FTD Respiratory pathogens 21*

Clinical utility of syndromic testing in respiratory infections

Compendium of scientific literature

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Epidemiology of respiratory infections among adults in Qatar (2012–2017)

Hamad Eid Al-Romaihi, Maria K. Smatti, Nandakumar Ganesan, Shazia Nadeem, Elmoubasher Farag, Peter V. Coyle, Joanne Daghfal Nader, Hebah A. Al-Khatib, Emad B. Elmagboul, Said Al Dhahry, Salih A. Al-Marri, Asmaa A. Al Thani, Abdullatif Al Khal, Muna A. Al Maslamani, Hadi M. Yassine.

PLoS ONE. 2019;14(6):e0218097. DOI: https://doi.org/10.1371/journal.pone.0218097.

Abstract

Background
Limited data is available about the etiology of influenza like illnesses (ILIs) in Qatar.

Objectives
This study aimed at providing preliminary estimates of influenza and other respiratory infections circulating among adults in Qatar.

Methods
We retrospectively collected data of about 44,000 patients who visited Hamad General Hospital clinics, sentinel sites, and all primary healthcare centers in Qatar between 2012 and 2017. All samples were tested for influenza viruses, whereas about 38,000 samples were tested for influenza and a panel of respiratory viruses using Fast Track Diagnostics (FTD) RT-PCR kit.

Results
Among all ILIs cases, 20,278 (46.5%) tested positive for at least one respiratory pathogen. Influenza virus was predominating (22.6%), followed by human rhinoviruses (HRVs) (9.5%), and human coronaviruses (HCoVs) (5%). A detection rate of 2–3% was recorded for mycoplasma pneumonia, adenoviruses, human parainfluenza viruses (HPIVs), respiratory syncytial virus (RSV), and human metapneumovirus (HMPV). ILIs cases were reported throughout the year, however, influenza, RSV, and HMPV exhibited strong seasonal peaks in the winter, while HRVs circulated more during fall and spring. Elderly (>50 years) had the lowest rates of influenza A (13.9%) and B (4.2%), while presenting the highest rates of RSV (3.4%) and HMPV (3.3%). While males had higher rates of HRVs (11.9%), enteroviruses (1.1%) and MERS CoV (0.2%), females had higher proportions of influenza (26.3%), HPIVs (3.2%) and RSV (3.6%) infections.

Conclusion
This report provides a comprehensive insight about the epidemiology of ILIs among adults in the Qatar, as a representative of Gulf States. These results would help in improvement and optimization of diagnostic procedures, as well as control and prevention of the respiratory infections.

FTD Respiratory pathogens 21 was used to identify the aetiology of influenza-like illnesses in this large retrospective study in Qatar. In the study, 46.5% of the samples tested positive for at least one respiratory pathogen included in the assay.

FTD Respiratory pathogens 21 is a multiplex PCR assay that simultaneously detects 20 viruses and 1 bacterium involved in respiratory tract infections.

For more information: fast-trackdiagnostics.com

FTD Respiratory pathogens 21 (FTD 2.1) is CE-IVD marked for diagnostic use in the EU. A research use only (RUO)-labeled product is also available. RUO labeled product is not for clinical or diagnostic use. Product availability may vary from country to country and is subject to varying regulatory requirements. Please contact your local representative for availability.

Clinical characteristics of influenza virus-induced lower respiratory infection during the 2015 to 2016 season

Kazuhiro Uda, Kensuke Shoji, Chitose Koyama-Wakai, Munehiro Furuichi, Noriyasu Iwase, Seiichiro Fujisaki, Shinji Watanabe, Isao Miyairi.

Journal of Infection and Chemotherapy. 2018;24(6):407-13. DOI: https://doi.org/10.1016/j.jiac.2018.01.002.

Abstract

Background
Influenza A(H1N1)pdm09 virus infections often manifest severe respiratory symptoms, particularly in patients with a past history of allergic disease. Most of these findings were reported during the 2009 pandemic. The purpose of this study was to detail the clinical characteristics of influenza virus-induced lower respiratory infection (LRI) during the A(H1N1)pdm09-predominant 2015–2016 season.

Methods
We retrospectively reviewed the clinical characteristics of influenza-induced LRI cases in children admitted to a tertiary children's hospital. Molecular diagnostic evaluation was performed on samples obtained from the most severe cases.

Results
We identified 66 patients with influenza-associated hospitalization and included 21 patients with influenza virus-induced LRI for analyses. Twelve patients (57%) were admitted to the pediatric intensive care unit, seven (33%) required mechanical ventilation, and three (14%) required extracorporeal membrane oxygenation. Plastic bronchitis (PB) was identified in six patients (29%), among whom a past medical history of asthma or food allergy were noted in all six patients. A past history of allergic disease was more common among patients with, than among those without, PB ($p = 0.009$). A(H1N1) pdm09 was detected from all the PB cases, and phylogenetic analyses of the hemagglutinin and neuraminidase genes demonstrated that this virus belonged to subclades 6B.1 and 6B.2. In the six PB cases, we found one patient with H275Y mutation in neuraminidase.

Conclusion
Allergic disease was a risk factor for developing PB due to influenza A(H1N1) pdm09 infection during the 2015–16 season.

FTD Respiratory pathogens 21 was used to identify influenza virus-induced lower respiratory infections in hospitalized children with severe cases.

FTD Respiratory pathogens 21 is a multiplex PCR assay that simultaneously detects 20 viruses and 1 bacterium involved in respiratory tract infections.

This kit detects and differentiates influenza A, 2009-pandemic influenza A(H1N1) virus (swine-lineage), and influenza B.*

**Inclusivity study, kit instruction for use.*

For more information: fast-trackdiagnostics.com

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Two cases of primary human parechovirus pneumonia in adults

Takashi Nishida, Takashi Ishiguro, Kenji Takano, Taisuke Isono, Yoichi Kobayashi, Yoshihiko Shimizu, Noboru Takayanagi.

Respiratory Medicine Case Reports. 2019;28:100949. ISSN 2213-0071.
DOI: https://doi.org/10.1016/j.rmcr.2019.100949.

Abstract

Human parechoviruses (HPeV) are mainly isolated from upper respiratory tract infections and gastroenteritis in children. HPeV has not been screened for in the past studies of community-acquired pneumonia (CAP) in adults, and its association with CAP is unknown. We present two cases that HPeV was detected by multiplex polymerase chain reaction for respiratory viruses using bronchoalveolar lavage fluid and diagnosed as pneumonia caused by HPeV.

FTD Respiratory pathogens 21 was used to detect human parechovirus from respiratory specimens in two adults with pneumonia in Japan.

FTD Respiratory pathogens 21 is a multiplex PCR assay that simultaneously detects 20 viruses and 1 bacterium involved in respiratory tract infections.

This FTD kit detects human parechovirus subtypes 1–8, 10, 14, and 16–18.*

**Inclusivity study, kit instruction for use.*

For more information: fast-trackdiagnostics.com

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Epidemiology of Human Parechovirus Type 3 Upsurge in 2 Hospitals, Freiburg, Germany, 2018

Roland Elling, Sindy Böttcher, Florian du Bois, Alexandra Müller, Christiane Prifert, Benedikt Weissbrich, Jörg Hofmann, Klaus Korn, Anna-Maria Eis-Hübinger, Markus Hufnagel, Marcus Panning.

Emerging Infectious Diseases. 2019;25(7):1384-8. DOI: https://doi.org/10.3201/eid2507.190257.

Abstract

In 2018, a cluster of pediatric human parechovirus (HPeV) infections in 2 neighboring German hospitals was detected. Viral protein 1 sequence analysis demonstrated co-circulation of different HPeV-3 sublineages and of HPeV-1 and -5 strains, thereby excluding a nosocomial outbreak. Our findings underline the need for HPeV diagnostics and sequence analysis for outbreak investigations.

FTD Respiratory pathogens 21 was used to detect human parechovirus from respiratory specimens in this investigational study in Freiburg, Germany.

FTD Respiratory pathogens 21 is a multiplex PCR assay that simultaneously detects 20 viruses and 1 bacterium involved in respiratory tract infections.

The FTD kit detects human parechovirus subtypes 1–8, 10, 14, and 16–18.*

**Inclusivity study, kit instruction for use.*

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Adenovirus types associated with severe respiratory diseases: A retrospective 4-year study in Kuwait

Wassim Chehadeh, Anfal Al-Adwani, Sonia Elezebeth John, Shaikhah Al-Dhufairi, Hessa Al-Dousari, Maha Alkhaledi, Widad Al-Nakib.

Journal of Medical Virology. 2018;90(6):1033-9. DOI: https://doi.org/10.1002/jmv.25059.

Abstract

Human adenovirus (HAdV) infection can result in a severe respiratory disease. The aim of this study was to identify HAdV types detected in patients hospitalized for severe respiratory illness. The study population consisted of 743 patients with severe respiratory disease admitted to four major hospitals in Kuwait between January 2013 and December 2016. Respiratory specimens were retrospectively screened for 20 respiratory viruses by real-time PCR. The HAdV hexon gene was amplified and directly sequenced, and HAdV types were identified by performing Bayesian phylogenetic analysis. HAdV DNA was detected in 27 (3.6%) patients, with peaks in November and March. Most patients were infants and young children suffering from pneumonia or acute bronchiolitis. The detected HAdV types were C1, C2, C5, B3, and B7. Clusters of HAdV C1, C2, and C5 were observed with high posterior probability. All patients infected with HAdV C5 and 50% of patients infected with HAdV C2 or B7 were admitted to the intensive care unit (ICU). Co-infection with other viruses was detected in 44.4% of patients. The most common co-infecting virus was rhinovirus (HRV). HAdV/HRV co-infection was detected in two children who presumably developed disseminated HAdV infection and died. This is the first report describing the circulation of HAdV types associated with severe outcomes in Kuwait. These findings highlight the need for a national surveillance system to monitor changes in predominant HAdV types and increased numbers of severe respiratory infections.

FTD Respiratory pathogens 21 was used to assess the presence of adenovirus as the etiological agent for severe respiratory diseases.

FTD Respiratory pathogens 21 is a multiplex PCR assay that simultaneously detects 20 viruses and 1 bacterium involved in respiratory tract infections.

This test detects seven species of HAdV (A to G).*

**Inclusivity study, kit instruction for use.*

For more information: fast-trackdiagnostics.com

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Role of multiplex PCR analysis in children with febrile seizures

Jelena Naric, Jürgen Rissland, Arne Simon, Martin Poryo, Ludwig Gortner, Sascha Meyer.

Wien Med Wochenschr. 2017;167:246-50. DOI: https://doi.org/10.1007/s10354-016-0462-1.

Abstract

Background
The aim of this study was to assess multiplex PCR analysis in detecting causative viruses in children with febrile seizures.

Methods
The study was a retrospective analysis comparing data from a pre-multiplex era (2009) with a period after the introduction of routine respiratory multiplex analysis (2010–2013) in children with febrile seizures.

Results
We included 200 children with febrile seizures (mean age: 29.5 ± 1.4 months; 104 male) in the study. In 2009, in 10 out of 49 (20%) children, microbiology testing (bacterial/fungal) was positive compared with a rate of 74 out of 151 (49%) children during 2010–2013 ($p < 0.01$). The rate of positive virological studies increased from 10 (20%) in 2009 to 73 (48.3%) in the period 2010–2013 ($p < 0.01$). Multiplex PCR analysis confirmed viral infections in 52 of 73 cases (71.2%).

Conclusion
Routine multiplex PCR analysis fosters the detection of respiratory viruses in children with febrile seizure. The precise role of multiplex analysis in the management of these children awaits further clarification.

To evaluate the role of multiplex PCR in children with febrile seizures, **FTD Respiratory pathogens 21** was used to analyze respiratory samples of children admitted to a university children's hospital in Austria.

FTD Respiratory pathogens 21 is a multiplex PCR assay that simultaneously detects 20 viruses and 1 bacterium involved in respiratory tract infections.

For more information: fast-trackdiagnostics.com

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Viral aetiology of bronchiolitis in hospitalised children in Qatar

Ibrahim Janahi, Anas Abdulkayoum, Fawziya Almeshwesh, Mohamed Alkuwari, Ahmed Al hammadi, Marwah Alameri.

BMC Infect Dis. 2017;17:139. DOI: https://doi.org/10.1186/s12879-017-2225-z.

Abstract

Background
Bronchiolitis is considered one of the earliest and most common causes of hospitalization in young children. Development of molecular technologies allowed a better understanding of bronchiolitis aetiology. Results from cohort studies evaluating the association between single, multiple viral infections and clinical outcomes are conflicting. Data on viral bronchiolitis in children were found to be limited in Qatar. This study aimed to determine frequency and seasonal trends of viral pathogens causing acute bronchiolitis, and to explore association between viral pathogens, disease severity and length of stay (LOS).

Methods
This is a retrospective descriptive study, including children admitted in 2010 and 2011 with acute bronchiolitis. Presenting history, physical examination and respiratory viral co-infections as detected by molecular assays were analyzed.

Results
At least one virus was detected in 315/369 (85.4%) of included children with single and multiple viruses in 67 and 33% of cases respectively. Respiratory syncytial virus (RSV) was the most detected virus, accounting for 51.2% followed by rhinovirus (RV) in 25.5% of cases. Fall and summer admissions were associated with longer LOS. On multivariate logistic regression analysis, retraction (OR 3.96; 95% CI 1.64,9.59) and age group 1–3 months (OR 3.09; 95% CI 1.06,9.05) were associated with longer LOS. Crepitation (OR 9.15; 95% CI 1.58,53.13), retraction (OR 4.10; 95% CI 1.05,16.12) and respiratory rate (OR 1.46; 95% CI 1.28,1.66) were associated with moderate to severe bronchiolitis. Identifying the viral agent did not influence disease severity or LOS.

Conclusion
Clinical presentation is of more relevance to LOS and disease severity than the detected viruses. Future studies should investigate the interplay between climate characteristics, population's factors and the most detectable circulating viruses.

FTD Respiratory pathogens 21 was used to identify the aetiology of acute bronchiolitis in a retrospective study in Qatar.

FTD Respiratory pathogens 21 is a multiplex PCR assay that simultaneously detects 20 viruses and 1 bacterium involved in respiratory tract infections.

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The potential influence of human parainfluenza viruses detected during hospitalization among critically ill patients in Kuwait, 2013–2015

Sahar Essa, Haya Al-tawalah, Sarah AlShamali, Widad Al-Nakib.

Virol J. 2017;14:19. DOI: https://doi.org/10.1186/s12985-017-0681-0.

Abstract

Background
The four types of human parainfluenza viruses (PIV) are important causes of community-acquired pneumonia, particularly in children; however, limited information exists about the incidence of PIV in critically ill patients. The aim of this study is to describe the spectrum, incidence and clinical features of PIV-associated infections diagnosed during the hospital stay of patients admitted to pediatric intensive care unit (PICU) and intensive care unit (ICU) of 5 medical centers across Kuwait.

Methods
This was a population-based, retrospective study from 2013 to 2015. Specimens were analyzed by molecular methods. This analysis was performed using the database of Virology Unit, Mubarak Al-Kabeer Hospital. Data from 1510 admitted patients with suspected respiratory viral infections was extracted.

Results
The database contained a total of 39 (2.6%) patients infected with PIV (53.8% male and 46.2% females) and 20 (51.3%) were under 1 year of age. The most frequently isolated type was type 3 (28, 71.8%) followed by type 1 (9, 23.1%). At admission the most common clinical diagnosis was pneumonia in 12 patients (30.8%, $p < 0.05$) followed by bronchiolitis in 10 patients (25.6%).

Conclusion
PIV plays an important yet unrecognized role in the outcomes of PIUC and ICU patients. Our results contribute to the limited epidemiologic data of PIV in PIUC and ICU in this region.

FTD Respiratory pathogens 21 was used to detect human parainfluenza virus (HPiV) in a cohort of patients admitted to the pediatric intensive care and intensive care units of five medical centers across Kuwait.

FTD Respiratory pathogens 21 is a multiplex PCR assay that simultaneously detects 20 viruses and 1 bacterium involved in respiratory tract infections.

It detects and differentiates the 4 main human parainfluenza viruses: HPiV-1, HPiV-2, HPiV-3 and HPiV-4.*

**Inclusivity study, kit instruction for use.*

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Kit information

FTD Respiratory pathogens 21

Overview
Five-tube multiplex for detection of influenza A virus, influenza A(H1N1) virus (swine-lineage), influenza B virus, human rhinovirus, human coronaviruses NL63, 229E, OC43, and HKU1, human parainfluenza viruses 1, 2, 3, and 4, human metapneumoviruses A/B, human bocavirus, human respiratory syncytial viruses A/B, human adenovirus, enterovirus, human parechovirus, *Mycoplasma pneumoniae*; and internal control.

Principle
Multiplex real-time PCR for detection of pathogen genes by TAQMAN technology.

Targets

1. Primer/probe mix	influenza A virus influenza B virus influenza A(H1N1) virus (swine-lineage) human rhinovirus
2. Primer/probe mix	human coronavirus NL63 human coronavirus 229E human coronavirus OC43 human coronavirus HKU1
3. Primer/probe mix	human parainfluenza virus 2 human parainfluenza virus 3 human parainfluenza virus 4 internal control
4. Primer/probe mix	human parainfluenza virus 1 human metapneumoviruses A/B human bocavirus *Mycoplasma pneumoniae*
5. Primer/probe mix	human respiratory syncytial viruses A/B human adenovirus enterovirus human parechovirus

Specimen
This test is for use with extracted RNA and DNA from nasopharyngeal swab specimens of human origin.

Compatibility
FTD Respiratory pathogens 21 was validated with the Thermo Fisher Scientific APPLIED BIOSYSTEMS 7500 Real-time PCR System and the bioMérieux NUCLISENS EASYMAG. For other cyclers and extraction methods, refer to the compatibility list at www.fast-trackdiagnostics.com. The customer is fully responsible to validate the FTD SARS-CoV-2 assay on the instrument they select to use.

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