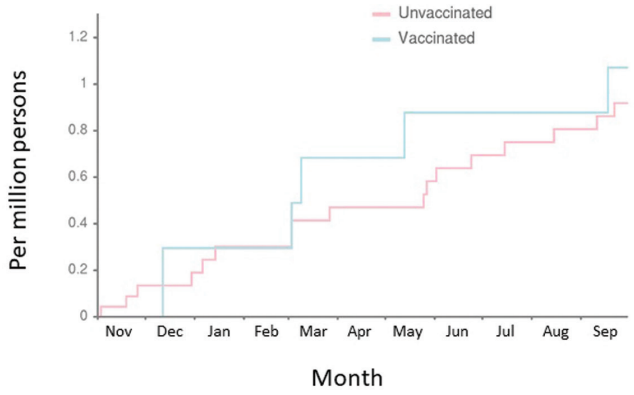
Background. In Taiwan, H1N1 vaccination began on November 1, 2009 and coincided with peak H1N1 pandemic activity. Nationwide ecological and case–control studies have identified no substantial association between the use of H1N1 vaccines and narcolepsy; however, wild-type H1N1 virus infection might have 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 vaccination. The vaccinated population had higher incidence (1.2 vs. 1.0 per million person-years, $P = 0.711$) (incidence rate ratio 1.24, 95% confidence interval [CI] 0.40–3.83), and higher cumulative risk (1.1 vs. 0.9 per million persons, $P = 0.772$) (risk ratio 1.16, 95% CI 0.43–3.14) of narcolepsy (figure). These differences, however, were not significant.

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

Figure. Daily cumulative risk of narcolepsy among the H1N1 vaccinated and unvaccinated groups, November 1, 2009–September 30, 2010.



Disclosures. **All authors: No reported disclosures.**

690. Bacterial Coinfections Among Adults Hospitalized with Community-Associated Influenza, 2016–2017

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Background. Influenza and bacterial coinfection are associated with increased symptom severity and worse health outcomes. We used data from the population based Influenza Hospitalization Surveillance Network (FluSurv-Net) California site to describe adult influenza hospitalizations with and without bacterial coinfections and evaluate the risk of severe disease.

Methods. We included data from adults hospitalized with laboratory confirmed influenza during the 2016/2017 influenza season who resided in San Francisco, Alameda or Contra Costa counties and had a bacterial culture performed ≤ 3 days after admission. We excluded records for healthcare facility-associated influenza. Univariate analyses were used to describe demographics, clinical characteristics and outcomes. Multivariate logistic regression was used to evaluate the effect of bacterial coinfection as a risk factor for severe outcome, defined as admission to an intensive care unit (ICU) or death during hospitalization.

Results. Among 2,029 adult influenza hospitalizations, 102 had ≥1 positive bacterial cultures. There were 119 bacterial isolates from blood (58), respiratory sites (60), and joint fluid (1). The most frequent blood isolates were *Streptococcus pneumoniae* (11), and *Staphylococcus aureus* (10). The most frequent respiratory isolates were *S. aureus* (30) and *S. pneumoniae* (7). Coinfected persons were younger (median age 71 vs. 78), and more likely to have past or current alcohol abuse or immunosuppression. Coinfected patients were more likely to be admitted to an ICU (45% vs. 15%) or die (16.0% vs. 3.6%). The median length of hospital stay was twice as long for coinfected patients (6 days vs. 3). In multivariate analyses, bacterial coinfection (aOR, 4.49; 95% CI, 2.99–6.72), chronic lung disease (aOR, 1.52; 95% CI, 1.18–1.95) and cardiovascular disease (aOR, 1.48; 95% CI, 1.15–1.90) were associated with a severe outcome.

Conclusion. Bacterial coinfection was associated with a four-fold higher risk of ICU admission and death during hospitalization. This study highlights the need for clinicians to maintain a high index of suspicion for the presence of bacterial coinfection among patients with influenza requiring hospitalization.

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691. Real-Time Local Influenza Forecasting Using Smartphone-Connected Thermometer Readings

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Background. Information regarding influenza activity can inform clinical and public health activities. However, current surveillance approaches induce 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, state-level forecasting accuracy improved by 23.9% compared with baseline time-series models. In many states, such as PA, New Mexico, MA, 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 2017–2018 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 local forecasts.

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

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Background. Transmission of WNV to humans in the United States typically occurs between June and September since warm temperatures accelerate mosquito life cycle. Precipitation can cause increase in aquatic breeding but outbreaks often depends upon human water management. We examine epidemiology, patterns of WNV disease transmission, and identification of high-risk areas in the United States from 2003 to 2014.

Methods. Trends and relationships of WNV cases and climatic factors were analyzed among the regions of the United States from 2003 to 2014. Human WNV tabulate data and climatic data were obtained from Centers for Disease Control, and NOAA and Climate Data Guide, respectively. Canonical correspondence analysis (CCA) was performed using variables: (i) neuroinvasive disease cases, non-neuroinvasive disease cases, deaths, presumptiveviremic blood donors, (ii) precipitation, temperature, Palmer Drought Severity Index (PDSI) and population density. The CCA ordination was explained the variability between WNV disease cases andclimatic variables. Biplots were used to visualize the associations between WNV cases and climatic anomalies.

Results. We compared the state wise WNV disease cases in relation to climatic and population density in the United States from 2003 to 2014. A total of 4,064 cases in 2006, 956 cases in 2010 and, 2,141 cases in 2014 were reported in the 32 states of the United States. Colorado state reported the highest WNV cases in 2003 (2,947 cases; 33%), followed by Texas in 2012 (1,868 cases; 35%) and California in 2014 (801 case; 37%). CCA ordination showed distinguishable clustering patterns between south central (Texas, Louisiana, Mississippi, Arkansas, and Oklahoma) and northern Great Plains (North Dakota, South Dakota, and Nebraska) regions (Figure 1). High temperature and prolong drought were the most important variable predictor for high WNV outbreak.