THE SEEPLEX® RV DETECTION KIT IDENTIFIES PATHOGENS IN THE MAJORITY OF RESPIRATORY OUTBREAKS FROM THE GREATER TORONTO AREA, ONTARIO, CANADA

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Abstract
Background: If we want to inform public health decisions in the timely detection of viral respiratory pathogens in outbreaks when culture-based methods are used as the sole-source of virus detection and identification, then molecular molecular methods may provide a better understanding of the etiology of respiratory virus outbreaks and may help prevent the spread of infection. Seegene, Inc. (Seegene, Inc., Rockville, MD 20850) has developed the Seeplex® RV Detection kit to identify respiratory virus pathogens; it is a multiplexed reverse transcriptase-polymerase chain reaction assay that detects 12 respiratory viruses including human rhinovirus A, human rhinovirus B, respiratory syncytial virus A/B, parainfluenza 1-4, coronavirus OC43, coronavirus 229E/NL63, parainfluenza 1, parainfluenza 2, parainfluenza 3, human metapneumovirus, and adenovirus. The distribution of outbreaks with a pathogen identified by molecular means was; 30% (n=19) no pathogen identified, 52.5% (n=33) 1 pathogen, 14.5% (n=9) 2 pathogens and 3.0% (n=2) 3 pathogens. In contrast, culture-based protocols identified pathogens in fewer outbreaks; 63% (n=40) no identification, 35% (n=22) 1 pathogen, 5% (n=3) 2 pathogens and 0% (n=0) 3 pathogens. Multiplexed molecular methods allow for the identification of a respiratory viral pathogen in the majority of respiratory outbreaks in our region. Given the uncertainty of culture-based protocols and the increased turnaround time associated with culture-based detection methods, multiplexed molecular methods are powerful tools for understanding and managing respiratory virus outbreaks.

Methods
All nasopharyngeal (NP) swabs from declared respiratory outbreaks in the GTA (September 1, 2007-February 1, 2008) were included in this analysis. All specimens were collected from long-term care facilities, schools, workplaces or healthcare facilities. Total nucleic acid was extracted from each specimen using the easyMag automated extraction system (Diagnostic Hybrids, Athens, OH, USA) followed by post-extraction analysis of cDNA by the Seeplex® RV Detection kit protocol. Fisher’s exact test was carried out using GraphPad Prism 5.01 (Graphad Software Inc.).

Results
Conclusions: Multiplexed molecular methods allow for the identification of a respiratory viral pathogen in the majority of respiratory outbreaks in our region. Molecular methods also detected larger numbers of human rhinovirus A and B and adenovirus-positive specimens than culture-based identification methods. Multiplexed molecular methods are a powerful tool for understanding and managing respiratory virus outbreaks.

References

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