Background. In Taiwan, H1N1 vaccination began on November 1, 2009 and coincided with peak H1N1 pandemic activity. Nationwide ecological and case–control studies have identified no substantial interaction between the use of H1N1 vaccines and narcolepsy; however, wild-type H1N1 virus infection might have triggered narcolepsy onset, or potentially confounded the findings.

Methods. Data collected in the nationwide case–control study was reanalyzed. Confirmed narcolepsy cases (Brighton levels 1–2 for ages 0–15 years and 1–4a for ages at least 16 years) with onset during November 1, 2009–September 30, 2010 were included and ascertained receipt of H1N1 vaccines. We compared incidence of narcolepsy between the H1N1 vaccinated and unvaccinated population and assessed daily cumulative risk throughout the study period, with adjustment for age. We applied population estimates (census data, 2009) and daily doses of H1N1 vaccines administered (Influenza Vaccine Information System) to calculate the number of persons and person-time for each group.

Results. There were 22 narcolepsy cases; five (23%) occurred after H1N1 vacc.

Conclusion. We found comparable average and cumulative risk of narcolepsy between the H1N1 vaccinated and unvaccinated Taiwanese population during the 2009–2010 pandemic.

Disclosures. All authors: No reported disclosures.

692. Effects of Regional Climatic Variability on West Nile Virus Outbreaks in the United States

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Session: 66. Public Health: Epidemiology and Outbreaks

Thursday, October 4, 2018: 12:30 PM

Background. Information regarding influenza activity can inform clinical and public health activities. However, current surveillance approaches delay a delay in influenza activity reports (typically 1–2 weeks). Recently, we used data from smartphone-connected thermometers to accurately forecast real-time influenza activity at a national level. Because thermometer readings can be geo-located, we used state-level thermometer data to determine whether these data can improve state-level surveillance estimates.

Methods. We used temperature readings collected by the Kinsa smart-thermometer and mobile device app to develop state-level forecasting models to predict real-time influenza activity (1–2 weeks in advance of surveillance reports). We used state-reported influenza-like illness (ILI) to represent state influenza activity for 48 US states with sufficient surveillance data. Counts of temperature readings, fever episodes and reported symptoms were computed by week. We developed autoregressive time-series models and evaluated model performance in an adaptive out-of-sample manner. We compared baseline time-series models containing lagged state-reported ILI activity to models incorporating exogenous thermometer readings.

Results. A total of 10,262,212 temperature readings were recorded from October 30, 2015 to March 29, 2018. In nearly all of the 48 states considered, weekly forecasts of ILI activity improved considerably when thermometer readings were incorporated. On average, 23.8% cold forecasting accuracy improved by 23.9% when integrated with baseline time-series models. In many states, such as PA, New Mexico, VA, Virginia, New York and SC, out-of-sample forecast error was reduced by more than 50% when thermometer data were incorporated. In general, forecasts were most accurate in states with the greatest number of device readings. During the 2018 influenza season, the average improvement in forecast accuracy was 24.4%, and thermometer readings improved forecasting accuracy in 41, out of 48, states.

Conclusion. Data from smart thermometers accurately track real-time influenza activity at a state level. Local surveillance efforts may be improved by incorporating such information. Such data may also be useful for longer-term forecasting.

Disclosures. I. Singh: Kinsa Inc.: Board Member, Employee and Shareholder, equity received and Salary. S. Pilewski: Kinsa Inc.: Employee and Shareholder, equity received and Salary. V. Petrovic: Kinsa Inc.: Employee and Shareholder, equity received and Salary.

Poster Abstracts • OFID 2018:5 (Suppl 1) • S249
Conclusion. Vector control methods focusing on prevention must be implemented to avoid epidemics of WNV if high temperature is leading to an unusual drought especially at the risk areas, such as Texas and California. However, high temperature with moist spell anomalies in the south central region showed a negative influence on WNV outbreak.

Disclosures. All authors: No reported disclosures.

693. Congenital Zika Syndrome: Assessing the Fatality Rate Since the 2015 Zika Outbreak

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Session: 66. Public Health: Epidemiology and Outbreaks
Thursday, October 4, 2018: 12:30 PM

Background. Many studies have demonstrated a causal link between Zika virus (ZIKV) infection, microcephaly (MCP) and other congenital abnormalities (CA). This study aimed to determine the perinatal case fatality rate in cases of Congenital Zika Syndrome (CZS) in the Rio Grande do Norte State (RN), a Brazilian Northeast State highly impacted by the Zika virus outbreak.

Methods. A cross-sectional study was conducted using data obtained through the State Health Department (SHD) for cases of MCP and CA in Rio Grande do Norte from April 2015 to December 31, 2017. Definition of perinatal period: commences at 22 completed weeks (154 days) of gestation and ends seven completed days after birth. Perinatal case fatality rate is defined as the number of deaths as a fraction of the number of sick persons with a specific disease (>100).

Results. During the study period, there were 519 cases of MCP and others CA notified in RN, of which 150 were confirmed and 126 remain under investigation. The remaining 243 cases have been ruled out by presenting normal exams or due to presenting microcephaly by non-infectious causes. Of the total confirmed cases, 30.0% (45/150) died after birth or during pregnancy. 64.4% (29/45) of confirmed deaths had ZIKV. Eleven cases remain under investigation and five were ruled out.

Conclusion. This study highlights a high rate of perinatal lethality (64.4%) in cases of CZS. Despite the growing number of CZS cases, the real incidence and prevalence might be higher due to the underreporting and lack of resources for confirmatory diagnostic tests (laboratory and imaging). Due to the high rate of lethality, findings predict an increase in the infant mortality rate in areas endemic for arboviruses. Because the severe neurological complications caused by CZS, it is likely to pose a substantial burden on public spending on healthcare. This study may be used to better describe the congenital Zika syndrome, its prognosis and natural history.

Disclosures. All authors: No reported disclosures.

694. The CAGE Study: Prevalence of Acute Gastroenteritis and Enteric Virus Infection in the Community

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Session: 66. Public Health: Epidemiology and Outbreaks
Thursday, October 4, 2018: 12:30 PM

Background. There are currently limited data about the occurrence and characteristics of sporadic acute gastroenteritis (AGE). In this study, we sought to (1) estimate the average point prevalence of AGE over a 1-year period; (2) describe health-seeking behaviors among those with AGE; and (3) calculate the proportion of stool samples testing positive for enteric viral pathogens.

Methods. Starting in October 2016, we recruited 52 weekly, age-stratified, random samples of Kaiser Permanente Northwest members to complete an online survey and, for a subset of participants, to submit a stool specimen. The survey included questions about the occurrence of vomiting and/or diarrhea within the previous 30 days and, for those reporting AGE, related health-seeking behaviors. Collected stool samples were tested for norovirus, astrovirus, sapovirus, and rotavirus by RT-qPCR.

Results. We received a total of 3,483 surveys from eligible participants, 417 (12%) of whom reported having had AGE symptoms (Figure 1). Of these, 70 (17%) sought related medical care across a spectrum of clinical encounter types (Figure 2). We also received a total of 531 stool samples, 74 from symptomatic and 457 from asymptomatic individuals. Among them, we detected norovirus in 12% and 3% of samples (P < 0.0005), respectively; astrovirus and sapovirus in 1% of samples in each group; and rotavirus in 8% and 7% of samples, respectively.

Conclusion. Our findings of AGE within the community are consistent with previous estimates using models of medically attended AGE occurrence and reported rates of health-seeking behavior. The prevalence of enteric viral infection among people in the community without AGE was generally low. These data can be used to generate age-stratified incidence estimates of community AGE and specifically that associated with enteric viral pathogens. Such disease burden data are needed to guide the development, targeting, and anticipated impacts of interventions, such as vaccines.

Disclosures. M. A. Schmidt, Takeda Vaccines, Inc.: Investigator, Research grant. S. B. Salas, Takeda Vaccines, Inc.: Investigator, Research grant. H. Groom, Takeda Vaccines, Inc.: Investigator, Research grant. G. Rosales, Takeda Vaccines, Inc.: Investigator, Research grant. J. Donald, Takeda Vaccines, Inc.: Investigator, Research grant. A. Naleway, Takeda Vaccines, Inc.: Investigator, Research grant.

695. Regional and Longitudinal Mapping of Escherichia coli Antibiotic Susceptibility

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Session: 67. Resistance Mechanisms: Gram-Negative
Thursday, October 4, 2018: 12:30 PM

Background. Antimicrobial resistance (AMR) is a serious threat to global health with local implications. AMR varies regionally; however, limited tools are available to aid practitioners in appropriate antibiotic selection based on statewide antimicrobial susceptibilities. The objective of this study was to map E. coli antibiotic susceptibility regionally and longitudinally in Wisconsin.

Methods. Antibiograms from 2009, 2013, and 2015 were collected from health systems, hospitals, and clinics in Wisconsin, resulting in 218 antibiograms representing 201,091 Gram-negative isolates. E. coli antibiotic susceptibility percentages were weighted by number of isolates and aggregated by county per year.

Results. Spatial interpolation methods (inverse distance weighted, Kriging) were tested by bootstrapping in appropriate antibiotic selection based on statewide antimicrobial susceptibilities. The objective of this study was to map E. coli antibiotic susceptibility regionally and longitudinally in Wisconsin.

Disclosures. No reported disclosures.