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Metagenomic analysis of viral diversity in respiratory samples from patients with respiratory tract infections in Kuwait

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A metagenomic approach based on target independent next-generation sequencing has become a known method for the detection of both known and novel viruses in clinical samples. This study aimed to use the metagenomic sequencing approach to characterize the viral diversity in respiratory samples from patients with respiratory tract infections. We have investigated 86 respiratory samples received from various hospitals in Kuwait between 2015 and 2016 for the diagnosis of respiratory tract infections. A metagenomic approach using the next-generation sequencer to characterize viruses was used. According to the metagenomic analysis, an average of 145, 019 reads were identified, and 2% of these reads were of viral origin. Also, metagenomic analysis of the viral sequences revealed many known respiratory viruses, which were detected in 30.2% of the clinical samples. Also, sequences of non-respiratory viruses were detected in 14% of the clinical samples, while sequences of non-human viruses were detected in 55.8% of the clinical samples. The average genome coverage of the viruses was 12% with the highest genome coverage of 99.2% for respiratory syncytial virus, and the lowest was 1% for Torque teno midi virus 2. Our results showed 47.7% agreement between multiplex real-time PCR and metagenomics sequencing in the detection of respiratory viruses in the clinical samples. Though there are some difficulties in using this method to clinical samples such as specimen quality, these observations are indicative of the promising utility of the metagenomic sequencing approach for the identification of respiratory viruses in patients with respiratory tract infections.

Recent Publications

1. Madi N, Al Nakib W, Mustafa A S, Khan M and Habibi N (2018) Metagenomic analysis of viral diversity in respiratory samples from patients with respiratory tract infections in Kuwait. *Journal of Medical Virology* 90(3):412-420.
2. Chehadeh W, Al Qaseer M, Albaksami O, Altawalah H, Suhail Ahmad, Madi N, John SE and Al Nakib W (2015) Phylogenetic analysis of HIV-1 subtypes and drug resistance profile in treatment-naïve people from Kuwait. *Journal of Medical Virology* 87(9):1521-6.
3. Madi N, Al Qasser M, Abdul Khalik D, Edan R and Al Nakib W (2015) Clinical utility of viral load management of CMV infection in SOT patients in Kuwait. *Transplantation Proceedings* 47(6):1802-7.
4. Al Tawalah H, Madi N and Al Qaseer M (2014) Prevalence of blood borne viruses in the dialysis unit, Mubarak Al-Kabeer Hospital. *Kuwait Medical Journal* 47(1):30-32.
5. Madi N, Al Tawalah H and Al Nakib W (2014) Clinical presentations of HHV-6 infection in infants and children in Kuwait: A retrospective study. *Advances in Microbiology* 4(15):1088-11094.

Biography

Nada Madi is an Assistant Professor in the Department of Microbiology, Faculty of Medicine at Kuwait University where she has been a Faculty Member since January 2015. She completed her PhD and MSc at Faculty of Medicine, Kuwait University and her Undergraduate study at Faculty of Science, Kuwait University. Her research interest lies in the area of developing advanced techniques in viral diagnostics such as metagenomics approach for the detection of viruses causing different diseases such as respiratory tract infections and gastroenteritis.

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