**Trip-Search:**

**1.: "infection" and "more than one virus"**

**2,: “viral coinfection” and “respiratory”**

**1. [Does Viral Co-Infection Influence the Severity of Acute Respiratory Infection in Children?](https://www.ncbi.nlm.nih.gov/pubmed/27096199%22%20%5Ct%20%22_blank) [Full Text available with Trip Pro](https://www.tripdatabase.com/account/upgrade)**

(OR: 0.324; P-value = 0.016) and oxygen necessity (OR: 0.328; P-value = 0.001). All these findings were replicated in the UK cohort.The presence of **more** **than** **one** **virus** in hospitalized children with ARI is very frequent but it does not seem to have a major clinical impact in terms of severity. However bacterial superinfection increases the severity of the disease course. On the contrary, pneumococcal vaccination plays a protective role. (...) Does Viral Co-**Infection** Influence the Severity of Acute Respiratory **Infection** in Children? Multiple viruses are often detected in children with respiratory **infection** but the significance of co-**infection** in pathogenesis, severity and outcome is unclear. To correlate the presence of viral co-**infection** with clinical phenotype in children admitted with acute respiratory **infections** (ARI).We collected detailed clinical information on severity for children admitted with ARI as part of a Spanish

**2016 PloS one**

**2. [Viral Agents Causing Acute Respiratory Infections in Children under Five: A Study from Eastern India](https://www.ncbi.nlm.nih.gov/pubmed/28018433%22%20%5Ct%20%22_blank) [Full Text available with Trip Pro](https://www.tripdatabase.com/account/upgrade)**

for detection of viruses using mono/multiplex real-time polymerase chain reaction. Results. A total of 300 children aged 2-60 months with ARIs were included. The most common age group affected with LRI was 2-12 mo and with URI was >12-60 mo. Viruses were detected in 248 cases. In URI, 77 were positive for single virus and 19 were positive for **more** **than** **one** **virus**; in LRI, 113 were positive for single virus and 12 were positive for **more** **than** **one** **virus**. The most common viruses isolated from URI cases were (...) Viral Agents Causing Acute Respiratory **Infections** in Children under Five: A Study from Eastern India Background. Acute respiratory **infections** (ARIs) are important cause of mortality and morbidity in children under five in developing country. Methods. This observational study was conducted over two-year period in a tertiary care teaching hospital of Eastern India. Nasal and throat swabs were collected, transported to the laboratory at 2-8°C in viral transport media, and then processed

**2016 International journal of pediatrics**

**3. [Viral coinfection is shaped by host ecology and virusâ€“virus interactions across diverse microbial taxa and environments](https://www.ncbi.nlm.nih.gov/pubmed/28469939%22%20%5Ct%20%22_blank) [Full Text available with Trip Pro](https://www.tripdatabase.com/account/upgrade)**

Viral coinfection is shaped by host ecology and virusâ€“virus interactions across diverse microbial taxa and environments **Infection** of **more** **than** **one** **virus** in a host, coinfection, is common across taxa and environments. Viral coinfection can enable genetic exchange, alter the dynamics of **infections**, and change the course of viral evolution. Yet, a systematic test of the factors explaining variation in viral coinfection across different taxa and environments awaits completion. Here I employ three (...) microbial data sets of virus-host interactions covering cross-**infectivity**, culture coinfection, and single-cell coinfection (total: 6,564 microbial hosts, 13,103 viruses) to provide a broad, comprehensive picture of the ecological and biological factors shaping viral coinfection. I found evidence that ecology and virus-virus interactions are recurrent factors shaping coinfection patterns. Host ecology was a consistent and strong predictor of coinfection across all three data sets: cross-**infectivity**

**2017 Virus Evolution**

**4. [Immunohistochemical assessment of respiratory viruses in necropsy samples from lethal non-pandemic seasonal respiratory infections. (Abstract)](http://www.ncbi.nlm.nih.gov/pubmed/20876328%22%20%5Ct%20%22_blank)**

 months. In 42.3% of cases, only one virus was detected: 11 (36.7%) RSV; 7 (23.3%) AdV; 4 (13.3%) PIV2; 3 (10%) FLU A; 2 (6.7%) FLU B; 2 (6.7%) PIV3; and 1 (3.3%) PIV1. Co-**infection** with **more** **than** **one** **virus** was observed in 41 (57.7%) cases. No positive correlations were observed between the presence of viral antigens and seasonality of the **infection**, sex, age or histopathological findings.Non-pandemic seasonal respiratory viruses are involved in a significant number of deaths in paediatric patients (...) Immunohistochemical assessment of respiratory viruses in necropsy samples from lethal non-pandemic seasonal respiratory **infections**. Acute respiratory **infections** are an important cause of childhood morbidity and mortality throughout the world, and viruses have often been reported to be an aetiological agent. This study aimed to identify respiratory viruses in paraffin-embedded samples of paediatric lung necropsy specimens, using immunohistochemistry on tissue microarray slides.Retrospective

**2010 Journal of Clinical Pathology**

**5. [Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study.](http://www.ncbi.nlm.nih.gov/pubmed/24055451%22%20%5Ct%20%22_blank) [Full Text available with Trip Pro](https://www.tripdatabase.com/account/upgrade)**

. Selection analysis of the MERS-CoV genomes reveals the expected accumulation of genetic diversity including changes in the S protein. The genetic diversity in the Al-Hasa cluster suggests that the hospital outbreak might have had **more** **than** **one** **virus** introduction.We present the largest number of MERS-CoV genomes (21) described so far. MERS-CoV full genome sequences provide greater detail in tracking transmission. Multiple introductions of MERS-CoV are identified and suggest lower R0 values. Transmission (...) Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. Since June, 2012, Middle East respiratory syndrome coronavirus (MERS-CoV) has, worldwide, caused 104 **infections** in people including 49 deaths, with 82 cases and 41 deaths reported from Saudi Arabia. In addition to confirming diagnosis, we generated the MERS-CoV genomic sequences obtained directly from patient samples to provide important information on MERS-CoV

**2013 Lancet**

8 results for

**“viral coinfection” and “respiratory”**

Primary Research

**1. [Epidemiology of Respiratory Syncytial Virus-related Hospitalizations and the Influence of Viral Coinfections in Southern Austria in a 7-year Period. (Abstract)](http://www.ncbi.nlm.nih.gov/pubmed/31651808%22%20%5Ct%20%22_blank)**

Epidemiology of **Respiratory** Syncytial Virus-related Hospitalizations and the Influence of **Viral** **Coinfections** in Southern Austria in a 7-year Period. The aim of this study was to determine the **respiratory** syncytial virus (RSV) epidemiology and to analyze the influence of risk factors and coinfections over the last years.Retrospectively all infants, children and adolescents hospitalized due to **respiratory** disease with positive RSV test [hospitalized for RSV infection (RSV-H)] between January 1 (...) . **Viral** **coinfection** (most common influenza virus, adenovirus and rhinovirus) was diagnosed in 37 cases (5%) resulting in a more severe course of disease. Main risk factors of coinfection were siblings and crowding. Mortality was 0.27% (2/745). Both children had coinfection with influenza A virus and were multihandicapped (15 and 20 years of age, respectively).Prematurity and underlying morbidities play a marked role in RSV-H. **Viral** **coinfections** aggravated disease with death in 2 multihandicapped

**2020 Pediatric Infectious Dsease Journal**

Primary Research

**2. [Systematic review and meta-analysis of respiratory viral coinfections in children.](http://www.ncbi.nlm.nih.gov/pubmed/26919484%22%20%5Ct%20%22_blank) [Full Text available with Trip Pro](https://www.tripdatabase.com/account/upgrade)**

Systematic review and meta-analysis of **respiratory** **viral** **coinfections** in children. **Respiratory** infections are a common cause of paediatric morbidity. Clinical outcomes in children hospitalized with single **respiratory** virus infection are compared with those with two or more viral-**viral** **coinfection**. Studies were restricted to those reporting on children aged less than 5 years (PROSPERO CRD#42014009133). Published data to calculate risk ratios (RR) comparing children with single viral infections (...) = 1.24, 95% confidence intervals (CI) = 1.00-1.55) and ICU admission (RR = 1.08 to RR = 1.31, 95% CI = 0.93-1.83) increased but remained non-significant. Point estimates suggested an increased risk of ICU admission in those coinfected with either **respiratory** syncytial virus or human metapneumovirus compared with those with single infection but was non-significant. Our findings suggest that coinfection is not associated with increased clinical severity, but further investigations by pathogen pairs

**2016 Respirology**

Primary Research

**3. [Viral coinfection in acute respiratory infection in Mexican children treated by the emergency service: A cross-sectional study](http://www.ncbi.nlm.nih.gov/pubmed/25903455%22%20%5Ct%20%22_blank) [Full Text available with Trip Pro](https://www.tripdatabase.com/account/upgrade)**

**Viral** **coinfection** in acute **respiratory** infection in Mexican children treated by the emergency service: A cross-sectional study Acute **respiratory** infections (ARIs) cause illness. Children under five years of age are highly vulnerable to these infections. **Viral** **coinfection** or multiple viral infection is a variable that can have a significant impact on the evolution of these diseases.This cross-sectional study was carried out in Mexican children (under five years of age) who had an ARI and who (...) syncytial virus (RSV) (14%), rhinovirus (hRV) (12%), bocavirus (hBoV) (9%), influenza virus (IF) (7%), and parainfluenza (PIF) (4%). The frequency of **viral** **coinfections** was 31.62%, and multiple logistic regression analysis revealed that hMPV, RSV, PIF, and hBoV were independently associated with multiple viral infection. No difference was found in the clinical manifestation of children with simple and multiple infections. Simple hMPV infection was associated with patients who presented with severe ARI

**2015** **Italian journal of pediatrics**

Primary Research

**4. [The burden of single virus and viral coinfections on severe lower respiratory tract infections among preterm infants: a prospective birth cohort study in Brazil. (Abstract)](http://www.ncbi.nlm.nih.gov/pubmed/25361184%22%20%5Ct%20%22_blank)**

The burden of single virus and **viral** **coinfections** on severe lower **respiratory** tract infections among preterm infants: a prospective birth cohort study in Brazil. **Respiratory** syncytial virus (RSV) is associated with severe lower **respiratory** tract infection (LRTI), especially in preterm infants. Other viruses, co-detected with RSV, may play a role in the severity of **respiratory** outcomes.This prospective epidemiologic study of severe LRTI incidence among children born ≤35 weeks gestational age (...) at 3 sites in Brazil (2008-2010) followed a birth cohort for 1 year post-enrollment. Nasal washes from subjects with LRTI were tested for **respiratory** viruses using polymerase chain reaction. The primary outcome was the incidence of severe LRTI requiring hospitalization associated with RSV infection. Secondary outcomes included identification of viruses associated with LRTI, alone or coinfections, and risk factors associated with severe LRTI.Among 303 subjects, 176 (58.1%) experienced LRTI. Among

**2014** **Pediatric Infectious Dsease Journal**

Primary Research

**5. [Respiratory viral coinfections identified by a 10-plex real-time reverse-transcription polymerase chain reaction assay in patients hospitalized with severe acute respiratory illness--South Africa, 2009-2010. (Abstract)](http://www.ncbi.nlm.nih.gov/pubmed/23169964%22%20%5Ct%20%22_blank)**

**Respiratory** **viral** **coinfections** identified by a 10-plex real-time reverse-transcription polymerase chain reaction assay in patients hospitalized with severe acute **respiratory** illness--South Africa, 2009-2010. Data about **respiratory** coinfections with 2009 pandemic influenza A virus subtype H1N1 during the 2009-2010 influenza pandemic in Africa are limited. We used an existing surveillance program for severe acute **respiratory** illness to evaluate a new multiplex real-time polymerase chain reaction (...) assay and investigate the role of influenza virus and other **respiratory** viruses in pneumonia hospitalizations during and after the influenza pandemic in South Africa.The multiplex assay was developed to detect 10 **respiratory** viruses, including influenza A and B viruses, parainfluenza virus types 1-3, **respiratory** syncytial virus (RSV), enterovirus, human metapneumovirus (hMPV), adenovirus (AdV), and rhinovirus (RV), followed by influenza virus subtyping. Nasopharyngeal and oropharyngeal specimens

**2012** **Journal of Infectious Diseases**

Ongoing systematic reviews

**6. [Respiratory viral coinfection and disease severity in children: a systematic review](http://www.crd.york.ac.uk/prospero/display_record.asp?src=trip&ID=CRD42014007250" \t "_blank)**

**Respiratory** **viral** **coinfection** and disease severity in children: a systematic review Print | PDF PROSPERO This information has been provided by the named contact for this review. CRD has accepted this information in good faith and registered the review in PROSPERO. CRD bears no responsibility or liability for the content of this registration record, any associated files or external websites. Email salutation (e.g. "Dr Smith" or "Joanne") for correspondence: Organisation web address: Timing

**2015** **PROSPERO**

Primary Research

**7. [Prevalence, clinical outcomes and rainfall association of acute respiratory infection by human metapneumovirus in children in Bogotá, Colombia.](http://www.ncbi.nlm.nih.gov/pubmed/31601181%22%20%5Ct%20%22_blank) [Full Text available with Trip Pro](https://www.tripdatabase.com/account/upgrade)**

, multiplex RT-PCR was performed on 502 and a virus was detected in 420 children with acute **respiratory** infection (ARI). The study group had a median age of 21 months (IQR 7-60), with similar proportion of males and females (56.4 and 43.6% respectively) and 5.2% (CI 95 3.3-7.8%) prevalence of HMPV infection. The group with HMPV infection showed a greater frequency of **viral** **coinfection** (22.7% vs 14% P = 0.03) compared with ARI caused by other viruses. The rate of bacterial coinfection (P = 0.31), presence (...) of comorbidities (p = 0.75), length of hospital stay (P = 0.42), need for mechanical ventilation (P = 0.75) and mortality (P = 0.22) were similar for HMPV and other viral infections. A moderate correlation was established between HMPV infection and rainfall peaks (Spearman's Rho 0.44 p = 0.02).Human metapneumovirus was the fifth most frequently isolated virus in children with ARI, had similar clinical behavior and severity to other viruses but a higher rate of **viral** **coinfection**. Its peaks seem to correlate

**2019** **BMC Pediatrics**Primary Research

**8. [A Single-Center Study of Viral Respiratory Tract Infections in Hospitalized Children From the Kurdistan Region of Iraq](http://www.ncbi.nlm.nih.gov/pubmed/30014009%22%20%5Ct%20%22_blank) [Full Text available with Trip Pro](https://www.tripdatabase.com/account/upgrade)**

detected in 203 out of 269 (75.5%) samples. The most frequent viruses were enterovirus/rhinovirus (n = 88; 32.7%), **respiratory** syncytial virus (n = 55; 20.4%), and human metapneumovirus (n = 36; 13.4%). In 42 samples (15.6%), coinfections with 2 or more **respiratory** viruses were detected, with enterovirus/rhinovirus, **respiratory** syncytial virus, human metapneumovirus, and adenovirus being identified as the most common agents in **viral** **coinfections** in these patients. (...) A Single-Center Study of Viral **Respiratory** Tract Infections in Hospitalized Children From the Kurdistan Region of Iraq Viral **respiratory** infections are among the most common causes of disease in humans, particularly in young children, and remain a major public health problem worldwide. For many geographic regions, there is limited epidemiological information on the main causative agents of these diseases. In this article, we investigated, in a prospective study, the viral agents leading

**2018** **Global pediatric health**