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Severe influenza pneumonia surveillance: clinical and translational epidemiology

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Objective

To present the development and implementation of the SIPS project, a statewide, hospital-based surveillance system for severe community-acquired pneumonia (sCAP) in Kentucky.

Introduction

The threat of epidemics due to nonhuman strains of influenza A viruses is ever present (1). Surveillance is a critical aspect of pandemic preparedness for early case detection (2). Identification of the index cases of a pandemic virus can trigger public health mitigation efforts (3). To develop an appropriate surveillance process, it is important to understand the two possibilities of pandemic evolution. A new pandemic may begin with mild cases, during which surveillance should be concentrated on work/school absenteeism and in physician offices. The other possibility begins with severe cases, characterized by sCAP, respiratory failure and ICU admission. As the syndrome of pneumonia is not reportable to health agencies for public health surveillance, a year-round, hospital-based surveillance mechanism may be an important tool for early case detection in the event of an epidemic of sCAP. To fill these gaps, we developed a statewide, hospital-based surveillance network for sCAP surveillance in Kentucky.

Methods

All acute care hospitals in Kentucky were invited to participate in the project. A case of sCAP was defined as a patient admitted to an ICU with the physician diagnosis of CAP. Upon patient identification, demographic and clinical characteristics were entered into an Internet-based data collection form. All patients had a nasopharyngeal swab sent to the University of Louisville Infectious Diseases Reference Laboratory for identification of viral pathogens. The Luminex xTAG respiratory viral panel multiplex PCR was used for viral identification. Clinical cultures were utilized to identify bacterial and fungal causes of sCAP. Statistical Process Control (SPC) charts were used to identify outbreaks. Chloropleth maps were used for spatial analysis. Each analytical mechanism was provided in real-time via the study website.

Results

Surveillance for sCAP began in December 2008, prior to the 2009 H1N1 influenza A pandemic. Six facilities representing all areas of the state, both rural and metropolitan were included. The website, www.kyflu.net was developed for study coordination. From December 1, 2008, through August 2011, 458 cases of sCAP were identified. There were multiple areas of special-cause variance on the SPC charts, though there were no unusual clusters upon spatial evaluation of the maps. The most common virus identified in patients with sCAP was rhinovirus (n = 39, 20%), followed by 2009 H1N1 influenza A virus (n = 34, 18%). These viruses were cultured in chicken eggs, genetically analyzed and further studied in mouse and ferret models to determine viral evolution and virulence mechanisms. One influenza virus was found to be hypervirulent compared to other strains.

Conclusions

The SIPS project is an ongoing effort that has thus far successfully identified patients with sCAP of viral etiology. Surveillance for sCAP is important not only for the early detection of cases in the event of a pandemic of influenza but for other etiologies as well. Furthermore, through translational research activities, we were able to identify novel strains of influenza and are working to further characterize the evolution of these viruses in our state.

Keywords

Influenza; respiratory virus; outbreak; pandemic; epidemic

References

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Citation: Emerging Health Threats Journal 2011, **4**: 11051 - DOI: 10.3402/ehtj.v4i0.11051