



April 2024

Rhinovirus, Adenovirus, RSV A and Influenza A detected in samples from persons with recent respiratory illness in Mombasa County

Issue Brief

Background

We received 15 respiratory specimens collected by Mombasa County Department of Health for diagnosis of potential respiratory pathogens. Nucleic acid extracts were obtained using the QIACUBE HT extraction platform and processed by reverse transcription RT-PCR (a molecular diagnostic assay we have processed with such samples since 2008 at the KEMRI-Wellcome Trust Research Programme). The assay targets 9 respiratory virus pathogens including SARS-CoV-2, respiratory syncytial virus (RSV; type A and B), influenza viruses (type A, B and C), human metapneumovirus, rhinovirus.

Findings

Viral respiratory pathogens were detected in 11/15 (73%) samples analysed. Rhinovirus, adenovirus, RSV A and influenza A and were detected in 4, 4, 2 and 1 sample, respectively. No sample was found positive for RSV B, influenza B, influenza C, human metapneumovirus or SARS-CoV-2. These results are summarised in the appended table (see next page) while also indicating the RT-PCR cycle thresholds (Ct) for the positive samples which are indicative of the viral quantities in the patients. The lower the Ct value, the higher the virus quantities.

Interpretation

Our findings indicate multiple respiratory viruses have recently circulated in Mombasa County, and the noted surge of respiratory illness cases is likely caused by multiple respiratory viral pathogens. We detected RSV A, influenza A and adenovirus in the samples that the Mombasa Department of Health shared. These are well known as agents of acute respiratory illness (ARI). Most of the detections were associated with Ct values of less than 25.0 which strongly implicates a causative role of the detected viruses (see table below) in the observed illness. Notably 4 samples had rhinovirus detected which is also commonly detected in healthy individuals. However rhinovirus has also been found in persons with lower respiratory track illness. The samples that tested negative for all the targets we assayed could be either: (a) infected with a virus that we did not attempt diagnosis/ analysis e.g. endemic coronaviruses (OC43, NL63, 229E or HKU1), parainfluenza 1-4, or pneumococcus or (b) the samples were not properly collected or (c) the samples were collected late into the illness course when pathogen quantities had declined to below the limit of detection of our detection method. Such samples can be in future processed by metagenomic sequencing.

Conclusion

Whereas SARS-COV-2 is now widely recognised to be one of the top causes of ARI, it should be noted that there are several other respiratory viruses that have potential to cause serious respiratory disease. Testing of the full range of known respiratory pathogens for persons with acute respiratory illness is important for better patient management and to provide data for prioritisation of pathogen interventions.

Table: Summary finding of respiratory virus screen of 15 samples received from Mombasa – March 2024

Sample_name	Human metapneumovirus	Rhinovirus	Influenza A	Influenza B	Influenza C	Adenovirus	RSV A	RSV B	SARS-CoV-2	Comment
001	-	-	-	-	-	-	-	-	-	None of our targets detected
002	-	-	23.2	-	-	-	-	-	-	Influenza A positive, like cause of ARI
003	-	-	-	-	-	-	-	-	-	None of our targets detected
004	-	-	-	-	-	-	22.5	-	-	RSV A positive, like cause of ARI
005	-	28.4	-	-	-	-	-	-	-	Rhinovirus detected, can be just a bystander
006	-	35.7	-	-	-	-	29.7	-	-	RSV A positive, like cause of ARI
007	-	-	-	-	-	20.8	-	-	-	Adenovirus positive, like cause of ARI
008	-	-	-	-	-	-	-	-	-	None of our targets detected
009	-	27.5	-	-	-	-	-	-	-	Rhinovirus detected, can be just a bystander
010	-	-	-	-	-	27	-	-	-	Adenovirus positive, like cause of ARI
011	-	-	-	-	-	-	-	-	-	None of our targets detected
012	-	31.4	-	-	-	-	-	-	-	Rhinovirus detected, can be just a bystander
013	-	-	-	-	-	20.1	-	-	-	Adenovirus positive, like cause of ARI
014	-	29	-	-	-	-	-	-	-	Rhinovirus detected, can be just a bystander
015	-	-	-	-	-	19.1	-	-	-	Adenovirus positive, like cause of ARI

Notes: In the comments section, red font is for diagnosis we identified the most likely causative agent, blue only partially certainty that the causative agent was identified and grey no agent was detected and further analysis is required. The grey and blue font samples can be processed in future by metagenomic approaches. Ideally more samples need to be analyzed and the metadata for the samples e.g. age of patients, sex, travel history, symptom range, co-morbidities should be provided for a better understanding of the illness context and risk factors for improved recommendations.