from all analyses. Furthermore, to be included in analysis, a specimen must have been positive for at least one virus. We excluded specimens from individuals for whom medical record abstraction was not possible.

Severity of acute respiratory tract infection was the outcome of interest and was included as a categorical variable (defined as outpatient or hospitalized). Secondary analyses were conducted to identify associations between ARTI coinfection and other potential indicators of severe infection. Among hospitalized patients, secondary outcomes of interest included intensive care unit admission, number of days hospitalized (required linear regression), and requirement for mechanical ventilation. Among all patients, additional outcomes of interest included requirement for supplemental oxygen, oxygen saturation less than 90%, and use of a bronchodilator.

The exposures of interest were presence of any respiratory coinfection or presence of an HRV-positive coinfection. Subjects with an acute respiratory tract infection caused by a single pathogen were considered unexposed for the purpose of analysis. Secondary analyses of virus-bacteria coinfections were limited to children with confirmed or suspected ARTI for whom (1) any bacterial test was ordered or (2) any respiratory bacterial test was ordered (not limited to respiratory culture).

Univariate descriptive statistics were calculated for categorical (frequency, percent) and continuous (mean, standard deviation, maximum and minimum values) variables. Continuous variables (i.e., age) were re-classified as categorical variables where a linear effect was not considered biologically plausible. Bivariate analyses were performed to identify covariates of interest, potential confounders associated either with exposure and outcome, and potential effect modifiers. Identified confounders remained in the final model even if the confounder itself was not statistically significant. Bivariate logistic regression was used to determine crude unadjusted odds ratios (and 95% confidence intervals) for hospitalization among exposed as compared to

unexposed. Odds ratios and 95% confidence intervals were adjusted for the effect of potential confounders (identified in the literature or in bivariate analyses) using multivariate logistic regression. The potential for effect modification by history of chronic respiratory disease and history of immunosuppressive condition was also of interest to the investigator; hence, interaction terms including these variables with the exposure variable (coinfection) were included in analyses and remained in the final model if significant. Beginning with a saturated model, manual backwards elimination and multivariate logistic regression modeling was used to decide which of the remaining covariates of interest identified in bivariate analyses, if any, were to be included in the model.

The following variables were included in the analysis: patient gender, age, race/ethnicity, rural or urban residence as determined by zip code, current or recent use of antimicrobials, exposure to second-hand tobacco smoke (when available), history of chronic respiratory conditions, history of chronic medical conditions that may lead to immunosuppression, payor (insurance coverage), white blood cell count, and C-reactive protein levels.

3.7 Quality assurance/quality control

3.7.1 Laboratory analysis

All laboratory tests were performed by trained CEID laboratory personnel with approximately 95% of all laboratory testing completed by the principal investigator. Appropriate positive and negative method (i.e., nucleic acid extraction and PCR) controls were analyzed alongside clinical respiratory specimens. Additionally, nucleic acid extraction and amplification procedures were physically separated into different laboratory suites in order to avoid contamination of clinical specimens by amplicons.

3.7.2 Data analysis

Clinical and demographic data from the patient medical record were checked for completeness and accuracy by the principal investigator using SAS v9.2. Incomplete, missing, or erroneous data were corrected following further review of the patient medical record by the principal investigator.

Table 2 Clinical covariates abstracted from the medical record

Table 2 Continued

Note: HCIS (Health Care Information Systems), MR (Medical Record), H&P (History and Physical)

CHAPTER 4 – RESULTS

4.1 Overview of specimen population

We conducted a retrospective study of 559 archived respiratory specimens from children under the age of 10 years collected from March 28, 2008 through June 30, 2009 and stored by the University of Iowa Hospital and Clinics Clinical Microbiology Laboratory. Primary analysis was limited to the first specimen collected from the first ARTI episode per child during the study period thereby excluding duplicates (n=421), specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI (n=349), and to children with accessible medical records (n=346). Details regarding the number of eligible, included, and excluded respiratory specimens appear in Figure 1.

Not all respiratory specimens collected from children less than 10 years of age from the study period were archived and available for study. A total of 116 specimens were unavailable for the following reasons – 39 virus-negative specimens had no remaining volume to archive following routine UIHC testing, 75 virus-positive specimens were not archived at the discretion of the laboratory technician, and 2 virus-positive specimens were set aside for validation of inhouse diagnostic assays. These 116 specimens represented 105 unique individuals and 100 children with accessible medical records.

Additional data from all 559 included specimens (with duplicates) and all 116 unavailable specimens (with duplicates) appears in the Appendix.

4.2 Specific aim 1

4.2.1 Virus-specific mono-infection and co-infection prevalence estimates

 A virus was identified in 56.3% of the 421 respiratory specimens arising from unique individuals (no duplicates) (Table 3). The most prevalent respiratory viruses were HRV (24.5%), RSV (18.5%), HBoV (7.6%), hMPV (6.7%), and all PIV (6.2%), which include PIV 1-3 and PIV not otherwise specified. Of the 103 HRV-positive specimens, HRV A was the most common group detected (45.6%) followed by HRV C (41.8%), and HRV B (0.9%). Non-typeable HRVs represented 11.7% of the HRV-positive specimens. A coinfection was identified in 21.1% of the 237 virus-positive specimens. Coinfections were detected more often for Ad (53.3% of 15 Ad-positive specimens), HBoV (50.0% of 32 HBoVpositive specimens), all PIV (42.3% of 26 PIV-positive specimens), HRV (34.9% of 103 HRV-positive specimens), and RSV (34.6% of 78 RSV-positive specimens). Among the 50 specimens with detected coinfections, the most frequent virus-virus combinations (Table 4) were HRV-RSV (n=14), HRV-HBoV (n=6), and HRV-PIV 3 (n=4). Among the 103 HRV-positive specimens, 58.3% of the non-typeable HRV specimens, 36.2% of the HRV A specimens, 27.9% of the HRV C specimens, and the single HRV B specimen were involved in coinfections.

 When limiting the analysis to the 349 respiratory specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, a virus was identified in 61.3% of the specimens (Table 5). HRV (27.5%), RSV (18.9%), HBoV (8.3%), hMPV (7.7%) and all PIV (6.6%) remained the most prevalent viruses detected. Of the 96 HRV-positive specimens, HRV A was the most common group detected (46.3%) followed by HRV C (41.1%), and non-typeable HRVs (12.6%). A coinfection was identified in

21.5% of the 214 virus-positive specimens. Coinfections were again detected more often for Ad (53.3% of 15 Ad-positive specimens), HBoV (51.7% of 29 HBoV-positive specimens), all PIV (43.5% of 23 PIV-positive specimens), HRV (35.4% of 96 HRV-positive specimens), and RSV (34.8% of 66 RSV-positive specimens). Among the 46 specimens with detected coinfections, the most frequent virus-virus combinations (Table 6) were HRV-RSV (n=12), HRV-HBoV (n=6), and HRV-PIV 3 (n=4). Among the 96 HRV-positive specimens, 58.3% of the non-typeable HRV specimens, 36.4% of the HRV A specimens, and 30.8% of the HRV C specimens were involved in coinfections.

 When including specimens from children for whom physicians had a concern for ARTI in the absence of traditional symptoms (n=56) in the analysis alongside confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, a virus was identified in 56.5% of the 405 specimens (Table 7). Of the 103 HRV-positive specimens, HRV A was the most common group detected (46.5%) followed by HRV C (41.6%), and non-typeable HRVs (11.9%). A coinfection was identified in 21.0% of the 229 virus-positive specimens. Coinfections were detected more often for Ad (53.3% of 15 Ad-positive specimens), HBoV (50.0% of 30 HBoV-positive specimens), all PIV (44.0% of 25 PIV-positive specimens), HRV (34.6% of 101 HRV-positive specimens), and RSV (34.2% of 73 RSV-positive specimens). Among the 48 specimens with detected coinfections, the most frequent virus-virus combinations (Table 8) were HRV-RSV (n=13), HRV-HBoV (n=6), and HRV-PIV 3 (n=4). Among the 101 HRVpositive specimens, 58.3% of the non-typeable HRV specimens, 36.2% of the HRV A specimens, and 28.6% of the HRV C specimens were involved in coinfections.

 When examining the 105 specimens from eligible children excluded from study due to an unavailable specimen, a virus was identified in 70.5% of the

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specimens (Table 9). The most prevalent respiratory viruses were RSV (53.3%), all PIV (8.6%), and influenza B (4.8%). A coinfection was identified in 2.7% of the 74 virus-positive specimens. The 2 coinfections detected included RSV-Ad and RSV-PIV 2 (Table 10). The latter part of this study coincided with the emergence of the novel H1N1 (nH1N1) influenza virus; 1 of the excluded specimens was identified as influenza A virus-positive during this time period and was subsequently characterized as nH1N1.

4.2.2 Summary of demographic and clinical characteristics of the study population with accessible medical records

Results presented here are limited to unique individuals (no duplicates) with accessible medical records. Of the 421 unique individuals included in this study, 407 had accessible medical records. Of the 105 eligible individuals excluded due to an unavailable specimen, 100 had accessible medical records. Additional data from (1) all 559 included specimens (with duplicates), (2) children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, (3) children for whom physicians had a concern for ARTI in the absence of traditional symptoms in addition to those with confirmed or suspected ARTI, and (4) all 116 unavailable specimens (with duplicates) appears in the Appendix. Results are comparable to those presented here.

Among the 407 children included in the study, 54.0% were male, 86.2% were under the age of 5 years, 72.9% were Caucasian, 47.8% used Medicaid as the primary payor for medical services, and 60.1% resided in an urban area (Table 11). Among those residing in rural areas, 54.0% used Medicaid as the primary payor; whereas among those residing in urban areas, 44.5% used Medicaid as the primary payor (p=0.061, data not shown). The mean age was 2.07 years (Table 12).

A large proportion of the children were hospitalized (76.9%), and of those that were hospitalized, 36.1% were patients in an intensive care unit at the time of specimen collection (Table 13). Hypoxemia (oxygen saturation less than 90%) was common (33.7% of children). Additionally, 44.5% required supplemental oxygen and 17.0% were mechanically ventilated. A bronchodilator was administered to 28.0% of the children. The median total length of hospitalization was 5.00 days (Table 14). Antimicrobials were frequently administered prior to the UIHC visit (29.7%), any time during the UIHC visit (59.7%), and as takehome prescriptions (26.0%) (Table 15). Data with regard to white blood cell count and C-reactive protein (CRP) levels were missing in a large proportion of individuals (23.3% and 37.1%, respectively); among those with complete information, elevated white blood cell count/leukocytosis (26.0%) and elevated CRP levels (67.2%) were common.

In 46.7% of the children, an ARTI-specific physician diagnosis was identified; respiratory tract infection, pneumonia, and bronchiolitis were common diagnoses (Table 16). Additionally, for 38.3% of the children a physician documented ARTI symptoms, though no ARTI diagnosis code was recorded in the medical record. It is interesting to note that of the 232 virus-positive specimens, 3.5% of the children did not have an acute respiratory tract infection. Common symptoms included fever (54.6%), cough (54.1%), and nasal congestion/runny nose (40.3%) (Table 17). Chronic respiratory conditions were common in this group (35.4%), as were chronic medical conditions that could lead to increased frequency of respiratory infection (29.7%) and history of prematurity (22.4%) (Table 18).

Specimens most often originated from nasal washes (85.8%), and overall, respiratory viruses were most commonly detected in the winter and spring months (January through June) (Table 19).

 Among the 100 children excluded from the study due to unavailable specimens, 60.0% were male, 90.0% were under the age of 5 years, 75.0% were white, and 78.0% resided in an urban area (Table 20). The mean age was 1.64 years (Table 21). Less than half of the children (44.0%) were hospitalized, and of those that were hospitalized, 27.3% were ever patients in an intensive care unit (Table 22). The median total length of stay was 2.00 days (Table 23). Specimens most often originated from nasal washes (84.0%), and overall, respiratory viruses were most commonly detected in the winter and early spring months (January through March) (Table 24).

 Compared to those children for whom specimens were included in the study, children for whom specimens were unavailable were significantly younger (p=0.035), were more likely to reside in an urban area (p=0.009), and were less likely to be admitted to the hospital (p<0.001).

4.2.3 Summary of demographic and clinical characteristics of the HRV-positive study population with accessible medical records

Figure 2 demonstrates the phylogeny of all HRV-positive specimens according to PCR assays utilizing the VP4/VP2 protocol. Figure A1 in the appendix demonstrates the phylogeny according to PCR assays utilizing the 5'NCR protocol. The HRV group data presented here are based upon the VP4/VP2 typing strategy.

Of the 407 unique specimens with accessible medical records, 102 (25.1%) tested positive for HRV; of these 30.4% were characterized as HRV C, 28.2% as HRV A, 0.1% as HRV B, and 3.9% as non-typeable HRVs. Of the 102 HRV-positive specimens, 56.9% were male, 85.3% were under the age of 5 years, 75.0% were white, 46.1% used Medicaid as the primary payor for medical services, and 62.8% resided in an urban area (Table 25). The mean age was 2.07 years (Table 26).

A large proportion of the children were hospitalized (75.5%), and of those that were hospitalized, 24.7% were patients in an intensive care unit at the time of specimen collection (Table 27). Additionally, 35.3% required supplemental oxygen and 33.0% were administered a bronchodilator. Few required mechanical ventilation (7.8%). The median total length of stay was 3.00 days (Table 28). Antimicrobials were frequently administered prior to the UIHC visit (32.4%), any time during the UIHC visit (54.9%), and as take-home prescriptions (30.4%) (Table 29). Data with regard to white blood cell count and C-reactive protein (CRP) levels were missing in a large proportion of individuals (23.3% and 37.1%, respectively); among those with complete information, elevated white blood cell count/leukocytosis (25.7%) and elevated CRP levels (61.8%) were common.

In 52.9% of the children, an ARTI-specific physician diagnosis was identified (Table 30). Additionally, for 40.2% of the children a physician documented ARTI symptoms, though no ARTI diagnosis code was recorded in the medical record. Of the 102 HRV-positive specimens, 2.0% of the children did not have an acute respiratory tract infection. Common symptoms included cough (63.7%), nasal congestion/runny nose (50.0%), fever (46.1%) and wheeze (30.4%) (Table 31). Chronic respiratory conditions were common in this group (46.1%) (Table 32).

Specimens most often originated from nasal washes (88.0%), and overall, HRVs were commonly detected in all seasons, though HRV A was more commonly detected in the spring and summer months whereas HRV C was more commonly detected in the late winter and early spring (Table 33).

 Compared to HRV A-positive specimens, HRV C-positive specimens were less likely to be male (p=0.028), to be Caucasian (p=0.037), to be given antibiotics prior to their first UIHC appointment (p=0.007), and to be admitted to the hospital (0.054). HRV C-positive specimens were more likely to be associated with cough (p=0.053) and wheeze (p=0.007).

4.3 Specific aim 2

4.3.1 Bivariate and multivariate analysis of selected host-specific factors and coinfection among viruspositive specimens with accessible medical records

 Results presented here are limited to analyses using virus-positive specimens with accessible medical record information from unique children (no duplicates) with confirmed (physician diagnosed) or suspected (physiciandocumented symptoms) ARTI (n=212). Results were similar when including a third group of children, those with physician concern for ARTI in the absence of traditional symptoms (data not shown).

 Table 34 details results from bivariate logistic regression models of selected host-specific factors and virus-virus coinfection (versus viral monoinfection). Table 35 provides the final model selected following a backwards elimination strategy beginning with a saturated model. While none of the covariates in the final model are significant at p < 0.05, the results are suggestive. Males were at increased odds of coinfection compared to females (OR 1.70, 95% CI 0.83-3.46). Children aged 6 months to 1 year had increased odds of coinfection as compared to children aged less than 6 months (OR 2.15, 95% CI 0.75-6.19) and the odds of coinfection decreased with increasing age after 1 year though this trend was not statistically significant (p for trend 0.5881). Children with a history of any chronic condition that may result in immunosuppression, and specifically increased risk of ARTI, had increased odds of coinfection as compared to children with no history of such conditions (OR 2.05, 95%CI 0.99-4.23).

4.3.2 Bivariate and multivariate analysis of selected host-specific factors and coinfection among viruspositive specimens with accessible medical records and complete tobacco smoke exposure data

 Results presented here are limited to analyses using virus-positive specimens with accessible medical record information from unique children (no duplicates) with confirmed (physician diagnosed) or suspected (physiciandocumented symptoms) ARTI with complete tobacco smoke exposure (n=96).

 Table 36 details results from bivariate logistic regression models of selected host-specific factors and virus-virus coinfection (versus viral monoinfection). Table 37 provides the final model selected following a backwards elimination strategy beginning with a saturated model. While none of the covariates in the final model are significant at $p < 0.05$, the results are suggestive. Children aged 6 months to 1 year had increased odds of coinfection as compared to children aged less than 6 months (OR 3.27, 95% CI 0.72-14.94) and the odds of coinfection decreased with increasing age after 1 year thought this trend was not statistically significant (p for trend 0.5265). Children with a history of any chronic condition that may result in immunosuppression, and specifically increased risk of ARTI, had increased odds of coinfection as compared to children with no history of such conditions (OR 2.26, 95%CI 0.63- 8.15). Children with direct exposure to tobacco smoke (adults smoke with child present in same room) had increased odds of coinfection as compared to children with no tobacco exposure (OR 4.26, 95% 0.88-20.67).

4.3.3 Bivariate and multivariate analysis of selected host-specific factors and coinfection among HRVpositive specimens with accessible medical records

 Results presented here are limited to analyses using HRV-positive specimens with accessible medical record information from unique children (no duplicates) with confirmed (physician diagnosed) or suspected (physiciandocumented symptoms) ARTI (n=95). Results were similar when including a third group of children, those with physician concern for ARTI in the absence of traditional symptoms (data not shown).

 Table 38 details results from bivariate logistic regression models of selected host-specific factors and HRV-specific coinfection (versus HRV monoinfection). Table 39 provides the final model selected following a backwards elimination strategy beginning with a saturated model. While none of the covariates in the final model are significant at $p < 0.05$, the results are suggestive. Males were at increased odds of HRV coinfection compared to females (OR 1.89, 95% CI 0.71-5.03). Children aged 6 months to 1 year had increased odds of HRV coinfection as compared to children aged less than 6 months (OR 3.70, 95% CI 0.87-15.67), and the odds of HRV coinfection decreased with increasing age after 1 year thought this trend was not statistically significant (p for trend 0.7025). Children residing in large rural areas had increased odds of HRV coinfection as compared to children living in urban areas (OR 3.17, 95% 0.77-13.1), and the odds of HRV coinfection decreased as the rural characterization increased though this trend was not statistically significant (p for trend 0.3864). Children with a history of any chronic condition that may result in immunosuppression, and specifically increased risk of ARTI, had increased odds of HRV coinfection as compared to children with no history of such conditions (OR 2.24, 95%CI 0.81-6.22).

4.4 Specific aim 3

Crude odds ratios for all indicators of severity other than ICU admission (for all coinfections and HRV-specific coinfection) and bronchodilator administration (for HRV-specific coinfection only) were not significant or marginally significant, and multivariate logistic regression models were not generated.

4.4.1 Modeling odds of ICU admission associated with virus-virus coinfection

 Results presented here are limited to analyses using virus-positive specimens with accessible medical record information from unique children (no duplicates) with confirmed (physician diagnosed) or suspected (physiciandocumented symptoms) ARTI who were hospitalized (n=160). Results were similar when including a third group of children, those with physician concern for ARTI in the absence of traditional symptoms (data not shown).

 Table 40 details the results from bivariate logistic regression models of selected factors (potential confounders as identified in the literature or stratified analyses) and odds of virus-virus coinfection (versus viral mono-infection). No significant effect modifiers were identified. Table 41 details the results from bivariate logistic regression models of selected factors (potential confounders as identified in the literature or stratified analyses) and odds of ICU admission. A significant trend was observed for the association between urban/rural residence and ICU admission (p for trend 0.032); as characterization of residence became more rural, the odds of ICU admission decreased. A significant trend was also observed for the association between tobacco smoke exposure and ICU admission (p for trend 0.030); as the degree of tobacco smoke exposure increased so did the risk of ICU admission. History of chronic respiratory

condition and history of immunosuppression did not significantly modify the association between coinfection and ICU admission.

The unadjusted odds ratio for ICU admission associated with virus-virus coinfection was 0.30 (95% CI 0.09-1.04). After controlling for potential confounders, the adjusted odds ratio was 0.32 (0.08-1.27) (Table 42). Male gender (OR 3.11, 95% CI 1.20-8.06), history of any immunosuppressive condition (OR 3.20, 95% CI 1.12-9.17), history of prematurity (OR 5.06, 95% CI 1.61-15.93), and leukocytosis (OR 4.44, 95% CI 1.68-11.74) were significantly associated with increased odds of ICU admission in this population.

4.4.2 Modeling odds of ICU admission associated with HRV coinfection

 Results presented here are limited to analyses using HRV-positive specimens with accessible medical record information from unique children (no duplicates) with confirmed (physician diagnosed) or suspected (physiciandocumented symptoms) ARTI who were hospitalized (n=73). Results were similar when including a third group of children, those with physician concern for ARTI in the absence of traditional symptoms (data not shown).

 Table 43 details the results from bivariate logistic regression models of selected factors (potential confounders as identified in the literature or stratified analyses) and odds of HRV coinfection (versus HRV mono-infection). No significant effect modifiers were identified. Table 44 details the results from bivariate logistic regression models of selected factors (potential confounders as identified in the literature or stratified analyses) and odds of ICU admission. No significant effect modifiers were identified.

The unadjusted odds ratio for ICU admission associated with HRV coinfection was 0.34 (95% CI 0.09-1.33). After controlling for potential confounders, the adjusted odds ratio was 0.51 (0.09-2.80) (Table 45). Rural

residence was significantly associated with decreased odds of ICU admission in this population (OR 0.15, 95% CI 0.03-0.83). History of any immunosuppressive condition (OR 5.48, 95% CI 0.79-38.05), history of prematurity (OR 11.72, 95% CI 0.81-169.35), and leukocytosis (OR 4.84, 95% CI 0.82-28.66) were associated with marginally increased odds of ICU admission (p < 0.10).

4.4.3 Modeling odds of bronchodilator administration associated with HRV coinfection

 Results presented here are limited to analyses using HRV-positive specimens with accessible medical record information from unique children (no duplicates) with confirmed (physician diagnosed) or suspected (physiciandocumented symptoms) ARTI and includes inpatients and outpatients (n=95). Results were similar when including a third group of children, those with physician concern for ARTI in the absence of traditional symptoms (data not shown).

 Table 46 details the results from bivariate logistic regression models of selected factors (potential confounders as identified in the literature or stratified analyses) and odds of HRV coinfection (versus HRV mono-infection). No significant effect modifiers were identified. Table 47 details the results from bivariate logistic regression models of selected factors (potential confounders as identified in the literature or stratified analyses) and odds of bronchodilator administration. Age 6 months to 5 years and history of asthma were significantly associated with increased odds of bronchodilator administration (p <0.05). History of any immunosuppressive condition was significantly associated with decreased odds of bronchodilator administration (p < 0.05). No significant effect modifiers were identified.

The unadjusted odds ratio for bronchodilator administration associated with HRV coinfection was 2.60 (95% CI 1.08-6.23). After controlling for potential
confounders, the adjusted odds ratio was 3.02 (1.06-8.65) (Table 48). Age 6 months to 1 year (OR 5.70, 95% CI 1.26-25.73, as compared to age less than 6 months) and history of asthma (OR 6.62, 95% CI 1.60-27.52) were significantly associated with increased odds of bronchodilator administration.

4.5 Secondary analysis – viral-bacterial coinfection

Table 49 details the prevalence estimates for virus-specific mono-infection and virus-bacteria coinfections for specimens from hospitalized children (no duplicates) with confirmed (physician diagnosed) or suspected (physiciandocumented symptoms) ARTI for whom any bacterial test was ordered (not limited to respiratory sources) (n=217). Compared to children who did not have a bacterial test ordered, those who did were more likely to be older (age 1-5 years p=0.035, age greater than 5 years p=0.025), to have a history of cancer (p=0.022), to have an elevated white blood cell count (p=0.048), to have a fever (p=0.005), and to be hospitalized (p <0.001). They were also less likely to have nasal congestion/runny nose ($p=0.002$) and wheeze ($p < 0.001$).

Crude odds ratios for all indicators of severity other than ICU admission (for all coinfections) were not significant or marginally significant, and multivariate logistic regression models were not generated.

Results presented here are limited to analyses using virus-positive specimens with accessible medical record information from hospitalized children (no duplicates) with confirmed (physician diagnosed) or suspected (physiciandocumented symptoms) ARTI for whom any bacterial test was ordered (not limited to respiratory sites) (n=124). Coinfection is defined as infection with at least one virus and one bacterium. The comparison group is defined as infection with a single virus.

 Table 50 details the results from bivariate logistic regression models of selected factors (potential confounders as identified in the literature or stratified analyses) and odds of virus-bacteria coinfection (versus viral mono-infection). No significant effect modifiers were identified. Age 1 to 5 years was associated with significantly decreased odds of virus-bacteria coinfection (OR 0.37, 95% CI 0.16-0.83). Rural residence (OR 2.14, 95% CI 1.03-4.43) and history of prematurity (OR 3.14, 95% CI 1.37-7.18) were associated with significantly increased odds of virus-bacteria coinfection. Table 51 details the results from bivariate logistic regression models of selected factors (potential confounders as identified in the literature or stratified analyses) and odds of ICU admission. Age 1 to 5 years, history of a chronic respiratory condition (structural defect or asthma), and history of prematurity were associated with significantly increased odds of ICU admission (p <0.05). A significant trend was observed for the association between age and ICU admission (p for trend 0.048); as age increased, the odds of ICU admission decreased. A significant trend was also observed for the association between urban/rural residence and ICU admission (p for trend 0.037); as characterization of residence became more rural, the odds of ICU admission decreased.

The unadjusted odds ratio for ICU admission associated with virusbacteria coinfection was 6.00 (95% CI 2.51-14.33). After controlling for potential confounders, the adjusted odds ratio was 5.58 (1.95-15.96) (Table 52). History of prematurity (OR 3.17, 95% CI 1.03-9.77) was also significantly associated with increased odds of ICU admission.

Table 53 details the prevalence estimates for virus-specific mono-infection and virus-bacteria coinfections for specimens from hospitalized children (no duplicates) with confirmed (physician diagnosed) or suspected (physiciandocumented symptoms) ARTI for whom any respiratory bacterial test was

ordered (n=93). Compared to children who did not have a respiratory bacterial test ordered, those who did were more likely to have a history of a structural respiratory condition (p=0.014) and an elevated white blood cell count (p=0.005). They were also less likely to have a history of cancer (p=0.026).

Crude odds ratios for all indicators of severity other than ICU admission (for all coinfections) were not significant or marginally significant, and multivariate logistic regression models were not generated.

Results presented here are limited to analyses using virus-positive specimens with accessible medical record information from hospitalized children (no duplicates) with confirmed (physician diagnosed) or suspected (physiciandocumented symptoms) ARTI for whom any respiratory bacterial test was ordered (n=60). Coinfection is defined as infection with at least one virus and one bacterium present. The comparison group is defined as infection with a single virus.

 Table 54 details the results from bivariate logistic regression models of selected factors (potential confounders as identified in the literature or stratified analyses) and odds of virus-bacteria coinfection (versus viral mono-infection). No significant effect modifiers were identified. History of asthma was associated with increased likelihood of coinfection; however, this result was only marginally significant (p=0.056). Table 55 details the results from bivariate logistic regression models of selected factors (potential confounders as identified in the literature or stratified analyses) and odds of ICU admission.

The unadjusted odds ratio for ICU admission associated with virusbacteria coinfection in this group is 9.75 (95% CI 2.54-37.40). The sample size was insufficient to allow for multivariate logistic regression modeling to control for potential confounders.

Figure 1. Description of eligible, included, and excluded respiratory specimens MR=Medical record, unique refers to first specimen of first ARTI (no duplicates)

Figure 2. Evolutionary relationships of 125 HRV taxa (VP4/VP2 protocol). The evolutionary history was inferred using the Neighbor-Joining method [1]. The bootstrap consensus tree inferred from 1000 replicates [4] is taken to represent the evolutionary history of the taxa analyzed [4]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [2] and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 348 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 [3]. Prefix ARTI.RS denotes study specimens.

Source: 1. Saitou N & Nei M (**1987**) The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* **4**:406-425.

^{2.} Tamura K, Nei M & Kumar S (**2004**) Prospects for inferring very large phylogenies by using the neighbor-joining method. *Proceedings of the National Academy of Sciences* (*USA*) **101**:11030-11035.

^{3.} Tamura K, Dudley J, Nei M & Kumar S (**2007**) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Molecular Biology and Evolution* **24**:1596-1599.

^{4.} Felsenstein J (**1985**) Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* **39**:783-791.

Figure 3. Detail of Figure 2, HRV A phylogeny.

Figure 4. Detail of Figure 2, HRV B and Coxsackievirus phylogeny.

Figure 5. Detail of Figure 2, HRV C phylogeny.

Table 3 Virus-specific mono-infection and coinfection prevalence estimates for all specimens, without duplicates (n=421)

Note: CoxS (coxsackievirus), Flu A (influenza A virus), Flu B (influenza B virus), PIV NOS (parainfluenza virus not otherwise specified).

^a Denominator is virus-specific total number of positive specimens.

 b Denominator is total number of specimens, n=421.</sup>

^c 95% binomial confidence interval associated with prevalence percent estimate for total number of positive specimens.

^d Ad genotypes include Ad1 (n=1, 0% coinfected), Ad2 (n=4, 75.0% coinfected), Ad3 (n=7, 57.1% coinfected), Ad5 (n=1, 0% coinfected), Ad41 (n=1, 100% coinfected), and non-typeable (n=1, 0% coinfected).

| Co-detected Viruses | N | |
|----------------------------|----------------|--|
| 2 Viruses | | |
| HRV + RSV | 14 | |
| HRV + HBoV | 6 | |
| $HRV + PIV3$ | 4 | |
| $HRV + hMPV$ | 3 | |
| HBoV + RSV | $\overline{2}$ | |
| $Ad + RSV$ | $\overline{2}$ | |
| $Ad + HRV$ | $\overline{2}$ | |
| PIV 3 + HBoV | $\overline{2}$ | |
| PIV 3 + RSV | $\overline{2}$ | |
| hMPV + RSV | $\overline{2}$ | |
| PIV 3 + $hMPV$ | 1 | |
| PIV NOS + RSV | | |
| hMPV + CoxS | | |
| HBoV + Ad | | |
| 3 Viruses | | |
| Ad + HRV + HBoV | $\overline{2}$ | |
| $HRV + HBoV + hMPV$ | 1 | |
| HRV + HBoV + RSV | | |
| HRV + hMPV + RSV | | |
| HRV + PIV NOS + RSV | | |
| hMPV + PIV NOS + RSV | | |
| $Ad + HRV + RSV$ | | |
| Total | 50 | |

Table 4 Frequency of viral coinfections for all specimens, without duplicates (n=421)

Note: CoxS (coxsackievirus), PIV NOS (parainfluenza virus not otherwise specified).

Table 5 Virus-specific mono-infection and coinfection prevalence estimates for specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=349)

Note: CoxS (coxsackievirus), Flu A (influenza A virus), Flu B (influenza B virus), PIV NOS (parainfluenza virus not otherwise specified).

^a Denominator is virus-specific total number of positive specimens.

 b Denominator is total number of specimens, n=349.</sup>

^c 95% binomial confidence interval associated with prevalence percent estimate for total number of positive specimens.

^d Ad genotypes include Ad1 (n=1, 0% coinfected), Ad2 (n=4, 75.0% coinfected), Ad3 (n=7, 57.1% coinfected), Ad5 (n=1, 0% coinfected), Ad41 (n=1, 100% coinfected), and non-typeable (n=1, 0% coinfected).

Table 6 Frequency of viral coinfections for specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=349)

Note: CoxS (coxsackievirus), PIV NOS (parainfluenza virus not otherwise specified).

Table 7 Virus-specific mono-infection and coinfection prevalence estimates for specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI or concern for ARTI in the absence of traditional symptoms, without duplicates (n=405)

Note: CoxS (coxsackievirus), Flu A (influenza A virus), Flu B (influenza B virus), PIV NOS (parainfluenza virus not otherwise specified).

^a Denominator is virus-specific total number of positive specimens.

^b Denominator is total number of specimens, n=405.

^c 95% binomial confidence interval associated with prevalence percent estimate for total number of positive specimens.

^d Ad genotypes include Ad1 (n=1, 0% coinfected), Ad2 (n=4, 75.0% coinfected), Ad3 (n=7, 57.1% coinfected), Ad5 (n=1, 0% coinfected), Ad41 (n=1, 100% coinfected), and non-typeable (n=1, 0% coinfected).

Table 8 Frequency of viral coinfections for specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI or concern for ARTI in the absence of traditional symptoms, without duplicates (n=405)

Note: CoxS (coxsackievirus), PIV NOS (parainfluenza virus not otherwise specified).

Table 9 Virus-specific mono-infection and coinfection prevalence estimates for specimens from eligible children excluded from study due to unavailable specimen, without duplicates $(n=105)$

Note: CoxS (coxsackievirus), Flu A (influenza A virus), Flu B (influenza B virus), PIV NOS (parainfluenza virus not otherwise specified).

^a Limited to UIHC Clinical Microbiology Laboratory virological assays.

^b Denominator is virus-specific total number of positive specimens.

 \textdegree Denominator is total number of specimens, n=105.

^d 95% binomial confidence interval associated with prevalence percent estimate for total number of positive specimens.

e Ad genotypes not determined.

Table 10 Frequency of viral coinfections for specimens from eligible children excluded from study due to unavailable specimen, without duplicates (n=105)

Table 11 Demographic characteristics of children for all specimens with accessible medical record information, without duplicates (n=407)

Table 11 Continued

 Note: Excludes 14 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table 12 Mean age of children for all specimens with accessible medical record information, without duplicates (n=407)

Note: Excludes 14 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table 13 Clinical characteristics (indicators of severity) associated with specimens for all children with accessible medical record information, without duplicates (n=407)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table 14 Clinical characteristics (length of hospitalization) associated with specimens for all children with accessible medical record information, without duplicates (n=407)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Includes non-UIHC hospitalizations when applicable.

Table 15 Clinical characteristics (antimicrobial use and inflammation markers) associated with specimens for all children with accessible medical record information, without duplicates (n=407)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Denotes antibiotics used prior to UIHC episode during which specimen was collected.

Table 16 Clinical characteristics (diagnoses) associated with specimens for all children with accessible medical record information, without duplicates (n=407)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table 17 Clinical characteristics (symptoms) associated with specimens for all children with accessible medical record information, with duplicates (n=407)

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table 18 Clinical characteristics (medical history) associated with specimens for all children with accessible medical record information, without duplicates (n=407)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table 19 Laboratory characteristics for all specimens with accessible medical record information, without duplicates (n=407)

Note: Excludes 14 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Other may include bronchial wash/biopsy, lung aspirate/biopsy, nasopharyngeal swab, nasal swab, THS, and tissue biopsy.

Table 20 Available demographic characteristics of children with accessible medical record information from eligible specimens excluded from study due to unavailability of specimen, without duplicates (n=100)

 Note: Excludes 3 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table 21 Mean age of children with accessible medical record information from eligible specimens excluded from study due to unavailability of specimen, without duplicates (n=100)

Note: Excludes 3 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table 22 Clinical characteristics (indicators of severity) associated with specimens with accessible medical record information from eligible children excluded from study due to unavailable specimen, without duplicates (n=100)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table 23 Clinical characteristics (length of hospitalization) associated with specimens with accessible medical record information from eligible children excluded from study due to unavailable specimen, without duplicates (n=100)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Includes non-UIHC hospitalizations when applicable.

Table 24 Laboratory characteristics of clinical specimens with accessible medical record information from eligible children excluded from study due to unavailable specimen, without duplicates (n=100)

Note: Excludes 3 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table 25 Demographic characteristics of children for HRV-tested specimens with accessible medical record information, without duplicates (n=407)

Table 25 Continued

Note: Excludes 14 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

a The category HRV Other includes 1 HRV B and 4 non-typeable HRVs.

Table 26 Mean age of children for HRV-tested specimens with accessible medical record information, without duplicates (n=407)

Note: Excludes 14 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category HRV Other includes 1 HRV B and 4 non-typeable HRVs.

Table 27 Clinical characteristics (indicators of severity) associated with HRV-tested specimens with accessible medical record information, without duplicates (n=407)

a The category HRV Other includes 1 HRV B and 4 non-typeable HRVs.

Table 28 Clinical characteristics (length of hospitalization) associated with HRV-tested specimens with accessible medical record information, without duplicates (n=407)

Table 28 Continued

a The category HRV Other includes 1 HRV B and 4 non-typeable HRVs.

b Includes non-UIHC hospitalizations when applicable.

Table 29 Clinical characteristics (antimicrobial use and inflammation markers) associated with HRV-tested specimens with accessible medical record information, without duplicates (n=407)

^a The category HRV Other includes 1 HRV B and 4 non-typeable HRVs.

Table 30 Clinical characteristics (diagnoses) associated with HRV-tested specimens with accessible medical record information, without duplicates (n=407)

a The category HRV Other includes 1 HRV B and 4 non-typeable HRVs.

Table 31 Clinical characteristics (symptoms) associated with HRV-tested specimens with accessible medical record information, without duplicates (n=407)

a The category HRV Other includes 1 HRV B and 4 non-typeable HRVs.

Table 32 Clinical characteristics (medical history) associated with HRV-tested specimens with accessible medical record information, without duplicates (n=407)

^a The category HRV Other includes 1 HRV B and 4 non-typeable HRVs.

^b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table 33 Laboratory characteristics of HRV-tested specimens with accessible medical record information, without duplicates (n=407)

Note: Excludes 14 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category HRV Other includes 1 HRV B and 4 non-typeable HRVs.

b Other may include bronchial wash/biopsy, lung aspirate/biopsy, nasopharyngeal swab, nasal swab, THS, tissue biopsy.

Table 34 Prevalence and odds ratio of viral coinfection by risk factor among children with confirmed or suspected ARTI, without duplicates^a

Table 34 Continued

^a Bivariate analysis of selected risk factors and viral coinfection includes only virus-positive specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical records, without duplicates (n=212).

^b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table 35 Adjusted odds ratio of viral coinfection by risk factor among children with confirmed or suspected ARTI, without duplicates^a

^a Multivariate analysis of selected risk factors and viral coinfection includes only virus-positive specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical records, without duplicates (n=212).

^b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table 36 Prevalence and odds ratio of viral coinfection by risk factor among children with confirmed or suspected ARTI with complete tobacco smoke exposure data, without duplicates $^{\rm a}$

Table 36 Continued

^a Bivariate analysis of selected risk factors and viral coinfection includes only virus-positive specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI and with complete tobacco smoke exposure data, without duplicates (n=96).

b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table 37 Adjusted odds ratio of viral coinfection by risk factor among children with confirmed or suspected ARTI with complete tobacco smoke exposure data, without duplicates^a

^a Multivariate analysis of selected risk factors and viral coinfection includes only virus-positive specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI and with complete tobacco smoke exposure data, without duplicates (n=96).

b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table 38 Prevalence and odds ratio of HRV-specific coinfection by risk factor among HRV-positive children with confirmed or suspected ARTI, without duplicates $^{\rm a}$

Table 38 Continued

^a Bivariate analysis of selected risk factors and viral coinfection includes only HRV-positive specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical record information, without duplicates (n=95).

b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table 39 Adjusted odds ratio of HRV-specific coinfection by risk factor among HRV-positive children with confirmed or suspected ARTI, without duplicates^a

^a Bivariate analysis of selected risk factors and viral coinfection includes only HRV-positive specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical record information, without duplicates (n=95).

b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table 40 Prevalence and odds ratio of viral coinfection by risk factor among hospitalized children with confirmed or suspected ARTI, without duplicates^a

Table 40 Continued

^a Bivariate analysis of selected risk factors and viral coinfection includes only virus-positive specimens from hospitalized children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical record information, without duplicates (n=160).

^b p for trend 0.401

 \degree p for trend 0.609

^d Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

^e p for trend 0.652

Table 41 Prevalence and odds ratio of ICU admission by risk factor among hospitalized children with confirmed or suspected ARTI, without duplicates^a

Table 41 Continued

^a Bivariate analysis of selected risk factors and ICU admission includes only virus-positive specimens from hospitalized children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical record information, without duplicates (n=160).

^b p for trend 0.087

 \degree p for trend 0.032

^d Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

^e p for trend 0.030

 $p < 0.05$

Table 42 Adjusted odds ratio of ICU admission by risk factor among hospitalized children with confirmed or suspected ARTI, without duplicates^a

^a Multivariate analysis of selected risk factors and ICU admission includes only virus-positive specimens from hospitalized children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical record information, without duplicates (n=160).

b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

 $p < 0.05$

Table 43 Prevalence and odds ratio of HRV-specific coinfection by risk factor among hospitalized HRV-positive children with confirmed or suspected ARTI, without duplicates^a

Table 43 Continued

^a Bivariate analysis of selected risk factors and viral coinfection includes only HRV-positive specimens from hospitalized children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical record information, without duplicates (n=73).

 $^{\rm b}$ p for trend 0.854

 \degree p for trend 0.671

^d Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

^e p for trend 0.822

Risk Factor N % Admitted to ICU (95% CI) OR (95% CI) p Gender Female 28 28 17.9 (6.1-36.9) 1.00 Male 45 24.4 (12.9-39.5) 1.49 (0.46-4.76) 0.510 Age (years)^b 0 to < 1 35 31.4 (16.9-49.3) 1.00 1 to < 5 27 14.8 (4.1-33.7) 0.38 (0.11-1.36) 0.137 > 5 11 9.10 (0-41.3) 0.22 (0.03-1.92) 0.170 Race (4 level) Caucasian 52 15.4 (6.9-28.1) 1.00 African-American 6 50.0 (11.8-88.2) 5.5 (0.94-32.25) 0.059 Hispanic 6 33.3 (4.3-77.7) 2.75 (0.43-17.61) 0.286 Other 3 33.3 (1.0-90.6) 2.75 (0.22-34.04) 0.431 Race (2 level) Caucasian 62 15.4 (6.9-28.1) 1.00 Other 15 15 40.0 (16.3-67.7) 3.67 (1.02-13.17) 0.046[†] Medicaid No 39 15.4 (5.9-30.5) 1.00 Yes 34 29.4 (15.1-47.5) 2.29 (0.73-7.17) 0.154 Urban/Rural $(4 \text{ level})^c$ Urban 1.00 Large rural 10 10 20.0 (2.5-55.6) 0.63 (0.12-3.38) 0.585 Small rural 11 18.2 (2.3-51.8) 0.56 (0.10-2.96) 0.491 Isolated rural 10 10 0 (0-30.9) NA NA Urban/Rural (2 level) Urban 1.00 Rural 31 28.6 (3.6-29.8) 0.37 (0.11-1.29) 0.118 History of chronic respiratory condition No 36 13.9 (4.7-29.5) 1.00 Yes 37 29.7 (15.9-47.0) 2.62 (0.81-8.53) 0.109 History of structural respiratory condition No 47 17.0 (7.7-30.8) 1.00 Yes 26 26 30.8 (14.3-51.8) 2.17 (0.70-6.69) 0.179 History of asthma No 60 23.3 (13.4-36.0) 1.00 Yes 13 13 15.4 (1.9-45.5) 0.60 (0.12-3.02) 0.533 History of cancer No 66 24.2 (14.5-36.4) 1.00 Yes 7 0 (0-41.0) NA NA History of transplant No 68 22.1 (12.9-33.8) 1.00 Yes 30.0 (0-71.6) 0.88 (0.09-8.51) 0.915

Table 44 Prevalence and odds ratio of ICU admission by risk factor among hospitalized HRV-positive children with confirmed or suspected ARTI, without duplicates^a

Table 44 Continued

^a Bivariate analysis of selected risk factors and ICU admission includes only HRV-positive specimens from hospitalized children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical record information, without duplicates (n=73).

 $^{\text{b}}$ p for trend 0.065

 \degree p for trend 0.057

^d Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

^e p for trend 0.207

 $p < 0.05$

Table 45 Adjusted odds ratio of ICU admission by risk factor among hospitalized HRV-positive children with confirmed or suspected ARTI, without duplicates^a

a Multivariate analysis of selected risk factors and ICU admission includes only HRV-positive specimens from hospitalized children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical record information, without duplicates (n=73).

b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

 $p < 0.05$

Table 46 Prevalence and odds ratio of HRV-specific coinfection by risk factor among HRV-positive children with confirmed or suspected ARTI, without duplicates^a

Table 46 Continued

^a Bivariate analysis of selected risk factors and HRV-specific coinfection includes only HRV-positive specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical record information, without duplicates (n=95).

 b p for trend 0.703</sup>

 \degree p for trend 0.386

^d Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

^e p for trend 0.537

Table 47 Prevalence and odds ratio of bronchodilator administration by risk factor among HRV-positive children with confirmed or suspected ARTI, without duplicates^a

Table 47 Continued

^a Bivariate analysis of selected risk factors and bronchodilator administration includes only HRV-positive specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical record information, without duplicates (n=95).

 b p for trend 0.268</sup>

 \degree p for trend 0.696

^d Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

^e p for trend 0.278

 $p < 0.05$

Table 48 Adjusted odds ratio of bronchodilator administration by risk factor among HRV-positive children with confirmed or suspected ARTI, without duplicates^a

a Multivariate analysis of selected risk factors and bronchodilator administration includes only HRV-positive specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI with accessible medical record information, without duplicates (n=95).

 $p < 0.05$

Table 49 Virus-specific mono-infection and virus-bacteria coinfection prevalence estimates for specimens from children with any bacterial tests completed (not limited to respiratory sites) and hospitalized with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=217)

Note: Flu A (influenza A virus), Flu B (influenza B virus), PIV All (parainfluenza virus 1-3 and not otherwise specified).

^a Denominator is virus-specific total number of positive specimens.

 b Denominator is total number of specimens, n=217.</sup>

^c 95% binomial confidence interval associated with prevalence percent estimate for total number of positive specimen.

Table 50 Prevalence and odds ratio of virus-bacteria coinfection (any site) by risk factor among hospitalized virus-positive children with confirmed or suspected ARTI, without duplicates^a

Table 50 Continued

^a Bivariate analysis of selected risk factors and virus-bacteria coinfection includes only virus-positive specimens from children with any bacterial tests completed (not limited to respiratory sites), accessible medical records, and hospitalized with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=124).

b Coinfection is defined as infection with at least one virus and one bacterium. "No coinfection" is defined as infection with a single virus.

 \degree p for trend 0.091

^d p for trend 0.500

^e Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

 f p for trend 0.856

 $p < 0.05$

Table 51 Prevalence and odds ratio of ICU admission by risk factor among hospitalized virus-positive children tested for bacterial infection (any site) with confirmed or suspected ARTI, without duplicates^a

Table 51 Continued

^a Bivariate analysis of selected risk factors and ICU admission includes only virus-positive specimens from children with any bacterial tests completed (not limited to respiratory sites), accessible medical records, and hospitalized with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=124).

^b p for trend 0.048

 \degree p for trend 0.037

^d Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

^e p for trend 0.687

 $p < 0.05$

Table 52 Adjusted odds ratio of ICU admission by risk factor among hospitalized virus-positive children tested for bacterial infection (any site) with confirmed or suspected ARTI, without duplicates^a

^a Multivariate analysis of selected risk factors and ICU admission includes only virus-positive specimens from children with any bacterial tests completed (not limited to respiratory sites), accessible medical records, and hospitalized with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=124).

b Coinfection is defined as infection with at least one virus and one bacterium. "No coinfection" is defined as infection with a single virus.

 $p < 0.05$

Table 53 Virus-specific mono-infection and virus-bacteria coinfection prevalence estimates for specimens from children with any respiratory bacterial tests completed and hospitalized with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=93)

Note: Flu A (influenza A virus), Flu B (influenza B virus), PIV All (parainfluenza virus 1-3 and not otherwise specified).

a Denominator is virus-specific total number of positive specimens.

 b Denominator is total number of specimens, n=93.</sup>

^c 95% binomial confidence interval associated with prevalence percent estimate for total number of positive specimen.

Table 54 Prevalence and odds ratio of virus-bacteria coinfection (respiratory site) by risk factor among hospitalized virus-positive children with confirmed or suspected ARTI, without duplicates^a

Table 54 Continued

^a Bivariate analysis of selected risk factors and virus-bacteria coinfection includes only virus-positive specimens from children with any respiratory bacterial tests completed, accessible medical records, and hospitalized with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=60).

b Coinfection is defined as infection with at least one virus and one bacterium. "No coinfection" is defined as infection with a single virus.

 \degree p for trend 0.724

 $^{\text{d}}$ p for trend 0.294

^e Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

^f p for trend 0.916

Table 55 Prevalence and odds ratio of ICU admission by risk factor among hospitalized virus-positive children tested for bacterial infection (respiratory site) with confirmed or suspected ARTI, without duplicates^a

Table 55 Continued

^a Bivariate analysis of selected risk factors and virus-bacteria coinfection includes only virus-positive specimens from children with any respiratory bacterial tests completed, accessible medical records, and hospitalized with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=60).

^b p for trend 0.777

 \degree p for trend 0.184

^d Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

^e p for trend 0.826

CHAPTER 5 – DISCUSSION

 Polymicrobial infections were common in our study of hospital-based pediatric inpatients and outpatients with acute respiratory tract infections. We conducted a retrospective study of 559 archived respiratory specimens from 421 children under the age of 10 years collected between March 28, 2008 and June 30, 2009. This population was comprised mostly of very young (86.2% under the age of 5 years, mean age 2.07 years), Caucasian (72.9%) children many of whom relied on Medicaid as a primary payor for medical services (47.8%). This study included several children who resided in rural areas (39.9%). A large proportion of the children were hospitalized (76.9%), and of those that were hospitalized, 36.1% were patients in an intensive care unit at the time of specimen collection.

A virus was identified in 61.3% of 349 respiratory specimens from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI. HRV (27.5%), RSV (18.9%), HBoV (8.3%), hMPV (7.7%), and PIV (6.6%) were the most common viruses detected. Of the 96 HRV-positive specimens, HRV A was the most common group detected (46.3%) followed by HRV C (41.1%), and non-typeable HRVs (12.6%). A viral coinfection was identified in 21.5% of the 214 virus-positive specimens and was most often detected for Ad (53.3% of 15 Ad-positive specimens), HBoV (51.7% of 29 HBoVpositive specimens), PIV (43.5% of 23 PIV-positive specimens), HRV (35.4% of 96 HRV-positive specimens), and RSV (34.8% of 66 RSV-positive specimens). Among the 46 specimens with dual or triple viral coinfections detected, the most frequent virus-virus combinations were HRV-RSV (n=12), HRV-HBoV (n=6), and HRV-PIV 3 (n=4). Among the 96 HRV-positive specimens, 58.3% of the non-

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typeable HRV specimens, 36.4% of the HRV A specimens, and 30.8% of the HRV C specimens were involved in coinfections.

These results are similar to previously published studies. Coinfection rates vary widely among these studies and are estimated to account for between 8.4% and 36.1% of ARTIs for which at least one virus was detected [3, 4, 6, 7, 9, 14-16, 19, 20]. Direct comparison of results from this study to previous studies is made difficult due to the number of design factors that vary from study to study, such as differences in patient population (e.g., ages included, inclusion of inpatients and/or outpatients, hospital or community source), definition of ARTI (e.g., lower or upper ARTI, pneumonia only, bronchiolitis only), timing of the study (e.g., season), diagnostic methods used (e.g., cell culture or molecular assays such as PCR), and pathogens under review (e.g., viral and/or bacterial, inclusion or exclusion of newly recognized agents such as HBoV).

We hypothesized that certain host-specific risk factors were associated with the likelihood of viral coinfection (Specific aim 2). While none of the covariates in our final model were significant, the results were suggestive. Male gender (OR 1.70, 95% CI 0.83-3.46), age between 6 months to 1 year (as compared to children less than 6 months old, OR 2.15, 95% CI 0.75-6.19), and history of any chronic condition that may result in immunosuppression (OR 2.05, 95% CI 0.99-4.23) were each associated with increased odds of viral coinfection (p > 0.05). Similar results were observed when limiting the analysis to viral coinfections that included HRV; in addition to male gender (OR 1.89, 95% CI 0.71-5.03), age between 6 months to 1 year (as compared to children less than 6 months old, OR 3.70, 95% CI 0.87-15.67), and history of any chronic condition that may result in immunosuppression (OR 2.24, 95% CI 0.81-6.22), children residing in large rural areas, as compared to those residing in urban areas, also

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had greater odds of HRV-specific coinfection (OR 3.17, 95% 0.77-13.10) though this increase was not statistically significant ($p > 0.05$).

Few studies have made an effort to identify host factors that may predispose a child to respiratory coinfections. In a study of 316 pediatric patients (less than 14 years old) hospitalized for either upper or lower ARTI in China, Peng et al. noted that coinfection was more common in children aged 3 to 6 years [14]. In a study of viruses in community-acquired pneumonia in hospitalized and non-hospitalized children aged less than 3 years old, Cilla et al. noted that children aged less than 12 months were more likely than older children to have a viral coinfection [7].

We also hypothesized that children with viral coinfections would be more likely to have severe ARTI (requiring hospitalization or greater medical intervention such as bronchodilator administration, supplemental oxygen requirement, or need for mechanical ventilation) than those children with single virus infections (Specific aim 3). No significant association was identified between any virus-virus coinfection and the following indicators of severity – hospitalization, bronchodilator administration, oxygen saturation less than 90% (hypoxemia), requirement for supplemental oxygen, requirement for mechanical ventilation, or total length of hospitalization. The unadjusted odds ratio for ICU admission associated with virus-virus coinfection was marginally significant (OR 0.30, 95% CI 0.09-1.04). After controlling for gender, age, history of any chronic condition that may result in immunosuppression, history of prematurity, and leukocytosis, the OR was no longer marginally significant (OR 0.32, 95%CI 0.08- 1.27).

With respect to virus-virus coinfections, our results are similar to studies that have found no significant association between coinfection and severity of illness [6, 9, 10, 12, 14]. However, these studies did not use multivariate

regression modeling to test hypotheses regarding severity of illness, and they do not report any measures of association (e.g., odds ratio). In our study, children with a viral coinfection were less likely to be admitted to the intensive care unit than children with a single virus infection, though this association was not statistically significant (OR 0.32, 95% CI 0.08-1.27) after controlling for potential confounders.

With respect to reasons for hospitalization and ICU admission in cases of pediatric ARTI, a number of factors may be considered, but oftentimes no set algorithm is in place and decisions regarding admission are made at the physician's discretion based upon the evidence at hand. We hypothesized that perhaps the observed reduced likelihood of admission to the ICU associated with virus-virus coinfections was an artifact associated with physician behavior when deciding what child is admitted to the ICU and when they are admitted. Most studies focusing on the need for major medical intervention in pediatric populations with ARTI have focused on bronchiolitis and RSV. Parker et al. identified 4 factors associated with major intervention (i.e., oxygen administration, IV fluid bolus, any treatment for apnea, or admission to critical care unit) in infants with bronchiolitis; these factors were severe retractions on arrival, baseline oxygen saturation 92% or less, increased respiratory rate, and history of poor fluid intake [112]. Weigl et al. identified young age, presence of underlying condition, pneumonia or bronchiolitis, prematurity, and retractions as factors that increased the duration of hospitalization in children under 2 years old admitted with ARTI [113]. In a study of dual viral infection in infants with severe bronchiolitis, Richard et al. identified young age, prematurity, underlying illness, and male gender as factors associated with admission to a pediatric intensive care unit [114]. Factors such as age, oxygen saturation, work of breathing, ability of the guardians to monitor the child at home, ability to feed, dehydration,

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complexity of care, and pre-existing conditions (i.e., underlying heart or pulmonary disease) are often considered by the evaluating physician at the University of Iowa Hospital and Clinics (personal communication with Dr. Jody Murph). We assessed the importance of several of these variables in our analyses. However, even after controlling for potential confounders, the direction of effect remained consistent in several sub-analyses (data not shown).

We next hypothesized that perhaps concurrent bacterial infections were playing a role in influencing the paradoxical viral coinfection data. We limited secondary analyses to hospitalized children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI for whom any bacterial test (not limited to respiratory sites) had been ordered during the same hospitalization that a viral test had been ordered and for whom a virus was detected (n=124). A virus-bacteria coinfection was identified for 33 children, and a virus-virus-bacteria coinfection was identified in 7 children. Children with virusbacteria coinfection, as compared to children with viral mono-infection, were more likely to be admitted to an intensive care unit (OR 5.58, 95% CI 1.95-15.96) even after controlling for potential confounders including age, history of prematurity, urban/rural residence, and leukocytosis. Similar results were observed when further limiting the population to children with respiratory bacterial tests ordered, though the sample size was insufficient to allow for control of confounding through multivariate logistic regression modeling (crude OR 9.75, 95% CI 2.54-37.40).

Given these data, we hypothesize the following explanation for the observed decreased likelihood of ICU admission among children with virus-virus coinfection as compared to children with viral mono-infection. The 33 children with single virus/single bacterium coinfections (26.6% of the children with viruspositive specimens) would have been classified as having a viral mono-infection

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in the primary analyses limiting exposure to virus-virus coinfection (no bacterial data included). It is also likely that a number of children not tested for bacterial pathogens may have had a concurrent bacterial infection. Though these cases would likely be distributed between viral mono-infection and virus-virus coinfections, we suspect that a higher proportion of viral mono-infections would also be positive for bacterial pathogens as evidenced by the data presented in Table 49 (virus-bacteria coinfections represented 26.6% of virus-positive specimens whereas virus-virus-bacteria coinfections represented only 5.7% of virus-positive specimens). Given that 33 of the 40 children with these virusbacteria coinfections would have been classified as having viral mono-infections in our primary analyses and that our secondary analyses suggest these children are at increased risk of ICU admission compared to viral mono-infections, children with virus-virus coinfections would appear to be less likely to be admitted to the ICU as compared to children with viral mono-infections when bacterial coinfections are not accounted for. When the children with virus-bacteria coinfections were removed from the analysis of virus-virus coinfection versus virus mono-infection, the observed odds ratio estimating the association between viral coinfection and ICU admission moved closer to the null hypothesis (OR 0.53, 95% CI 0.11-2.49). This suggests that at least part of the observed protective effect of virus-virus coinfection ($p > 0.05$) can be explained by virusbacteria coinfection, and that perhaps undetected bacterial coinfections could account for the remaining effect.

Examples of coinfecting bacterial and viral pathogens are common in the literature, but reports tend to be virus-specific [115]. For example, most deaths associated with epidemics of influenza are associated with secondary bacterial infections including *Streptococcus pneumoniae* and *Haemophilus influenzae*. In children, RSV has been associated with *S. pneumoniae*, *Bordetella pertussis*,

and *Staphylococcus aureus*. Additionally, associations between adenovirus and *B. pertussis* have been noted in severe respiratory disease in children. The body of evidence describing the importance of viral and bacterial cooperation in cases of pneumonia is growing [116]. Jennings et al. conducted a study among 304 patients admitted to the hospital with community-acquired pneumonia (CAP) and demonstrated that HRV-pneumococcal coinfection was independently associated with severe pneumonia [11]. Templeton et al. included both inpatients and outpatients in their study of CAP and demonstrated that individuals with HRVbacterial or coronavirus-bacterial coinfections were independently association with severe pneumonia [17]. Additional evidence of the interaction between bacterial and viral pathogens comes from animal studies [115]. Several mechanisms have been postulated to further explain this interaction [115]. Viruses may increase the ability of bacteria to infect or adhere to mucosal surfaces through changes induced in host cell membranes. It has also been postulated that perhaps exudates on mucosal surfaces resulting from viral infection may increase bacterial growth. The host immune defense against bacteria could also be affected by viral infection through the inhibition of nonspecific phagocytosis by neutrophils and macrophages. It has also been postulated that perhaps viral infection can exacerbate the effect of bacterial toxins.

The original intent of this study was to focus attention on coinfections involving HRV, HBoV, and Ad. Our sample size was insufficient to examine hypotheses regarding illness severity in the cases of HBoV-specific and Adspecific coinfections. With respect to HRV-specific coinfections, our results are similar to other published studies. Recent studies report HRV coinfection rates ranging from 17.7% to 47% [47, 52, 54-59]. In our sample of 349 children with confirmed (physician diagnosed) or suspected (physician-documented

symptoms) ARTI, 96 children (27.5%) were HRV-positive, 35.4% of which were co-infected with HRV and at least one other virus. Some studies have suggested that coinfection with HRV leads to more severe disease manifestations such as lower respiratory tract infections, requirement for supplemental oxygen, and longer stays in the hospital [54, 58, 59]. In the current study, no significant association was identified between coinfection involving HRV (as compared to HRV mono-infection) and the following indicators of severity – hospitalization, ICU admission, oxygen saturation less than 90% (hypoxemia), requirement for supplemental oxygen, requirement for mechanical ventilation. However, children with coinfection involving HRV (as compared to HRV mono-infection) were significantly more likely to be administered a bronchodilator (OR 3.02, 95% CI 1.06-8.65) even after controlling for age, history of asthma, and race. Like RSV, HRVs have been known to be associated with wheezing and asthma exacerbations in children [49, 117]. The most common combination among detected coinfections involving HRV was HRV-RSV (47% of 34 coinfections). We hypothesize that it is dual infection with RSV that drives the increased likelihood of bronchodilator administration in children with HRV-specific coinfections as compared to HRV mono-infections.

We must acknowledge the limitations of this study. The use of archived respiratory specimens proves to be problematic with respect to biases associated with sampling and exposure misclassification. First, not all individuals with ARTIs may be symptomatic; and furthermore, not all symptomatic individuals with ARTI may seek medical care. Thus, only those individuals who sought medical care were eligible for inclusion into this study. Additionally, not every individual who seeks medical care for an ARTI will have a viral respiratory test ordered. Therefore, it is likely that certain cases of ARTI (e.g., symptomatic infections requiring medical attention or more severe infections eliciting increased effort to

identify an etiologic agent) may be overrepresented in the sample population. Indeed, over 75% of our population was hospitalized.

An additional limitation was the unavailability of all eligible specimens collected during the study period. Specimens were not available for the following reasons: (1) the specimen tested negative for all viruses and was not archived because the entire volume of sample was used for clinical testing, (2) the specimen tested positive for at least one virus and the laboratory technician decided not to archive the remaining volume of the sample, or (3) the remaining volume of the sample was retained for in-house validation studies. Compared to those children for whom specimens were included in the study, children for whom specimens were unavailable (n=105) were significantly younger (p=0.035), were more likely to reside in an urban area (p=0.009), and were less likely to be admitted to the hospital (p<0.001). If children whose specimens were excluded were more likely to be coinfected than those children whose specimens were included (a large proportion were RSV-positive), then our observed measures of association between coinfection and severity of illness, specifically ICU admission, would be biased away from the null hypothesis of no association.

Underestimation of respiratory coinfections likely occurred for several reasons. First, every possible respiratory pathogen was not included in the respiratory panel so this study was limited to coinfections involving influenza A and B, parainfluenza 1, 2, and 3, respiratory syncytial virus, adenovirus, rhinovirus, human bocavirus, and human metapneumovirus. However, those viruses included are the most common respiratory viral pathogens infecting children. Second, if a clinician ordered a virus-specific DFA in addition to a viral culture panel and the DFA was positive, viral culture would not be completed. Case in point - among the 105 specimens not included in this study, which were therefore limited to UIHC routine testing procedures alone, only 2 viral

coinfections were detected. Third, additional coinfections may have been missed as the viral culture and DFA methods utilized for influenza A and B, parainfluenza 1, 2, and 3, respiratory syncytial virus, and adenovirus are less sensitive than the molecular methods utilized for rhinovirus, human bocavirus, human metapneumovirus, and adenovirus. Finally, only a limited proportion of our sample had information regarding bacterial pathogens. When available in the patient medical record, information regarding results from additional bacterial tests performed by the UIHC Clinical Microbiology Laboratory or the University Hygienic Laboratory (UHL) on other specimens (collected at the time a specimen for viral culture was collected) was included in secondary analyses.

This was a cross-sectional study using archived respiratory specimens that were collected as a part of routine medical care. As such, we are unable to establish causality with regard to coinfections and severe ARTI in children as we cannot firmly establish a temporal sequence of events.

It is likely that further under-ascertainment of coinfections occurred as a result of the disconnect between the timing of potential coinfection and specimen collection; for example, a patient may be infected with a single pathogen at time A, then infected with a second pathogen at time B, and at time C the first infection has resolved but the second has not. Sampling at time A, B, or C may therefore produce different results with respect to the presence of a coinfection. Unless multiple samples were taken over the duration of the illness, little can be done to address to this problem or to identify the significance of concurrent versus consecutive infections.

Over-estimation of respiratory coinfections due to co-detection of asymptomatic viral shedding post-infection and acute infection with a second virus may have also occurred. Among the 407 children for whom medical records were available, 3.5% of virus-positive children did not have a

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symptomatic ARTI. Molecular methods may have over-estimated the presence of viable virus through detection of viral particles or nonviable virus. Some would argue that co-detection is a more appropriate term for what we define as coinfection in this study. Some studies have attempted to address this concern by measuring viral load in respiratory specimens with quantitative, real-time PCR assays. The underlying assumption is that high viral loads represent acute infection whereas low viral loads may represent shedding of virus from a previous infection. Due to financial constraints, we were unable to use these methods for this study.

Data quality and completeness was expected to vary among covariates selected for abstraction from electronic medical records. Attempts were made to correct inaccurate or incomplete data. Any misclassification of clinical covariates is expected to be non-differential as the investigator was blinded to coinfection and illness severity status at the time of abstraction. Exclusion of incomplete information from analysis may lead to biased estimates of association as this assumes that the observations with complete data are representative of all observations. Furthermore, exclusion of observations may result in an insufficient sample size for subsequent analyses. Some specimens originated from children outside the UIHC medical system (e.g., tests could not be conducted at local hospital and were sent to the UIHC Clinical Microbiology Laboratory) and were not accompanied by additional data from the patient medical record. These samples were excluded from the analysis.

Finally, our sample size may have been insufficient to detect certain measures of association. Though we began with 559 archived respiratory specimens, the effective sample size was whittled down as children with multiple specimens were limited to the first specimen collected during the first episode of ARTI, children without accessible medical records were excluded, children not

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meeting the primary or secondary definition of ARTI were excluded, and as outpatients were excluded from analyses focused on ICU admission, requirement for mechanical ventilation, and length of hospitalization.

 Despite these limitations, the methodology of the current study sets it apart from earlier studies. Unlike many of its predecessors, this study was designed with an *a priori* hypothesis in mind concerning a role for coinfections in severe ARTI. Furthermore, few studies have attempted to control for potential confounders, and to our knowledge, none have explored the role of potential effect modifiers.

The University of Iowa Hospital and Clinics is a comprehensive academic medical center and regional referral center. Our results may not be applicable to other hospital-based settings due to the composition of the patients seeking care at UIHC and the behavior of the physicians providing care; however, the underlying biological theory suggests that an association could still exist if virusbacteria coinfections do in fact result in more severe illness, though the measure of association may be attenuated.

Further studies are needed to elucidate the clinical significance of polymicrobial infections, particularly with respect to severity of illness and the role of certain viruses as they occur in coinfections, such as HRV, HBoV, and Ad. Many of the studies published thus far have been retrospective in nature, relying on archived respiratory specimens. Those that do rely on prospective collection of respiratory specimens and accompanying medical record data are often limited by small sample sizes and do not attempt to estimate a measure of association (either odds ratio or risk ratio) for severity of illness as it relates to coinfection. Those that do generate a measure of association often do not control for important confounders. Future studies should include both viral and bacterial pathogens for consideration. *S. pneumoniae*, *Streptococcus pyogenes*,

H. influenzae, *Staphylococcus aureus*, *B. pertussis*, *Moraxella catarrhalis*, *Mycoplasma pneumonia*, and *Chlamydophila pneumoniae* have been identified as bacterial pathogens of the respiratory tract in immunocompetent children [118] and their role in virus-bacteria coinfections should warrant further consideration.

In summary, the results of this study suggest that polymicrobial infections are common in this pediatric population and that these infections, particularly those involving bacteria, may lead to more severe disease outcomes. It is our hope that this study will inform medical and public health professionals with regard to the epidemiology of polymicrobial infections and their potential importance as a cause of severe acute respiratory tract infection in children. Furthermore, the results of this study could contribute to the ongoing discussion of the importance of diagnostic ability to reliably detect multiple concurrent pathogens in a single patient.

APPENDIX

Figure A1. Evolutionary relationships of 174 HRV taxa (5'NCR protocol). The evolutionary history was inferred using the Neighbor-Joining method [1]. The bootstrap consensus tree inferred from 1000 replicates [2] is taken to represent the evolutionary history of the taxa analyzed [2]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [3] and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 174 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 [4]. Prefix ARTI.RK denotes study specimens.

Source: 1. Saitou N & Nei M (**1987**) The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* **4**:406-425.

2. Felsenstein J (**1985**) Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* **39**:783-791.

3. Tamura K, Nei M & Kumar S (**2004**) Prospects for inferring very large phylogenies by using the neighbor-joining method. *Proceedings of the National Academy of Sciences* (*USA*) **101**:11030-11035.

4. Tamura K, Dudley J, Nei M & Kumar S (**2007**) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Molecular Biology and Evolution* **24**:1596-1599.

 $\frac{}{0.005}$

Figure A2. Evolutionary relationships of 37 HBoV taxa. The evolutionary history was inferred using the Neighbor-Joining method [1]. The bootstrap consensus tree inferred from 1000 replicates [2] is taken to represent the evolutionary history of the taxa analyzed [2]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [3] and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 151 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 [4]. Prefix ARTI.BV denotes study specimens.

Source: 1. Saitou N & Nei M (**1987**) The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* **4**:406-425.

2. Felsenstein J (**1985**) Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* **39**:783-791.

3. Tamura K, Nei M & Kumar S (**2004**) Prospects for inferring very large phylogenies by using the neighbor-joining method. *Proceedings of the National Academy of Sciences* (*USA*) **101**:11030-11035.

4. Tamura K, Dudley J, Nei M & Kumar S (**2007**) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Molecular Biology and Evolution* **24**:1596-1599.

Table A1 Virus-specific mono-infection and coinfection prevalence estimates for all specimens, with duplicates (n=559)

Note: CoxS (coxsackievirus), Flu A (influenza A virus), Flu B (influenza B virus), PIV NOS (parainfluenza virus not otherwise specified).

^a Denominator is virus-specific total number of positive specimens.

 b Denominator is total number of specimens, n=559.</sup>

^c 95% binomial confidence interval associated with prevalence percent estimate for total number of positive specimens.

^d Ad genotypes include Ad1 (n=1, 0% coinfected), Ad2 (n=6, 66.7% coinfected), Ad3 (n=8, 50.0% coinfected), Ad5 (n=1, 0% coinfected), Ad41 (n=1, 100% coinfected), and non-typeable (n=2, 50.0% coinfected).

| Co-detected Viruses | N |
|----------------------------|----------------|
| 2 Viruses | |
| HRV + RSV | 17 |
| HRV + HBoV | 7 |
| $HRV + PIV3$ | 5 |
| $HRV + hMPV$ | 4 |
| HBoV + RSV | 3 |
| $Ad + RSV$ | 3 |
| $Ad + HRV$ | 3 |
| PIV NOS + RSV | $\overline{2}$ |
| PIV 3 + HBoV | $\overline{2}$ |
| $PIV2 + HBOV$ | $\overline{2}$ |
| PIV 3 + RSV | 1 |
| PIV 3 + $hMPV$ | 1 |
| hMPV + RSV | |
| hMPV + CoxS | 1 |
| HBoV + Flu A | 1 |
| HBoV + Ad | 1 |
| 3 Viruses | |
| $Ad + HRV + HBoV$ | $\overline{2}$ |
| HRV + HBoV + hMPV | 1 |
| HRV + HBoV + RSV | 1 |
| $HRV + hMPV + RSV$ | |
| HRV + PIV NOS + RSV | |
| hMPV + PIV NOS + RSV | |
| $Ad + HRV + RSV$ | |
| Total | 61 |

Table A2 Frequency of viral coinfections for all specimens, with duplicates (n=559)

Note: CoxS (coxsackievirus), Flu A (influenza A virus), PIV NOS (parainfluenza virus not otherwise specified).

Table A3 Virus-specific mono-infection and coinfection prevalence estimates for specimens from eligible children excluded from study due to unavailable specimen, with duplicates (n=116)

Note: CoxS (coxsackievirus), Flu A (influenza A virus), Flu B (influenza B virus), PIV NOS (parainfluenza virus not otherwise specified).

^a Limited to UIHC Clinical Microbiology Laboratory virological assays.

^b Denominator is virus-specific total number of positive specimens.

 \textdegree Denominator is total number of specimens, n=116.

^d 95% binomial confidence interval associated with prevalence percent estimate for total number of positive specimens.

e Ad genotypes not determined.

Table A4 Frequency of viral coinfections for specimens from eligible children excluded from study due to unavailable specimen, with duplicates (n=116)

Table A5 Demographic characteristics of children for all specimens with accessible medical record information, with duplicates (n=529)

Table A5 Continued

 Note: Excludes 30 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Note: Excludes 30 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A7 Clinical characteristics (indicators of severity) associated with specimens for all children with accessible medical record information, with duplicates (n=529)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A8 Clinical characteristics (length of hospitalization) associated with specimens for all children with accessible medical record information, with duplicates (n=529)

Table A8 Continued

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Includes non-UIHC hospitalizations when applicable.

Table A9 Clinical characteristics (antimicrobial use and inflammation markers) associated with specimens for all children with accessible medical record information, with duplicates (n=529)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Denotes antibiotics used prior to UIHC episode during which specimen was collected.

Table A10 Clinical characteristics (diagnoses) associated with specimens for all children with accessible medical record information, with duplicates (n=529)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A11 Clinical characteristics (symptoms) associated with specimens for all children with accessible medical record information, with duplicates (n=529)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.
Table A12 Clinical characteristics (medical history) associated with specimens for all children with accessible medical record information, with duplicates (n=529)

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

^b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table A13 Laboratory characteristics for all specimens with accessible medical record information, with duplicates (n=529)

Note: Excludes 30 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Other may include bronchial wash/biopsy, lung aspirate/biopsy, nasopharyngeal swab, nasal swab, THS, tissue biopsy.

Table A14 Demographic characteristics of children with accessible medical record information and confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=346)

Table A14 Continued

 Note: Excludes 3 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A15 Mean age of children for specimens with accessible medical record information and confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=346)

Note: Excludes 3 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A16 Clinical characteristics (indicators of severity) associated with all specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=346)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A17 Clinical characteristics (length of hospitalization) associated with all specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=346)

Table A17 Continued

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Includes non-UIHC hospitalizations when applicable.

Table A18 Clinical characteristics (antimicrobial use and inflammation markers) associated with all specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=346)

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Denotes antibiotics used prior to UIHC episode during which specimen was collected.

Table A19 Clinical characteristics (diagnoses) associated with all specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates $(n=346)$

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A20 Clinical characteristics (symptoms) associated with all specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=346)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A21 Clinical characteristics (medical history) associated with all specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=346)

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table A22 Laboratory characteristics of specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI, without duplicates (n=346)

Note: Excludes 3 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Other may include bronchial wash/biopsy, nasal swab, THS, tissue biopsy.

Table A23 Demographic characteristics of children with accessible medical record information and confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI or concern for ARTI in the absence of traditional symptoms, without duplicates (n=392)

Table A23 Continued

 Note: Excludes 13 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A24 Mean age of children for specimens with accessible medical record information and with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI or concern for ARTI in the absence of traditional symptoms, without duplicates (n=392)

Note: Excludes 13 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A25 Clinical characteristics (indicators of severity) associated with specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI or concern for ARTI in the absence of traditional symptoms, without duplicates (n=392)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A26 Clinical characteristics (length of hospitalization) associated with specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI or concern for ARTI in the absence of traditional symptoms, without duplicates (n=392)

Table A26 Continued

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Includes non-UIHC hospitalizations when applicable.

Table A27 Clinical characteristics (antimicrobial use and inflammation markers) associated with specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI or concern for ARTI in the absence of traditional symptoms, without duplicates (n=392)

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Denotes antibiotics used prior to UIHC episode during which specimen was collected.

Table 28 Clinical characteristics (diagnoses) associated with specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI or concern for ARTI in the absence of traditional symptoms, without duplicates (n=392)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A29 Clinical characteristics (symptoms) associated with specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI or concern for ARTI in the absence of traditional symptoms, without duplicates (n=392)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A30 Clinical characteristics (medical history) associated with specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI or concern for ARTI in the absence of traditional symptoms, without duplicates (n=392)

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

^b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table A31 Laboratory characteristics of specimens with accessible medical record information from children with confirmed (physician diagnosed) or suspected (physician-documented symptoms) ARTI or concern for ARTI in the absence of traditional symptoms, without duplicates (n=392)

Note: Excludes 13 specimens for which medical record information was accessible Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

^b Other may include bronchial wash/biopsy, lung aspirate/biopsy, nasopharyngeal swab, nasal swab, THS, tissue biopsy.

Table A32 Available demographic characteristics of children with accessible medical record information from eligible specimens excluded from study due to unavailability of specimen, with duplicates (n=108)

Note: Excludes 8 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A33 Mean age of children with accessible medical record information from eligible specimens excluded from study due to unavailability of specimen, with duplicates (n=108)

Note: Excludes 8 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A34 Available clinical characteristics (indicators of severity) associated with specimens with accessible medical record information from eligible children excluded from study due to unavailable specimen, with duplicates (n=108)

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A35 Clinical characteristics (length of hospitalization) associated with specimens with accessible medical record information from eligible children excluded from study due to unavailable specimen, with duplicates (n=108)

Table A35 Continued

a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

b Includes non-UIHC hospitalizations when applicable.

Table A36 Laboratory characteristics of specimens with accessible medical record information from eligible children excluded from study due to unavailable specimen, with duplicates (n=108)

Note: Excludes 8 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category All PIV combines frequencies for PIV 1-3 and PIV NOS.

Table A37 Demographic characteristics of children for HRV-tested specimens with accessible medical record information, with duplicates (n=529)

Table A37 Continued

Note: Excludes 30 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

a The category HRV Other includes 1 HRV B and 5 non-typeable HRVs.

Table A38 Mean age of children for HRV-tested specimens with accessible medical record information, with duplicates (n=529)

Note: Excludes 33 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category HRV Other includes 1 HRV B and 5 non-typeable HRVs.

Table A39 Clinical characteristics (indicators of severity) associated with HRV-tested specimens with accessible medical record information, with duplicates (n=529)

a The category HRV Other includes 1 HRV B and 5 non-typeable HRVs.

Table A40 Clinical characteristics (length of hospitalization) associated with HRV-tested specimens with accessible medical record information, with duplicates (n=529)

Table A40 Continued

^a The category HRV Other includes 1 HRV B and 5 non-typeable HRVs.

b Includes non-UIHC hospitalizations when applicable.

Table A41 Clinical characteristics (antimicrobial use and inflammation markers) associated with HRV-tested specimens with accessible medical record information, with duplicates (n=529)

^a The category HRV Other includes 1 HRV B and 5 non-typeable HRVs.

b Denotes antibiotics used prior to UIHC episode during which specimen was collected.

Table A42 Clinical characteristics (diagnoses) associated with HRV-tested specimens with accessible medical record information, with duplicates (n=529)

a The category HRV Other includes 1 HRV B and 5 non-typeable HRVs.

Table A43 Clinical characteristics (symptoms) associated with HRV-tested specimens with accessible medical record information, with duplicates (n=529)

a The category HRV Other includes 1 HRV B and 5 non-typeable HRVs.

Table A44 Clinical characteristics (medical history) associated with HRV-tested specimens with accessible medical record information, with duplicates (n=529)

^a The category HRV Other includes 1 HRV B and 5 non-typeable HRVs.

^b Includes history of cancer, transplant, and chronic conditions that may lead to increased risk of ARTI (see Table 2).

Table A45 Laboratory characteristics of HRV-tested specimens with accessible medical record information, with duplicates (n=529)

Note: Excludes 30 specimens for which medical record information was inaccessible. Percentages may not add to 100.0 due to rounding. Virus-specific estimates exclude coinfections.

^a The category HRV Other includes 1 HRV B and 5 non-typeable HRVs

b Other may include bronchial wash/biopsy, lung aspirate/biopsy, nasopharyngeal swab, nasal swab, THS, tissue biopsy

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