

2511. Estimating Numbers of Influenza Excess Deaths and Hospitalizations at the State-Level

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Background. Influenza surveillance activities inform the state public health response to influenza but may under-detect influenza events. We applied modeling methods to estimate influenza excess pneumonia and influenza (P&I) and respiratory and circulatory (R&C) deaths and hospitalizations to Colorado data from July 1, 2007 through June 30, 2016.

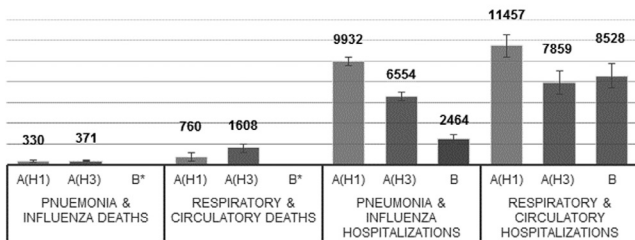
Methods. Data included P&I and R&C deaths and hospitalizations (events) listed as underlying or primary diagnoses on death certificates and hospital discharge records, respectively, and local sentinel lab surveillance for influenza A and B. We evaluated four negative binomial models for each event type. Model 1 estimated a seasonal baseline of events from a weekly time series of diagnoses and included coefficients for excess events due to influenza A and B. In Model 2, we created influenza A subtype coefficients by applying subtype proportions from national surveillance to the percent of local specimens positive for influenza A. Models 3 and 4 were similar to Models 1 and 2, except influenza-specific diagnoses were removed from the baseline model and added to final estimates. We calculated 95% confidence intervals (CI) using bootstrap methods. Statewide laboratory-based surveillance was a reference.

Results. Model 2 better captured seasonal variability than Model 1. Models 3 and 4 inconsistently predicted events. According to Model 2 (figure), during 9 influenza seasons there were 701 P&I deaths (median 37 A(H1) and 52 A(H3) per year), 2,368 R&C deaths (median 73 A(H1) and 203 A(H3) per year), 18,950 P&I hospitalizations (median 1,068 A(H1), 1,021 A(H3), and 272 B per year), and 27,844 R&C hospitalizations (median 1,156 A(H1), 1,112 A(H3), and 1,037 B per year) due to influenza. While A(H3) was most frequently associated with death, A(H1) was more often associated with hospitalization. Compared with laboratory-based surveillance, we estimated 1.2 and 4.0 times as many P&I/R&C deaths and 1.3 and 1.9 times as many P&I/R&C hospitalizations.

Conclusion. Robust statistical models applied to state-level data better estimate local influenza burden, and augment those of laboratory-based surveillance. Such models may be useful for prevention planning and more accurate public information about the burden of influenza.

Figure.

Estimates of Total Number of Influenza Excess Deaths and Hospitalizations with 95% Confidence Intervals--CO, 2007-8 through 2015-16



* Influenza B not included in influenza excess death models.

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2512. The Trend in the Incidence of Herpes Zoster and Effect of Immune Status on Severity and Healthcare Utilization: Population-Based Study of Korea, 2003–2015

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Background. An increase in the incidence of herpes zoster (HZ) is observed in South Korea. However, the effects of changes in population structure and immune status on the incidence and severity of HZ have not been well studied. We investigated longitudinal changes in the incidence of HZ and disease severity over time and according to age and comorbidities.

Methods. We used population-based medical records from the National Health Insurance Service for approximately 50,000,000 subscribers from 2003 to 2015. Herpes

zoster cases (period 2003–2015) or its complications (period 2007–2015) were identified using ICD-10 codes (B02-B02.9) and comorbid conditions were also collected. The annual crude incidence rates and age-standardized rates of HZ were calculated using direct standardization to the 2010 Korean Census population. Negative binomial regression was used to analyze the yearly incidence rate ratio (IRR) and the impact of immune status on disease severity. Healthcare utilization was compared across age groups and comorbid conditions.

Results. The crude and age-sex standardized incidence rate of HZ annually increased over the study period (Figure 1). Such trend was also observed after adjusting for age, sex, immune status, and socioeconomic status (adjusted IRR 1.06, 95% CI 1.05–1.08). The incidence was highest in 61–80 year-olds whereas the relative increase was high in 11–30 year-olds (Figure 2). Incidences of HZ-associated hospitalizations and complications also steadily increased over time as well as across age groups (Figure 3) although the proportions among HZ cases remained stable. Among HZ cases, the risk of complications was higher among elderly population (71 years; IRR 1.1–1.23), patients with comorbidities (IRR 1.17, 95% CI 1.14–1.19), and male patients (IRR 1.19, 95% CI 1.09–1.38). The length of hospital stay (median 12 days [range: 7–25] vs. 8 days [range: 6–14], $P < 0.001$) was significantly greater in HZ patients with comorbidities than those without.

Conclusion. The incidence of HZ has rapidly increased independent of population structure change. It is necessary to establish strategies such as vaccination to reduce the incidence of HZ, and efforts should be made to reduce the disease burden among those with comorbidities.

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2513. The Utility of Next-Generation Sequencing for Detection of Causative Viruses in Sera of Patients With Acute Myocarditis

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Background. Myocarditis is an inflammatory disease of the myocardium with a wide range of clinical presentations, occasionally leading to cardiac dysfunction and heart failure. Although viral infections are considered to be the most common etiology of myocarditis, identification of the causative virus is still challenging. Recently, next-generation sequencing (NGS) has been applied in the diagnosis of infectious diseases. The aim of this study was to evaluate the utility of NGS for detection of causative viruses in sera of patients with acute myocarditis.

Methods. Twelve pediatric and five adult patients hospitalized for acute myocarditis were included in this study. Serum samples before initiation of treatment were collected in the acute phase and analyzed with NGS-based approach. To detect pathogen-derived sequencing reads, we performed DNA and RNA sequencing for each sample.

Results. An average of 20,062,443 and 19,506,189 total reads were obtained in DNA and RNA sequencing libraries, respectively. Viral sequence reads were detected in 7 (41%) of the 17 myocarditis patients. Substantial sequence reads of GB virus C (GBV-C) reads were detected from one patient by RNA sequencing; however, its pathogenicity to human is unknown. Detection of Epstein-Barr virus, human parvovirus B19, and respiratory syncytial virus reads by NGS was consistent with PCR or antigen test results. Conversely, the number of detected virus-derived reads was small in most cases. No significant bacterial or fungal reads other than normal bacterial flora was detected.

Conclusion. NGS-based approach may have potential to detect the causative viruses and contribute to clarification of the etiology of acute myocarditis.

Disclosures. All authors: No reported disclosures.

2514. Pediatric Medically Attended Shingles in Alberta, Canada 2016; Preliminary Results

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Background. Herpes zoster (shingles) is a reactivation of latent varicella virus. Shingles is uncommon in children and children vaccinated against varicella may be