

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Assessing the Reproducibility and Validity of a Zika Epidemiologic Risk Map

Abstract

BACKGROUND: Following the identification of imported Zika cases in Florida in late 2015, an epidemiologic risk map was created and disseminated to county health departments. This map displayed the proportions of women of childbearing age and sociodemographic factors (race, primary language, and low income) determined in a 2011 Key West study to approximate populations at risk for being missed in dengue (an epidemiologically similar arbovirus) prevention outreach campaigns. The goal of this analysis was to evaluate reproducibility of methodology used to generate risk level for a census tract and to evaluate correlation between case numbers and the designated census tract risk using the defined population risk factors.

METHODS: Epidemiologic risk maps were created county-by-county using census-tract level data from the 2010–2014 American Community Survey (ACS) 5-year estimates (Baseline) or the 2012–2016 ACS 5-year estimates (Updated) and standardized methodology. High-, medium-, or low-risk census tracts were defined based on natural breaks in the distribution of each variable within a county. Baseline map risk levels were compared to the original map (Original) created in 2015; the same data layers and methodology were used for both maps. Validation of risk level definition was conducted by overlaying residential address information from 1,680 confirmed and probable 2016–2017 ZIKV infection cases on both the Baseline and Updated maps and comparing the proportion of cases by risk level aggregate for all census tracts.

RESULTS: Map reproducibility was low. Census tract-defined risk on the Baseline map completely matched those on the Original map in only 20/67 (29.9%) counties; more than 10 census tracts were discordant in each of 12/67 (17.9%) counties. Although most cases (85.5% in Baseline; 84.6% in Updated) lived in high- or medium-risk census tracts, there was no gradient between the two, with an equal distribution of cases in each. Census tract-defined risk was not associated with being travel-related or locally acquired.

CONCLUSIONS: The epidemiologic risk map created and disseminated during the ZIKV outbreak in Florida was not reproducible, and defined risk did not consistently align with case distribution. Updating the map with population data accurate to the time of infections did not improve the map's ability to predict high risk areas. A different methodological approach other than using natural breaks to determine risk classification should be used when creating future maps. Factors influencing communication penetration are not necessarily indicative of risk of infection and should be evaluated further.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Epidemiologic Methods; Geographic Information Systems (GIS); Vectorborne Disease
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Comparison on Outcomes of Dogs and Cats Exposed to Rabies before and after Implementation of New Animal Management Recommendations, Kansas 2013-2018

Abstract

BACKGROUND: Rabies is a highly fatal zoonotic disease of mammals. Prior to 2016, Kansas regulation required out-of-date dogs and cats exposed to rabies to be managed like unvaccinated dogs and cats, euthanized or quarantined for six months. Quarantine presents a significant burden on public health resources and owner finances; causing many to opt for euthanasia. In 2016, the National Association of State Public Health Veterinarian's Animal Rabies Compendium recommendations were updated. Management of out-of-date dogs and cats significantly changed from a 6-month quarantine to a 45-day observation. Management of unvaccinated dogs and cats changed from a 6- to a 4-month quarantine.

METHODS: Rabies-positive animals reported to the Kansas Department of Health and Environment were entered into Kansas' electronic disease surveillance system. All dogs and cats exposed to rabies were evaluated for vaccination status, disposition, and outcome. Vaccination status was categorized as current, out-of-date, unvaccinated, or unknown. Disposition was classified as quarantined, observed, or euthanasia. Outcomes of dogs and cats exposed to a rabies-positive animal from January 1, 2013 – December 31, 2015 (period 1) were compared to those from January 1, 2016 – December 10, 2018 (period 2).

RESULTS: In period 1, 184 dogs and cats were exposed to rabies; 81 (44%) were currently vaccinated, 26 (14%) out-of-date, 67 (36%) unvaccinated, and 10 (6%) unknown. Of 26 out-of-date contacts, 13 (50%) were euthanized and 13 (50%) were quarantined for six months (11 survived, one exhibited signs and tested rabies negative, one was euthanized). Of 67 unvaccinated contacts, 51 (76%) were euthanized, 12 (18%) were quarantined for six months (8 survived, one exhibited signs and tested rabies positive, one lost to follow-up, two died from unrelated causes), and four (6%) were killed by the rabies-positive animal. In period 2, 126 dogs and cats were exposed to rabies; 43 (34%) were currently vaccinated, 20 (16%) out-of-date, 62 (49%) unvaccinated, and one unknown. Of 20 out-of-date contacts, three (15%) were euthanized and 17 (85%) were observed for 45 days (all survived). Of 62 unvaccinated contacts, 42 (68%) were euthanized and 20 (32%) were quarantined for four months (all survived).

CONCLUSIONS: No exposed out-of-date dogs or cats developed rabies during quarantine or observation. Fewer out-of-date and unvaccinated dogs and cats were euthanized following rabies exposure after new recommendations were implemented. The updated guidelines have reduced the number of animals euthanized, decreased the burden of public health follow-up, and continue to prevent the spread of rabies in Kansas.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Veterinary Public Health; One Health; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Factors Associated with Inappropriate Administration of Rabies Post-Exposure Prophylaxis in Suburban Cook County, Illinois, 2015-2018

Abstract

BACKGROUND: Rabies is nearly 100% fatal in humans but is preventable when post-exposure prophylaxis (PEP) is given promptly and correctly. The Advisory Committee on Immunization Practices (ACIP) publishes guidelines that detail when animal exposure circumstances warrant PEP administration. Failure to adhere to these guidelines results in unnecessary cost, inconvenience, and minor medical risks to the patient when PEP is given but not indicated. Potential human rabies exposures, including the initiation of PEP, are reportable in Illinois. Since 2015, the Cook County Department of Public Health (CCDPH) has engaged in continuous quality improvement initiatives to increase reporting and improve clinical quality measures related to rabies exposures. In this study, we assessed factors associated with inappropriate administration of PEP.

METHODS: Individuals who received PEP in Suburban Cook County between January 2015 and October 2018 were retrospectively evaluated for appropriateness of treatment according to ACIP guidelines. A multivariable logistic regression model was used to evaluate predictors of inappropriate PEP administration.

RESULTS: During our study period, 279 (54%) of 519 reported individuals received inappropriate administrations of PEP. Individuals who received PEP were 84% less likely to have been treated inappropriately if a local or state health department was consulted (OR 0.16, 95% CI 0.11-0.26). A health department was consulted for 163 (31%) reported PEP recipients. Exposing animal species was also associated with appropriateness of PEP administration. Compared to bats, exposure to a dog or cat was associated with greater odds of inappropriate PEP administration (OR 2.69, 95% CI 1.52-4.76; OR 5.61, 95% CI 1.73-18.14, respectively), while exposure to a raccoon was associated with reduced odds of inappropriate PEP administration (OR 0.25, 95% CI 0.09-0.72). Patient age and sex were not significantly associated with inappropriate PEP administration.

CONCLUSIONS: Consultation with a health department was the single most protective factor against inappropriate administration of PEP in Suburban Cook County. As the majority of patients were given PEP without consulting a health department, this is an area where substantial improvement can be made to reduce the burden of unnecessary PEP. Healthcare providers should be especially mindful when considering PEP for domestic animal exposures, as the likelihood of inappropriate PEP administration was significantly higher for dog and cat exposures than for bats or raccoons. The results from this analysis will allow CCDPH to implement more informed education efforts with local hospitals.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Vaccine-Preventable Diseases; Local Epidemiology; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Knowledge and Practices Regarding Zoonotic Disease Exposure Risks and Personal Protective Equipment Use Among Arizona Wildlife Professionals, 2008 and 2018

Abstract

BACKGROUND: Over half of all emerging infectious diseases are zoonotic; >70% of those are wildlife-associated. Wildlife professionals are at increased risk of occupational disease exposure. In 2008, after an Arizona wildlife biologist died from plague after necropsying an infected mountain lion without adequate personal protective equipment (PPE), the Arizona Department of Health Services (ADHS) surveyed wildlife professionals from multiple Arizona agencies. ADHS revised the survey in 2018 to assess changes in practice and culture, and to address additional factors identified since 2008. The purpose of both studies was to assess the risk of disease exposure to wildlife professionals, their PPE use, and zoonoses knowledge; these results would identify targets for education to improve practices.

METHODS: In 2008, a 12-question survey was distributed in-person at a state wildlife professional meeting using an anonymous email link to wildlife agency employees. In 2018, a revised 20-question survey was created in Qualtrics® and distributed using an anonymous email link to state and federal wildlife agencies, licensed wildlife rehabilitators, and other wildlife control groups through their own list serves.

RESULTS: We received 162 and 81 complete responses in the 2008 and 2018 surveys, respectively. Over half of respondents (54% in 2008; 59% in 2018) had >10 years of experience. In 2018, fifty-one percent were male, and respondents represented all 15 Arizona counties. Respondents reported similar bite frequencies in 2008 (27%) and 2018 (23%), but bites from rabies reservoir (bats, foxes, or skunks) or spillover species (bobcats and coyotes) was higher in 2008 (42%) than in 2018 (16%). Among the 58% of respondents in 2018 that performed necropsies or collected animal samples within the previous five years, only 60% always wore latex or nitrile gloves, and 79% never wore a facemask. In 2018, reasons for PPE non-use included: not necessary in given scenarios (79%), not readily available (27%), and practicality (19%). Respondents indicated awareness of certain zoonoses, including the risk of plague (96%), rabies (91%) and hantavirus (91%); however awareness was lower for brucellosis (72%), leptospirosis (60%), and tuberculosis (59%).

CONCLUSIONS: Approximately one quarter of Arizona wildlife professionals reported experiencing wildlife bites in 2008 and 2018, although the frequency of high-risk rabies exposures in 2018 was lower. In 2018, questions pertaining to zoonoses awareness and reasons for non-use of PPE highlighted targets for education to improve practices, which should be pursued. Development of educational materials and facilitation of personal protection training for wildlife professionals could prevent future disease transmission.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Occupational Health; Infectious Diseases; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Monitoring Rabies Epizootics in the United States: Balancing the Need for a Sensitive Rabies Surveillance System with Reasonable Expectations for Laboratory Monitoring

Abstract

BACKGROUND: A standardized rabies virus (RABV) surveillance system that includes virus characterization information could enhance early detection of: host-shift events, translocation of RABV variants, and discovery of novel variants. Given the severe implications that RABV have for both human and animal health, understanding the transmission dynamics of RABV variants within and between animal species is crucial. To date, there has been no systematic evaluation of either the representativeness or completeness of the virus characterization data in animals submitted to the U.S. national animal rabies surveillance system.

METHODS: The authors discussed epidemiologically important events likely to yield actionable information relevant to rabies control. Specimens likely to identify significant epidemiologic events (e.g. host-shift, translocation, novel variant, or epidemiologically unusual events) were considered of epizootiological importance (SEI). The 2010–2015 U.S. public health rabies surveillance data were used to project the additional burden for laboratory testing if all SEI underwent virus characterization. Data were analyzed and the total number of positive samples obtained for each SEI category across the six year time span was used to calculate the estimated number of samples and confidence intervals that public health laboratories could expect if all SEI underwent RABV characterization. Terrestrial animal data was included in this analysis; however, bats were not included.

RESULTS: Four epidemiologically relevant events critical to rabies surveillance were determined based on discussion and previous literature findings: introduction of novel RABV variants; translocation of variants; host-shift events; and rabies events that may affect future testing guidelines. Twelve SEI categories, based on one of the four events, were evaluated. During 2010–2015, there was an annual average of 855 (95% CI, 739–971) rabies positive SEI; an average of 270 (95% CI, 187–353) (31.6%) SEI underwent virus characterization. Virus characterization of all SEI would be expected to increase laboratory testing by approximately 584 (95% CI, 543–625) samples per year.

CONCLUSIONS: Prioritizing RABV characterization of SEI may improve early detection of rabies events associated with host-shifts, translocations, and importation. Characterization of SEI may help refine wildlife rabies management practices. Laboratory testing of SEI should be evaluated by each public health laboratory to ensure testing does not strain routine diagnostic laboratory capacity.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Surveillance; Zoonotic Diseases; Epidemiology
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11034
Abstract Type	Breakout
Abstract Title	Polar Bears in the Desert: Rickettsia Parkeri Rickettsiosis in Southern Arizona, 2016-2017

Abstract

BACKGROUND: *Rickettsia parkeri* is an emerging tick-borne disease in the United States (US), transmitted by the bite of *Amblyomma maculatum* (the Gulf Coast tick). Clinical manifestations can include fever, headache, fatigue, myalgia, and maculopapular rash. A characteristic eschar forms at the site of the tick bite. Arizona's index case of *R. parkeri* rickettsiosis was reported in 2014. In 2018, the Arizona Department of Health Services sought to describe and characterize additional cases of this emerging disease identified during 2016-2017.

METHODS: We identified cases through routine investigation in conjunction with electronic laboratory reports, and three cases self-reported to public health authorities. Serum samples were evaluated for IgG antibodies reactive with antigens of *Rickettsia rickettsii* and *R. parkeri* using indirect immunofluorescence antibody testing. Samples were initially screened at a 1/32 and diluted serially to endpoint; those with IgG antibody titers ≥ 64 were considered positive. DNA was extracted from eschar swab specimens and screened using a real-time PCR assay targeting a segment of the 23S rRNA gene of all known *Rickettsia* species.

RESULTS: We identified seven cases (3 confirmed, 4 probable) of *R. parkeri* rickettsiosis ; patients (6 male, 1 female) ranged in age from 29-69 years (median, 41 years), and became ill between July and September. Fever (6/7), myalgia (5/7), and arthralgia (5/7) were most commonly reported and 5/7 patients had a documented eschar. All patients reported a tick bite acquired in southern Arizona within 2-8 days prior to illness onset. Four patients worked as US border patrol agents. Antibodies reactive to *R. rickettsii*, *R. parkeri* , or to both antigens, were detected in all patients; titers reactive with *R. parkeri* were two- to four-fold greater for six patients. Seroconversions between acute and convalescent-phase samples were identified for two patients. The panRickettsia real-time assay was positive for two patients.

CONCLUSIONS: *R. parkeri* rickettsiosis is endemic to a region of the southwestern US and could present an occupational risk; prevention messaging could be provided to border patrol agents. Four cases initially misdiagnosed despite the presence of an eschar suggests a lack of regional clinician awareness. *R. parkeri* rickettsiosis is the second tick-borne rickettsiosis identified repeatedly in Arizona since 2003. Rocky Mountain spotted fever, a closely related and significantly more clinically severe spotted fever rickettsiosis, is also endemic in portions of Arizona. Public health agencies need to provide further information to clinicians to help distinguish these two infections clinically and apply species-specific diagnostic assays to improve surveillance.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Epidemiology; Vectorborne Disease; Occupational Exposure
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Probable Transfusion-Associated Transmission of Powassan Virus, 2018

Abstract

BACKGROUND: Powassan virus (POWV) is a tick-borne flavivirus and rare cause of encephalitis. In the United States, POWV disease is most commonly reported from the Northeast and Upper Midwest; no cases have been reported in Indiana. Transmission of POWV via blood transfusion or organ transplantation has not been documented. We investigated a case of encephalitis in an Indiana resident with recent history of kidney transplantation and red blood cell transfusions.

METHODS: Medical records of the encephalitis patient, the organ donor, and the recipient of a lung from the same donor were reviewed. The encephalitis patient and blood donors were interviewed. Specimens from the encephalitis patient, lung recipient, organ donor, and blood donors were tested for evidence of POWV infection by reverse transcription-polymerase chain reaction (RT-PCR), IgM capture enzyme-linked immunosorbent assay, and/or plaque reduction neutralization test. An environmental investigation was conducted to assess the encephalitis patient's risk of tick exposure.

RESULTS: The patient had onset of encephalitis in July 2018, approximately three weeks after a kidney transplant and three red blood cell transfusions. The patient was hospitalized, but survived. Serum and CSF collected 13 days after encephalitis onset had detectable POWV IgM antibodies but no detectable RNA. The POWV neutralizing antibody titer was 10 in this serum specimen and 320 in a serum specimen collected five days later. POWV neutralizing antibodies were not detected in the CSF. Serologic testing for other flaviviruses was negative. The patient's pre-transplant serum had no detectable POWV RNA, IgM, or neutralizing antibodies. Post-transplant serum from the lung recipient had no detectable POWV IgM or neutralizing antibodies. Banked organ donor serum had no detectable POWV RNA, IgM, or neutralizing antibodies. A plasma co-component from one of the three blood donors had no detectable POWV IgM or neutralizing antibodies, but RT-PCR test results were equivocal. A serum specimen collected from this donor 174 days after donation had detectable POWV IgM antibodies and a neutralizing antibody titer of 40. The blood donor lived in the Upper Midwest and reported a tick bite one month prior to donation. Follow-up sera from the other two blood donors had no detectable POWV neutralizing antibodies. The encephalitis patient's only reported outdoor exposure was in Indiana, at home and a park; no ticks were found at either location.

CONCLUSIONS: Blood transfusion was the likely mechanism of POWV transmission in this case. While POWV disease is rare, healthcare providers should consider POWV to be a possible transfusion-associated pathogen.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Infectious Diseases; Emerging Infections
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Syndromic Surveillance of Emergency Department Visits for Tick Bites and Lyme Disease — Three Regions, 2017

Abstract

BACKGROUND: Surveillance for Lyme disease can be resource intense in endemic areas due to high case volume. Syndromic surveillance of emergency departments (ED) visits may offer an efficient approach to monitor tick bite and Lyme disease cases. We described the frequency and seasonality for these outcomes in regions with high, medium, and low Lyme disease incidence. In addition, we evaluated the utility of tick bite visits to predict the seasonal peak in Lyme disease visits.

METHODS: We developed algorithms for tick bite and Lyme disease using combinations of *International Classification of Diseases* Tenth Revision (ICD-10) diagnostic codes and key word search terms in the chief complaint field of ED visit data. Algorithms were applied to data submitted through the National Syndromic Surveillance Program (NSSP) during 2017 in three regions with known high, medium, or low Lyme disease incidence. We compared number and seasonality of ED visits by region for tick bite and Lyme disease. We calculated Lyme disease incidence using total ED visits and compared to National Notifiable Diseases Surveillance System (NNDSS) data. We also calculated the time lag between peak number of ED visits for tick bite and for Lyme disease.

RESULTS: In 2017, the number of ED visits in the high, medium, and low incidence regions was 13,804 (346/100,000 ED visits), 6,536 (29/100,000 ED visits), and 764 (20/100,000 ED visits) for tick bite and 4,749 (119/100,000 ED visits), 3,946 (17/100,000 ED visits), and 170 (5/100,000 ED visits) for Lyme disease, respectively. For comparison, Lyme disease incidence was 53, 12, and 1 case per 100,000 persons in the high, medium, and low incidence regions, as reported through NNDSS. In the high incidence region, 44% of the ED visits for Lyme disease occurred during June and July, as compared with 53% of cases reported through NNDSS. Peak daily ED visits for tick bites preceded the peak for Lyme disease by 50 and 42 days in the high and medium incidence regions, respectively; no temporal pattern for Lyme disease ED visits was observed in the low incidence region.

CONCLUSIONS: Syndromic surveillance demonstrates substantial ED burden by patients with tick bite and Lyme disease. In high incidence areas, ED visits for Lyme disease have similar relative incidence and seasonality as data reported to NNDSS. In high and medium incidence areas, peak ED visits for tick bites may provide a guide for optimal timing of Lyme disease prevention messages.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Syndromic Surveillance; Vectorborne Disease
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Lightning
Abstract Title	Beyond Case Counts—Capturing Record Number of Deaths Due to West Nile Virus in Los Angeles County By Enhancing Monitoring of Patients

Abstract

BACKGROUND: Los Angeles County Department of Public Health (LACDPH) documents cases of West Nile virus (WNV) every year. As WNV can cause prolonged illness, case investigations frequently occur while the patient remains hospitalized. Patients alive at the time of case investigation have been recorded as surviving the disease. In 2017, the outcome monitoring protocol was enhanced for patients who remained hospitalized at the time of case investigation and LACDPH documented a record-breaking 27 deaths.

METHODS: Medical records were requested for each hospitalized WNV patient reported to LACDPH. Patients with discharge summaries unavailable at the time of investigation due to prolonged hospitalization were flagged for additional follow-up every two weeks and up to three months, until a discharge summary was available for review. For patients discharged to rehabilitation centers, death certificates were reviewed five months after the initial investigation.

RESULTS: In 2017, 18 deaths were identified through routine surveillance. Approximately 80 patients remained hospitalized at the time of case investigation and were flagged for additional follow-up. Nine more deaths were identified for a total of 27 deaths. Among all 27 deaths, the average length of time between disease onset and death was 29 days (range of 8 to 144 days). This average was longer among the nine additional deaths (45 days, range of 15 to 144 days) compared to deaths identified through routine surveillance (21 days, range of 8 to 46 days). The average length of hospitalization for those nine patients was also longer than those deaths identified by routine surveillance (41 vs. 14 days). All nine additional deaths died during hospitalization compared to 3 of the 18 deaths found through routine surveillance.

CONCLUSIONS: The additional deaths identified from the new protocol revealed that many WNV deaths can go unreported without active monitoring. Though the deaths all occurred in the hospital, reliance on passive reporting from the hospital is insufficient for deaths that can occur up to five months after onset. A substantial number of deaths also occurred after hospitalization. Under-estimation of fatalities contributes to a false perception that WNV is not a severe and significant threat to the public. The record number of deaths documented in 2017 prompted an unprecedented educational campaign in which approximately 100 public health teams distributed mosquito-borne disease materials to thousands of public venues across LAC. Having an accurate count of deaths played a key role in garnering public interest and promoting behavior change, which is imperative to preventing WNV.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Epidemiologic Methods; Epidemiology; Vectorborne Disease
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Lightning
Abstract Title	Hantavirus Infection on the Navajo Nation 1992-2016

Abstract

BACKGROUND: Hantavirus is a genus of viruses in the Bunyaviridae family. The primary species of hantavirus in the American Southwest is Sin Nombre Virus. Its main host, the deer mouse (*Peromyscus maniculatus*), can carry the virus in feces, urine, and saliva. The most common mode of transmission to humans is inhalation of aerosolized particles containing the virus. The purpose of the project was to assess the burden of hantavirus among Navajo residing in the Four Corners (AZ, NM, UT, CO) area. The goal of the project was to quantify available data in order to serve as a platform for future surveillance efforts and to reveal patterns that may assist in targeting prevention.

METHODS: The Navajo Epidemiology Center received data from the CDC Viral Special Pathogens Branch for 139 hantavirus cases between November 1992 and May 2016 that were linked to a city of residence or city of exposure in one of 10 counties in and around Navajo Nation. Two methods were used to restrict analysis to Navajo cases. First, data were included for all individuals listed as American Indian with a community of residence on the Navajo Nation. Second, cases with a community of residence outside Navajo Nation were evaluated individually. Data was managed in Microsoft Excel 2013 and analyzed using SAS 9.3.

RESULTS: One hundred and eight cases that were potentially Navajo occurred between November 1992 and May 2016. The highest numbers of cases occurred during the late spring and early summer months – April, May, June, and July – with a slight peak again in November. Women appear to have a higher risk of mortality compared to men. This difference is largest among women in the 40-49, 50-59, and 60-69 age groups. Approximately half of cases occurred in Eastern Agency (Navajo Nation contains five geopolitical regions called agencies). Most cases had exposure to mice in or around the home. Many cases lived in mobile homes, at altitudes between 6000 and 7000 feet, and in piñon/juniper woodland and/or high desert areas.

CONCLUSIONS: Hantavirus surveillance data suggest that persons in certain occupations and certain populations may be at increased risk because of potential for rodent exposure. Educational efforts and awareness focused on high-risk populations should continue so that persons can decrease their risk of acquiring hantavirus disease.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Tribal Epidemiology; Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11651
Abstract Type	Lightning
Abstract Title	Review of Pennsylvania's 2018 Arbovirus Season: A Blip on the Radar or Is This the New Norm?

Abstract

BACKGROUND: In response to the emerging threat of West Nile virus (WNV) and other arboviruses, a multi-agency task force was established in 2000 to reduce expected morbidity and mortality through comprehensive human and animal surveillance and a mosquito control program. Since its emergence in 1999, WNV has been the most frequently reported arbovirus in Pennsylvania; typically averaging 11 human, 4 equine, 25 avian cases and 1504 positive mosquito pools annually. The 2018 mosquito season created unique challenges in the wake of the National Weather Service reporting record rainfalls across the state. The purpose of this review is to describe the burden of WNV and other mosquito-borne arboviruses during 2018 and to illustrate the importance of an interagency response during a high burden season.

METHODS: The multi-agency task force includes three state agencies: Department of Environmental Protection (DEP), leading mosquito surveillance; Department of Health (DOH), leading human case surveillance; and Department of Agriculture, leading veterinary surveillance. As outlined in the Commonwealth of Pennsylvania's WNV and Other Arboviruses Prevention and Control Plan (WNV plan), interagency coordination and weekly data sharing updates promotes a targeted approach for mosquito control efforts in areas with elevated human and animal infection rates. The WNV plan was routinely monitored and response efforts by the appropriate agency were initiated when tiered thresholds were achieved (phases 0–4).

RESULTS: During 2018, routine surveillance identified 120 human, 111 equine, and 107 avian cases of WNV. A record 4,729 WNV-positive mosquito pools were identified in 63 of 67 Pennsylvania counties, requiring large mosquito-control efforts statewide. In addition, other rarely reported mosquito-borne arboviruses were identified including a human and emu case of Eastern Equine encephalitis, and a human case of Saint Louis encephalitis virus. For only the second time in Pennsylvania, DEP identified an *Aedes aegypti* mosquito. The highest phase of response (phase 4) in the WNV control plan was reached and prevention activities including health alerts and enhanced communication efforts were carried out accordingly.

CONCLUSIONS: Environmental factors, including record rainfall across Pennsylvania, promoted ideal mosquito breeding conditions which contributed to record numbers of WNV-infected mosquitoes and greater than expected human, equine, and avian cases. The established task force and WNV plan promoted a coordinated, rapid response and allowed for interagency sharing of key information necessary to reduce risk of human illness. As the threat from arbovirus diseases continues, it is crucial to remain vigilant with surveillance activities and coordinated mosquito control prevention efforts.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Collaboration; Data Sharing; Vectorborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11325
Abstract Type	Lightning
Abstract Title	Tail of a Rabid Puppy: Lessons Learned

Abstract

BACKGROUND: In Minnesota, skunks and bats are the main rabies reservoirs. Livestock and pets generally develop rabies following a bite from a rabid skunk. People are generally exposed to rabies by bats, livestock, and unvaccinated pets. The Minnesota Department of Health (MDH) utilizes interagency cooperation with the Minnesota Board of Animal Health (BAH) when investigating exposures to potentially rabid animals. On September 17, 2018, BAH notified MDH that a 4 month-old puppy with progressive paralysis and other neurological symptoms had been euthanized and submitted for rabies testing at a regional veterinary diagnostic laboratory (VDL). An interagency investigation was initiated to determine possible animal and human exposures.

METHODS: MDH contacted the puppy's owners and the submitting veterinarian and obtained names of persons who had contact with the puppy during September 2-17. All contacts were interviewed by MDH to discern potential exposures and, if needed, recommend post-exposure prophylaxis (PEP). BAH conducted field investigations to evaluate animal exposures to the puppy.

RESULTS: From interviews with the owners and two veterinarians on September 17, MDH learned that the puppy was attacked by a skunk July 1, and developed symptoms consistent with rabies September 12. Due to overwhelming clinical and epidemiological evidence for rabies, MDH initially interviewed 11 potential contacts obtained from initial owner interview, and advised 8 to initiate PEP on September 17. On September 18, the VDL notified the submitting veterinarian, MDH and BAH that the rabies direct fluorescent antibody (DFA) test was negative, resulting in some contacts discontinuing PEP. The VDL performed a second rabies DFA and rabies PCR test due to concerns of a false negative test. On September 21, the second rabies DFA and rabies PCR were positive. In total, 49 contacts were interviewed, many of whom expressed doubt about the positive results following the previous negative results. Twenty-five (51%) contacts were advised to start rabies PEP treatment, including 5 international visitors and 6 children. Coordination between four healthcare facilities in Minnesota and North Dakota was needed to ensure adequate PEP for contacts with high-risk exposures. BAH placed one animal into 180-day quarantine.

CONCLUSIONS: While typically very reliable, false-negative DFA results do occur, and repeat testing should be performed when the animal's clinical presentation and exposure history is consistent with rabies. Strong relationships and good communication between public health and animal health agencies and VDLs are essential for a successful rabies surveillance program and to empower all program participants to investigate unexpected results.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11585
Abstract Type	Poster
Abstract Title	A Review of Powassan Virus Cases in Pennsylvania Residents (2011–2017) and Novel Evidence Found in Locally Collected Adult Black-Legged Ticks (2013–2015)

Abstract

BACKGROUND: Powassan virus (POWV) is a zoonotic, tick-borne RNA virus that can infect the central nervous system and cause severe illness such as meningitis in humans. POWV is transmitted by the black-legged tick, *Ixodes scapularis*. Since surveillance began in 2003, more than 100 cases of POWV have been reported in the United States. Over half of these were reported in 2016–2017, suggesting an increase in incidence in recent years. The purpose of this review is to describe the epidemiology of recent human disease cases and better define the geographic areas of POWV risk in Pennsylvania.

METHODS: Pennsylvania residents were identified through passive surveillance when POWV lab results were reported to the Pennsylvania Department of Health (PADOH). Suspected POWV cases were investigated and reported to the national surveillance system, ArboNET, if they met case definition. Adult ticks were recovered from deer heads during late Fall hunting seasons. Ticks identified as adult *Ixodes scapularis* were grouped into pooled tick samples by year and region of collection. PCR testing was performed and ticks making up a positive pool were then tested individually for POWV.

RESULTS: There were a total of five human cases of POWV reported to PADOH, one case in 2011 and four cases in 2017. POWV patient characteristics include: all were male and resided in northeast Pennsylvania, four (80%) were >65 years old, none had traveled the month before symptom onset, all five were hospitalized with neuroinvasive symptoms, and two reported tick bites prior to symptom onset. During 2013–2015, 1,990 adult *Ixodes scapularis* ticks were recovered from 9,930 harvested deer heads. One of the 409 (0.2%) pooled tick samples tested positive for POWV. The positive tick sample was collected in 2014 from a collection site in southeast Pennsylvania, and the state-wide individual tick pathogen prevalence rate for the three-year collection period was 0.05%.

CONCLUSIONS: This study provides evidence that POWV is present in *Ixodes scapularis* ticks in Pennsylvania and suggests that the patients who tested positive for POWV could have acquired their infection locally. Considering the potential for severe disease, primary care physicians should become familiar with signs and symptoms of this emerging pathogen to properly diagnose and treat patients who become infected with POWV. Also, Pennsylvanians should be educated on prevention of tick-borne diseases such as practicing strict tick avoidance measures and locating and removing ticks as soon as possible after exposure.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases; Vectorborne Disease; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Poster
Abstract Title	Anticipating Years with Weather-Related Increased Risk of West Nile Virus to Humans in Nebraska

Abstract

BACKGROUND: To complement Nebraska's vector-borne disease surveillance, we looked for a statistical connection between weather and human cases of West Nile Virus (WNV) that would let us issue warnings of higher annual risk at the start of the infection season. We investigated which time lags of key variables explained most.

METHODS: We created 12, 18, 24, 30 and 36-month lags of temperature and drought data. Human cases per county-year was the response variable. From the number of cases, we computed cumulative incidence (previous exposure). We used the R package mgcv (Wood) to fit general additive models with functional smoothing curves, essentially letting the data speak for itself. We fit models based on 2002-2015, and used 2016 for out-of-sample predictions. We used Akaike information criterion to select models that best fit the data, and contrasted the performance of our best-fit models with the performance of the naïve model (the assumption that each year would be the same as the preceding one). Because more than half of the county-years in our data had zero cases, we converted predictions to presence-absence, and mapped predictions for which of Nebraska's 93 counties would have cases in 2016. We used McNemar's test of statistical significance.

RESULTS: The best-performing model used 24-month temperature lags, 12-month lags of the Standardized Precipitation and Evapotranspiration Index, cumulative incidence, county and year, and had an R-square of 0.917. It out-performed the naïve model in 10 out of 13 years, 2003-2015, and in 2016. In presence-absence predictions for 2016, our model outperformed the naïve in 30% of counties, with exponentially small probability of this difference happening by chance.

CONCLUSIONS: Our model has predictive value. We anticipate that different combinations of precipitation and temperature will work better for different places, and that the best-fit model may evolve over time, but that the method of identifying a best model and then using it to make predictions will be widely applicable, for West Nile Virus and for other annual effects of temperature and drought. To deploy this method operationally, we recommend model refitting and evaluation after each year's infection season, incorporating the most recent numbers of human cases, and then making predictions in May or June, as soon as drought indices can be computed. Timely availability of infection data and drought indices may be a constraint.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Risk Assessment; Vectorborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10735
Abstract Type	Poster
Abstract Title	Correlation between West Nile Virus Surveillance Data in Louisiana and National Data, 2002-2018

Abstract

BACKGROUND: West Nile virus (WNV) is a mosquito-borne disease that was introduced to the United States in 1999, with the first human case identified in Louisiana in 2001. Less than one percent of all WNV infections develop neuroinvasive disease (NID) that can be associated with encephalitis or meningitis. With the assumption that transmission is affected by local ecologic conditions, we intended to determine if Louisiana WNV-NID case counts would correlate with national data from 2002–2018 despite regional variances in ecologic factors.

METHODS: Suspected arboviral infections were reported to the Infectious Disease Epidemiology Section of the Louisiana Department of Health, Office of Public Health, through laboratory reports and physician inquiries. Clinical symptoms, exposure information and laboratory results were evaluated against the Council of State and Territorial Epidemiologists (CSTE) case definitions and entered into the Louisiana web-based surveillance system, Infectious Disease Reporting Information System (IDRIS). While diagnosis and reporting is incomplete, most cases of WNV-NID are severe enough to cause hospitalization and receive laboratory testing. Hence the reporting of WNV-NID cases is considered the best indicator for comparisons of WNV activity. Louisiana WNV-NID cases were extracted from IDRIS from 2002–2018 (only 1 case was reported in 2001); national WNV-NID data were obtained from CDC from 2002–2018. A linear regression analysis was performed and a coefficient of determination was calculated.

RESULTS: As of January 7, 2019 Louisiana has identified 1,095 WNV-NID cases and there have been 24,463 WNV-NID cases reported nationally. The number of WNV-NID cases in Louisiana has shown wide variations, ranging from a high of 204 cases in 2002 and 160 cases in 2012, to a low of 6 cases in 2011. The number of national WNV-NID cases also had wide variation, ranging from a high of 2,946 cases in 2002 and 2,873 cases in 2012, to a low of 386 cases in 2009. Over the past 17 years, Louisiana represented 4.48% of all WNV-NID national cases. The highest and lowest proportions for Louisiana data were respectively: in 2005 twice the national proportion (9.01%) and in 2011 less than half of that proportion (1.23%). The coefficient of determination equals 72.67%.

CONCLUSIONS: Overall, there is a strong positive linear relationship between the WNV-NID cases reported from Louisiana to the national data. This is supported by the coefficient of determination and similar variation in the high and low WNV-NID years. Future analysis may investigate how national factors determine local case counts despite regional variations in ecological factors.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Surveillance; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11705
Abstract Type	Poster
Abstract Title	Evaluation of a Community-Based Mosquito Trapping Program in Sedgwick County, Kansas, 2018

Abstract

BACKGROUND: In 2013, the Sedgwick County Division of Health (SCDOH) began collaborating on mosquito surveillance with the Kansas Department of Health and Environment (KDHE), the City of Wichita Stormwater Program (CoW), and the Kansas Biological Survey (KBS). In Sedgwick County, mosquito surveillance guides larvicidal mosquito abatement efforts to protect the health of Sedgwick County residents. From 2013 to 2017, mosquito trapping was performed by KBS. In 2018, changes to the program resulted in trapping performed by SCDOH-coordinated community volunteers and, also, a new ArcGIS application.

METHODS: Mosquito surveillance was conducted weekly from May 17 through October 25, 2018 (24 weeks). Encephalitis Vector Surveillance (EVS) traps were set in five pre-determined locations every Tuesday night and collected Wednesday morning (240 trap-days) by four trained Sedgwick County Master Gardeners volunteers, one student and, later in the summer, four SCDOH staff. Mosquitoes were packaged on dry ice and sent to the KBS for enumeration and species identification. Standing water around traps with >20 *Culex* species mosquitoes were treated with larvicidal dunks. One CoW field staff entered larvicidal dunk application into an ArcGIS online survey which SCDOH used to track mosquito numbers and abatement. A mosquito program survey was sent to all volunteers and analyzed by SCDOH at the end of the surveillance season.

RESULTS: In 2018, mosquito traps were set up and removed 100% of total season trap-days. Community volunteers spent 144 trap-days and accrued 3,864 mileage. After two volunteers dropped out of the program, SCDOH staff spent 96 trap-days and accrued 1,064 mileage to complete trapping. Of the participants, 78% responded to the end of season survey. Volunteers identified strong partnerships, an easy to understand program structure, and a well-organized SCDOH staff as the program's strengths. Volunteers identified insufficient volunteers, difficulty submitting mileage, commuting time, and insufficient dry ice as barriers. The ArcGIS application allowed field staff to easily identify trap and abatement location. The application was utilized consistently by CoW staff, who reported the system was easy to use and more efficient for reporting abatement. For SCDOH reports, the ArcGIS application saved approximately two hours in staff time compared to 2017.

CONCLUSIONS: Although more labor intensive when compared to previous years' trappings, Sedgwick County successfully coordinated a mosquito surveillance program in 2018. Community volunteers were dedicated to the program, but the logistics and sustained need from May through October were obstacles. Sustainability remains a top concern.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Surveillance; Vectorborne Disease; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11459
Abstract Type	Poster
Abstract Title	Evaluation of Immunoglobulin G Titers for Determining Spotted Fever Group Rickettsioses —Tennessee, 2013-2017

Abstract

BACKGROUND: Tick-borne disease cases more than doubled during 2004 – 2016 making up 77% of all vector-borne disease reports. Spotted fever group rickettsioses (SFGR) have been reported throughout most of the continental United States although >60% of cases are reported by North Carolina, Oklahoma, Arkansas, Tennessee, and Missouri. Surveillance approaches in these states vary. From 2013 – 2016, there was a 27% increase in reported SFGR cases. We reviewed clinical symptoms and testing of Tennessee SFGR cases to assess our surveillance approach.

METHODS: We analyzed cases with SFGR immunoglobulin G (IgG) titers $\geq 1:64$ during 01/01/2013 – 12/31/2017 collected through passive surveillance. Strengths and limitations of various SFGR IgG titers for determining case classifications were compared. Data in this retrospective cohort analysis were analyzed using two-way frequencies, Pearson's Chi-square test and Fisher's exact test to evaluate the distribution of the input variables, and logistic regression to measure associations between patient's IgG titers, onset and sample collection dates, and case classification status.

RESULTS: 7,459 cases were reported with 30% being probable cases. Investigations with a single IgG titer of 1:64 resulted in the highest number of non-case classifications (72%) and had the lowest positive predictive value (PPV), 27%. In comparison, investigations with a single IgG titer of 1:128 had a higher PPV (38%). Receiver operating characteristic (ROC) analyses indicated that eliminating 1:64 IgG titers and increasing the titer cut-off to 1:128 or above, increased the accuracy of single IgG tests in identifying clinically compatible cases.

CONCLUSIONS: In Tennessee, the number of people tested for SFGR continues to increase, causing a high burden of investigations. A single IgG titer of 1:64 was a poor indicator of a clinically compatible case. Convalescent titers are a more reliable approach for determining case status however, in practice, this is rarely performed. To prioritize the large volume of laboratory reports, health departments may consider giving highest priority to investigations of patients with IgG titers $\geq 1:128$. Investigations for patients with an IgG titer of 1:64 could be limited to those with a convalescent titer. Standardized approaches to surveillance will facilitate consistent case reporting and monitoring of SFGR trends.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10733
Abstract Type	Poster
Abstract Title	Kentucky's Mosquito Surveillance and Arbovirus Testing, 2018

Abstract

BACKGROUND: Diseases transmitted by mosquitoes and other arthropods are an important public health concern. To better understand the threat of potential mosquito-borne disease events, the Kentucky Department for Public Health (KDPH) along with partners, initiated a mosquito surveillance program in 2017 set out to identify and describe mosquito species present across our state. These surveillance efforts continued in 2018, applying lessons learned from 2017.

Kentucky completed its second Mosquito Surveillance season utilizing ELC funds provided by the CDC.

METHODS: Fourteen local health departments (LHD's) participated in mosquito surveillance during the 2018 mosquito season. Environmental staff collected mosquito pools at designated collection sites in 24 counties for 16 weeks between June and October. Mosquito pools were sent to one of three designated laboratories. The laboratories are testing for St. Louis Encephalitis virus (SLE), West Nile Virus (WNV), or Zika virus based on the anticipated presence of the viruses in the mosquito species and historical disease transmission patterns. Protocols are set in place for public health response to any positive pools.

RESULTS: During the 2018 mosquito season, 980 mosquito pools were collected. From those pools, 15,720 individual mosquitoes representing 29 species were identified. The most commonly identified species was *Culex pipiens* (n=4,392) at 28%. The next most commonly identified species was *Aedes albopictus* (n=2,618) at 17%. Of the 980 mosquito pools, 480 pools have been tested for WNV with 77 testing positive in five distinct geographic regions. In 2017, 119 mosquito pools were tested and 17 were positive for WNV in three distinct regions. In addition, in 2018, 374 of the mosquito pools were tested for SLE virus with no positives, as well as 370 of the mosquito pools tested for Zika virus with no positives.

CONCLUSIONS: Kentucky needs to increase surveillance more evenly across the state. Due to the 15.9% positivity rate for WNV, an increase in public awareness and intervention efforts are priority. For example, 75% of mosquito pools submitted from Daviess County was positive for WNV, and this was unexpected. This indicates Kentucky may have a higher rate for WNV than what is currently known. KDPH is increasing public awareness by utilizing surveillance efforts, so these will aid in developing additional prevention initiatives.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Surveillance; Vectorborne Disease; One Health
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	10935
Abstract Title	Poster
	Skunk Rabies Epizootic Impact on the Recommendation for Rabies Post-Exposure Prophylaxis El Paso County, CO 2017-2018

Abstract

BACKGROUND: Bats are the traditional rabies reservoir in Colorado, however, since 2009 the state has experienced a skunk rabies epizootic. Before 2009, the last rabid terrestrial animal in El Paso County (EPC) was a skunk in 1974. While relatively few skunks tested positive for the rabies virus between 2009 and 2016, the number increased dramatically to 21 skunks in 2017, followed by 61 in 2018. The increase in skunk rabies was most noticeable during March and April of 2018, which corresponds to the skunk mating season in Colorado. Prior to 2017, the only rabies season that had a higher number of positive skunks than bats was 2009. We hypothesized that due to the increase in rabid skunks, the number of people requiring post-exposure prophylaxis (PEP) would increase in EPC.

METHODS: All animal bites by a rabies reservoir species are reportable to the health department within 24 hours. El Paso County Public Health (EPCPH) receives calls from citizens to evaluate exposures from potentially rabid animals and utilizes REDCap, an open-source database, to triage them. If an animal tests positive for rabies it is recorded in the Colorado Zoonotic Disease Animal Surveillance Reporting Database; if a person is recommended PEP, the exposure is documented in the Colorado Electronic Disease Reporting System (CEDRS). A report was created in CEDRS to pull data on PEP recommendations for people and cross-referenced with the rabies-positive animals in EPC recorded in the zoonotic database. REDCap brings the two information streams together to associate a specific animal with the PEP recommendations.

RESULTS: Analysis included 179 people recommended for rabies PEP between January 2012 and December 2018. Of those people, 96 were exposed to bats, 25 to cats, 22 to skunks and 36 to other animals. By year: 38 people were recommended for PEP in 2018, 34 in 2017, 34 in 2016, 64 in 2015, 8 in 2014, 0 in 2013 and 1 in 2012.

CONCLUSIONS: Recommendations for Rabies PEP did not increase with the number of rabid skunks; the majority of PEP recommendations are due to bat exposures. Skunk exposures are more evident whereas bat exposures are often nuanced, requiring a more conservative approach to recommendations. This dynamic is reversed in pets, with more animals being recommended for rabies vaccines due to skunks than bats.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Vector-Borne & Zoonotic Diseases
Consider for Different Presentation?	Zoonotic Diseases
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11213
Abstract Type	Quick
Abstract Title	<i>Salmonella</i> Serovar Fluntern Illnesses Linked to Leopard Geckos— United States, 2018

Abstract

BACKGROUND: Reptile contact is an important cause of zoonotic non-typhoidal salmonellosis (NTS) in the United States. In April 2018, Oregon Public Health Division contacted CDC about a temporal cluster of four *Salmonella* serovar Fluntern (SF) illnesses in four states; ill people reported contact with geckos, a popular reptile pet. PulseNet, the national molecular subtyping network of foodborne disease surveillance, subsequently identified additional SF clinical isolates. We sought to characterize the magnitude of illness and prevent further transmission.

METHODS: A case was defined as isolation of SF from an ill patient during July 1, 2017, through March 1, 2018. Public health personnel interviewed patients to assess reptile exposure, and conducted traceback for reported purchase locations. Environmental samples were taken from patients' pet gecko habitats. Animal isolate data regarding SF from the U.S. Department of Agriculture National Veterinary Services Laboratories (NVSL) were obtained to determine if SF had been isolated from animal sources. Whole genome sequencing (WGS) core genome multi-locus sequence typing (cgMLST) was performed to determine relatedness between clinical and animal isolates.

RESULTS: We identified 12 cases in 11 states; 8 (67%) were female, and median age was 5 years (range: <1–58 years). Three patients were hospitalized; no deaths were reported. Of those with exposure information (n=10), all reported reptile exposure; 9 (90%) specified contact with leopard geckos. No common source of geckos was identified from reported purchase locations. Health officials in Los Angeles County (LAC) isolated SF from one patient's leopard gecko. Five reptile/gecko isolates were identified from NVSL from 2015–2018. WGS cgMLST analysis revealed substantial genetic diversity between clinical and animal isolates; however, gecko and clinical isolates from LAC were highly related (1 allele difference).

CONCLUSIONS: This investigation linking SF illness to leopard gecko exposure highlights an important public health risk of NTS transmission. A better understanding of how geckos are distributed in the United States could improve gecko traceability to points of origin and mitigate *Salmonella* transmission at breeders. Identification of historic gecko isolates suggests the potential for transmission of SF from geckos to humans in the United States has existed for several years. This investigation demonstrates a need to educate gecko breeders, retailers, and the public about the risk of *Salmonella* infection from pets, and the value of continual prevention efforts among those who own and care for leopard geckos.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Epidemiology
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Animal Bites and Rabies Post-Exposure Prophylaxis: An Evaluation of Public Health Surveillance Data in the United States—November 2018

Abstract

BACKGROUND: Rabies is a fatal viral illness that is preventable with post-exposure prophylaxis (PEP). Robust animal bite and PEP data would be useful in evaluating appropriate use of PEP, measuring public health costs, assessing adherence to PEP schedules, and monitoring supplies nationwide. However, neither are nationally notifiable and the quality of state-level data is unknown.

METHODS: The National Association of State Public Health Veterinarians with assistance from the Centers for Disease Control and Prevention designed a cross-sectional web-based survey to evaluate the availability and quality of surveillance data for animal bites and PEP. Surveys were sent to state public health veterinarians in the 50 U.S. states, Puerto Rico, New York City, and Washington DC in November 2018. Questions were designed to determine which jurisdictions have surveillance data at the state level, how those systems are managed, what data are collected and used, and which entities outside of public health participate in information flow. The survey included multiple choice questions, likert scales, and free text response fields organized with skip patterns.

RESULTS: Of 53 jurisdictions, 39 (73.5%) responded including 37 states, New York City and Philadelphia. No state-level data on animal bites or PEP was available in 7 (17.9%) jurisdictions; 3 (7.7%) jurisdictions had only ad hoc data available such as rabies hotline calls. Of the 29 jurisdictions with some state-level animal bite or PEP data available, 15 jurisdictions (38.4%) had data from animal bite surveillance; of those, 7 (46.7%) reported electronic reporting platforms and 5 (71.4%) reported platforms integrated with other reportable conditions. Models for capturing PEP data ranged from standard local health department follow-up of suspected rabies exposures to integrated electronic surveillance systems that collected more data. Jurisdictions reported inconsistent availability of personally identifying data (e.g., age) and type of animal exposure; they estimated 50% of data were shared between state and local jurisdictions. Few responders supported making PEP nationally notifiable but 30 (79.0%) of 38 supported improving standards for data collection.

CONCLUSIONS: PEP and animal bite surveillance is variable among jurisdictions. Lack of standardized definitions and protocols contributes to the inability to interpret data at the national level. Setting data standards for animal bite and PEP surveillance may facilitate improved data collection so that practices and burden of rabies, animal bites, and PEP across jurisdictions can be compared. Alternatively, data sources such as syndromic surveillance or distribution data from PEP manufacturers could circumvent the limitations of existing surveillance.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Surveillance; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11728
Abstract Type	Quick
Abstract Title	Eastern Equine Encephalitis Activity in Emus, Florida, 2018

Abstract

BACKGROUND: Eastern equine encephalitis virus (EEEV), an endemic arbovirus in Florida, can be transmitted year-round. Emus are particularly vulnerable to infection, typically resulting in rapid death following onset of severe gastrointestinal illness. Emus develop high levels of viremia and can infect competent vectors. Exposure to bodily fluids or feces from infected birds can lead to possible exposure for people and other animals. A EEEV horse vaccine is available for off-label use in emus. During 2018, the Florida Department of Health (Florida Health) and Florida Department of Agriculture and Consumer Services (FDACS) received reports of seven emu flocks with symptoms consistent with EEEV infection. Joint investigations were initiated with FDACS and local mosquito control.

METHODS: Emu owners were interviewed and provided recommendations related to proper personal protective equipment (PPE), mosquito bite prevention, carcass and egg disposal, and emu vaccination. Molecular testing was conducted by Florida Health on bloody fecal samples and when available, tracheal, cloacal, or choanal swabs or serum from recently deceased or sick birds. Representative tissues were collected from two emus that were autopsied. Symptom monitoring was conducted for 10 days post-exposure on individuals caring for the emus. Serum samples were also obtained for molecular and serologic testing to evaluate for possible EEEV exposure. Public health advisories were also issued to the public.

RESULTS: EEEV infections were confirmed in emus at seven of the farms, with five farms reporting illness in more than one emu. Symptom onset dates ranged from 2/13/18–11/1/18. Farm A had the highest rate of transmission, where more than half of the 28 emus were symptomatic. The remaining emus were euthanized due to the high rate of transmission at the location and lack of veterinary care. Overall, 44/60 (73%) of the emus among the seven locations became ill or were euthanized. Twenty-two samples were positive for EEEV by molecular testing, including six fecal samples, six tracheal swabs, two cloacal swabs, two serums, one heart, one brain, one spleen, two livers, and one intestine. A single ostrich was also symptomatic at one of the farms. EEEV testing was negative for 18 human contacts.

CONCLUSIONS: Most of the emu flocks had no history of previous vaccination. Investigations were complicated due to owners' limited resources, including no regular veterinary care. There were also differences in risk perception among individuals caring for infected emus; only two owners routinely used the provided PPE. The joint investigations were critical to preventing further spread of EEEV.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Environmental Health; Vectorborne Disease
Consider for Different Presentation?	Yes
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Affiliation	State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11310
Abstract Type	Quick
Abstract Title	Epidemiologic Features of an Outbreak of Human Jamestown Canyon Virus Disease, Wisconsin, 2017-2018

Abstract

BACKGROUND: Jamestown Canyon virus (JCV) is a mosquito-borne *Orthobunyavirus* that can cause neuroinvasive disease. Nationally, JCV disease is most commonly reported in Wisconsin. During 2012 to 2016, a median of five cases of JCV disease (range 1 – 11) were reported annually among Wisconsin residents. Then in 2017 and 2018, 43 cases and 20 cases of JCV were reported respectively, representing a >500% increase in the average annual number of cases compared to the previous five years. We report on the epidemiologic features of this JCV disease outbreak during 2017 and 2018.

METHODS: JCV cases were classified using both laboratory and clinical criteria from the arboviral diseases national surveillance case definition. Wisconsin State Laboratory of Hygiene (WSLH) performed JCV-specific IgM enzyme-linked immunoassay on specimens submitted to WSLH for arbovirus testing and on specimens from commercial laboratories with evidence of arboviral antibodies from patients with clinical evidence of an arboviral illness. Specimens with presumptive evidence of JCV IgM antibodies were confirmed at CDC using plaque reduction neutralization test. Clinical information, demographics, travel history, and potential modes of transmission were collected through patient interviews, and clinical information was confirmed by medical record abstraction.

RESULTS: A total of 63 cases of JCV disease were reported from 35 (49%) Wisconsin counties. Illness onsets occurred during each month of the year except February, March, and December, with 53 (84%) cases occurring between June and September. The median patient age was 57 years (range 19 – 83), and 41 (65%) were male. Fifty (79%) cases were classified as neuroinvasive disease, and 38 (60%) were hospitalized. The most common symptoms reported were fatigue (87%), fever (84%), headache (71%), chills (65%), myalgia (60%), and disorientation (57%). Encephalitis was diagnosed in 22 (35%) of the cases, meningitis in 11 (17%), and acute flaccid paralysis in 3 (5%). Infections were presumably transmitted by mosquitoes, since all patients denied blood transfusion, organ transplantation, or laboratory exposure in the 30 days prior to illness onset. Of the 63 cases, 13 cases also had laboratory evidence of another arboviral infection (West Nile, Powassan, or eastern equine encephalitis virus).

CONCLUSIONS: JCV infections in 2017 and 2018 contributed to significant morbidity among Wisconsin residents. The abrupt increase in cases, in the absence of substantial modifications in surveillance practices, suggests potential change(s) in disease transmission dynamics resulting in more human infections. Accurate diagnosis of JCV disease and further characterization of transmission dynamics in Wisconsin can inform public health prevention strategies.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Outbreaks; Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11410
Abstract Type	Quick
Abstract Title	Epidemiology of Ehrlichiosis Caused By Ehrlichia Chaffeensis and Ehrlichia Ewingii— United States, 2013–2016

Abstract

BACKGROUND: Human ehrlichiosis is a tickborne disease caused by bacteria from the *Ehrlichia* genus. The majority of reported cases in the United States are due to infection by *E. chaffeensis*. Ehrlichiosis can cause moderate to severe illness and is potentially fatal. Symptoms can include fever, headache, malaise, and myalgia. Rash is reported in approximately one-third of patients with *E. chaffeensis* infection. Infection caused by *E. ewingii* usually results in milder illness compared with *E. chaffeensis*. Presumptive treatment with doxycycline is recommended for patients of all ages with suspected ehrlichiosis. Presented here is a summary of *E. chaffeensis* and *E. ewingii* cases reported to the Centers for Disease Control and Prevention (CDC) with illness onset during 2013–2016.

METHODS: Cases of ehrlichiosis are reported to CDC through two national surveillance systems: the National Notifiable Diseases Surveillance System (NNDSS) and tickborne rickettsial disease case report forms (CRFs). Demographic data reported through NNDSS were used to calculate incidence rates. Data from CRFs describe clinical course and patient outcome.

RESULTS: From 2013–2016, a total of 5,733 cases of ehrlichiosis were reported through NNDSS (60.4% male, 68.0% white, median age 58 years). The majority of cases were reported as *E. chaffeensis* infection (n=5,648, 98.5%). The incidence rate (IR) of *E. chaffeensis* infection was 4.6 cases per million persons. Most cases reported illness onset from May–August (n=3,477, 79.1%). The hospitalization rate (HR) was 53.7%, and the case fatality rate (CFR) was <1.0%. No fatalities in persons under 30 years old were reported. Eighty-five (1.5%) cases were reported through NNDSS as *E. ewingii* infection. The IR of *E. ewingii* infection was 0.07 cases per million persons. Most cases reported illness onset between June and August (n=61, 78.2%). The HR was 57.9% and no deaths were reported.

CONCLUSIONS: The incidence of human ehrlichiosis cases in the United States has continued to rise since becoming nationally notifiable in 1999. A national surveillance summary of cases with illness onset during 2008–2012 showed children aged <5 years with ehrlichiosis were more than twice as likely to experience fatal outcome compared to the rest of the population. This report found no fatalities in persons aged <30 years, which may be due to educational efforts urging physicians to treat young patients with suspected rickettsial infection with doxycycline. Ongoing surveillance and reporting of tickborne diseases are critical in understanding the epidemiology of ehrlichiosis in the United States.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Surveillance; Vectorborne Disease; Epidemiology
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10632
Abstract Type	Quick
Abstract Title	Eschar-Associated Rickettsiales: Clinical Clue or Misunderstood Element?

Abstract

BACKGROUND: Eschars are necrotic lesions found at the site of tick or mite attachment and can be a common clinical feature of certain rickettsial diseases. Eschars result from a number of domestic pathogens, including *Rickettsia parkeri*, *R. species 364D* and *R. akari*, and several imported *Rickettsiae* including *R. africae* and *R. conorii*, but have not been linked to *Ehrlichia* and *Anaplasma* species. In 2010, the Centers for Disease Control and Prevention began collecting information on eschars on their tickborne rickettsial disease (TBRD) case report form (CRF). The purpose of this analysis is to summarize U.S. eschar-associated rickettsioses.

METHODS: We summarized supplemental data collected by state and local health departments and submitted to the Rickettsial Zoonoses Branch via CRFs or similar sources. Data with illness onset from 2010–2016 were included in this summary. Case classifications were made according to CSTE case definitions.

RESULTS: From 2010–2016, 484 TBRD cases were reported with the presence of an eschar. Of those, 387 (80.0%) were classified as a spotted fever rickettsiosis, 64 (13.2%) were *E. chaffeensis* ehrlichiosis, 30 (6.2%) were *A. phagocytophilum*, 1 (0.2%) was *E. ewingii* ehrlichiosis, and 2 (0.4%) were undetermined ehrlichiosis/anaplasmosis. Of eschar-associated spotted fever rickettsiosis cases, 11 identified *R. africae* as the suspected agent, 2 listed *R. parkeri*, and one case each specified *R. conorii*, *R. species 364D*, and *R. akari*. Only 8.7% of eschar-associated infections met the criteria for a confirmed case. Eschar-associated illnesses were more common in men than women (59.9% vs 39.0%), most were white (68.4%) and non-Hispanic (83.1%). Nineteen percent (n=90) of eschar-associated cases were hospitalized, and only one person reportedly died because of their illness. Thirty-four cases were positive by PCR, yet only six were reported as a spotted fever rickettsiosis.

CONCLUSIONS: The presence or absence of eschars can provide valuable data and help clinically differentiate spotted fever group rickettsioses; however, the value and validity of eschars in cases of ehrlichiosis and anaplasmosis have not yet been defined. Cases of eschar-associated ehrlichiosis and anaplasmosis are not reported in the literature, yet 20% of eschar-associated illnesses were reported as one of these agents. It is possible that some of these instances arise from misunderstanding of the term. Further clinical research is needed to clarify if these reports reflect a mistake, a new discovery, or if they are a result of co-infection with another eschar-causing rickettsial pathogen.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Surveillance
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Evaluating the Efficacy of Community-Level Interventions during Outbreaks of Flea-Borne Typhus Fever

Abstract

BACKGROUND: The city of Pasadena is a known endemic area for flea-borne typhus fever, with several documented outbreaks within the last 30 years. In 2016 and 2018, Pasadena experienced epidemic levels of typhus fever across the city. Our objective was to evaluate the effectiveness of community interventions, including educational mailers and media messaging, for the management of typhus fever outbreaks and assess the efficacy of these interventions.

METHODS: Face-to-face interviews were conducted among a simple random sample within a cluster area of flea-borne typhus fever using a semi-structured questionnaire. Among the 2,309 residential addresses that received the initial mailer, 200 were randomly selected to be interviewed, and a total of 37 (18.5%) interviews were completed. Participants were asked whether they had heard of typhus and from what source, what their level of concern was about the disease, and whether they took any preventive actions. Residents who voluntarily reported seeing the educational mailer and/or the press coverage following our health alert, were compared to those residents who heard about the typhus outbreak from other outlets or did not hear about it at all to assess the value of the educational materials for vectorborne disease prevention.

RESULTS: Among the respondents who completed the interview (n=37), almost 46% (17/37) of the sample reported seeing the educational mailer from the health department and nearly 22% (8/37) reported hearing about the outbreak from traditional news outlets (e.g. newspapers, television). Of those who reported seeing the mailer, 76% (13/17) did at least one preventive control activity to mitigate typhus fever risk. Specifically, all four of the pet owners who reported seeing the mailer discontinued backyard feeding. Finally, people who reported seeing the mailer reported higher, but not significant, levels of concern about flea-borne typhus fever ($p=0.14$) but more knowledge about how typhus is transmitted ($p=0.01$).

CONCLUSIONS: Broad, community-level mailers appear to be an effective strategy for motivating individuals in high-risk areas to change behaviors to prevent environmental infectious diseases like flea-borne typhus fever.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Local Epidemiology; Vectorborne Disease; Evaluation
Consider for Different Presentation?	Yes
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Presenting Author(s) Institution Affiliation	Matthew M Feaster City of Pasadena Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10992
Abstract Type	Quick
Abstract Title	Evaluation of Commercial Insurance Claims As a Component of Lyme Disease Surveillance

Abstract

BACKGROUND: In high incidence areas, traditional case-based surveillance for Lyme disease (LD) can require substantial resources while yielding little new information for public health action. Commercial claims data, a growing source of epidemiologic information, could supplement case-based surveillance to provide a more complete picture of disease burden, geographic spread, and factors linked to severe illness while requiring fewer resources. We evaluated population characteristics and LD patterns in a large national insurance claims database to evaluate its utility as a component of LD surveillance.

METHODS: We examined the annual variability of enrollee data in MarketScan[®] Commercial Claims and Encounters databases during 2010-2016 and its representativeness compared to the US population. Analyzed records were restricted to those with full-year enrollment and associated prescription data. We identified records of enrollees as clinician-diagnosed cases of LD using International Classification of Disease codes for LD and related clinical conditions with antimicrobial prescriptions for LD treatment. Case characteristics were compared to those in the National Notifiable Diseases Surveillance System (NNDSS). US Census regions were used to describe geographic distribution.

RESULTS: During 2010-2016, annual enrollment in the MarketScan database varied between 19,004,365 (in 2016) and 28,757,701 (in 2012). Proportions of the MarketScan population in each region remained consistent and closely aligned with the US population (regional proportions differed by 0-8% between the two populations). Females were slightly overrepresented in MarketScan, as were adults aged 45-55, compared to the US population. We identified 111,006 individuals diagnosed with LD; annual incidence per 100,000 enrollees ranged from 49 (2010) to 79 (2014) and was equal between sexes. Median annual incidence per 100,000 enrollees in the Northeast, North Central, South and West census regions was 277, 25, 29, and 14, respectively. Age-specific incidence in MarketScan was bimodal with a consistent peak in males 5-9 years and a second peak in adults that was variable across years. In NNDSS, annual incidence ranged from 10 to 12; a bimodal age distribution consistently occurred, with the majority of cases among males, irrespective of age group. Comparatively, relative incidence of LD in adult women was much higher in the MarketScan database.

CONCLUSIONS: Despite yearly variation in MarketScan enrollment, several epidemiologic characteristics of clinician-diagnosed LD were similar to those of national surveillance data. Differences between MarketScan and NNDSS data require further consideration; however, MarketScan could serve as a complementary surveillance tool and provide new insights into burden, demographics, and clinical picture of LD that inform education and prevention activities.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	ICD; Vectorborne Disease; Surveillance
Consider for Different Presentation?	Yes
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Affiliation	CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11281
Abstract Type	Quick
Abstract Title	Evaluation of the West Nile Virus Risk Level Model in Kansas, 2018

Abstract

BACKGROUND: West Nile virus (WNV) is the leading cause of domestically acquired arboviral disease in the United States and Kansas. *Culex* species mosquitoes are the primary vector for transmission. Mosquito-based surveillance (MS) is the primary tool for quantifying WNV transmission risk. WNV risk levels (RL) were developed in 2017 and modified in 2018. RLs were evaluated to determine if current factors used to calculate RLs accurately reflected the risk of transmission.

METHODS: MS was conducted weekly with fifteen traps among three counties, in 2 of 6 regions in Kansas, from 5/13/2018 to 10/23/2018. RL threshold measures were based on California's Mosquito-Borne Virus Risk Assessment. Percent change of *Culex spp.* mosquitoes from the same week the previous year, average daily temperature over the previous two weeks, and five-year historical case data were used (Model 1). Weekly average numerical values were calculated and assigned to one of four RLs (minimal, low, moderate, high). In post-season analysis, a second model was explored where, if ≥ 40 *Culex spp.* mosquitoes were trapped in a county during a week, that factor increased to the maximum value (Model 2). One week was subtracted from onset dates of cases to determine the region's RL during the likely exposure period. RLs in all six regions, positive predictive value (PPV), and sensitivity of both models were compared.

RESULTS: As of 12/11/18, 40 confirmed or probable WNV cases had completed investigations and were reported to ArboNet; two cases occurred prior to MS and were excluded from analysis. In Model 1, 23 weeks were high risk, 89 moderate, and 26 low. In Model 2, 28 weeks were high risk, 92 were moderate, and 18 were low. In Model 1, 10 (26%) persons had likely exposure during high risk weeks compared to 25 (66%) in Model 2. In Model 1, 28 (74%) persons had likely exposure during moderate risk weeks compared to 13 (34%) in Model 2. Zero cases in either model were likely infected during a low risk week. PPV increased from 0.22 in Model 1 to 0.38 in Model 2 and sensitivity increased from 0.19 in Model 1 to 0.56 in Model 2.

CONCLUSIONS: Addition of the two-tier factor for *Culex spp.* in Model 2 increased predictability and sensitivity of Kansas' WNV risk model. Routine evaluation of the WNV surveillance system is crucial to ensure stakeholders receive accurate RL classification to provide appropriate mosquito control and prevention messages to the public.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Risk Assessment; Vectorborne Disease; Disease Prevention
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10595
Abstract Type	Quick
Abstract Title	Increasing Incidence of Anaplasmosis in the United States, 2013–2017

Abstract

BACKGROUND: Anaplasmosis, caused by the bacterium *Anaplasma phagocytophilum*, is a tickborne disease of national concern due to its increasing incidence in the United States. The blacklegged tick, *Ixodes scapularis*, is the primary vector in the Northeastern and Midwestern United States where anaplasmosis is most commonly reported. Illness can range from mild to moderate, the most common symptoms are fever, chills, headache, myalgia, and malaise. While the reported case-fatality rate is <1%, predictors of a more severe course of illness include advanced age, immunosuppression, comorbid medical conditions, and delay in diagnosis and treatment. Doxycycline is the treatment of choice for rickettsial diseases in patients of all ages.

METHODS: Cases of anaplasmosis reported to the Centers for Disease Control and Prevention National Notifiable Diseases Surveillance System (NNDSS) during 2013–2017 were included in this analysis. Incidence rates (IRs) were calculated using U.S. Census Bureau population estimates.

RESULTS: During 2013–2017, 19,151 cases of anaplasmosis were reported to NNDSS, for an average annual IR of 1.3 cases per 100,000 persons. The number of cases doubled from 2,782 in 2013, to 5,762 in 2017, with IRs also increasing from 0.9 to 1.8, respectively. During this time period, the East North Central region reported the most cases with 9,553 (IR=4.1). When adjusting for population, New England had the highest IR of 10.7; this increased from 5.1 in 2013 to 19.0 in 2017. States with the highest IRs included Vermont (27.1), Maine (22.64), New Hampshire (13.1), Minnesota (11.2), Massachusetts (11.1), Rhode Island (10.9), and Wisconsin (10.5); these seven states accounted for 70.3% of all reported cases. Most cases (n=15,740; 82.2%) were reported in persons aged ≥40 years. While the number of cases was highest among persons aged 40–64 years (n=8,323), the IR was highest among persons aged ≥64 years in 2017 at 5.1. Only 78 cases were reported in children aged <5 years.

CONCLUSIONS: During 2013–2017, there was an increase in total number of cases and in the incidence rates of anaplasmosis reported through national surveillance. While anaplasmosis is endemic in the Northeastern and Midwestern states, the Northeastern states have experienced a dramatic increase in cases in recent years. Explanations for this trend may include expansion of the geographic range of *I. scapularis* and increased awareness and testing among providers. The older age predominance is also concerning given the risk of more severe outcomes in these vulnerable populations.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases; Surveillance; Vectorborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11460
Abstract Type	Quick
Abstract Title	Investigation of a Bite Inflicted By a Privately Owned Macaque on a Child – Indiana, 2018

Abstract

BACKGROUND: Primates belonging to the genus *Macaca*, also known as macaques, are reservoirs for *Macacine herpesvirus* (B virus), which is a rare cause of neurologic illness and death in humans. B virus can be transmitted via bites, scratches, or contact with body fluids of infected animals. Bites inflicted by nonhuman primates (NHPs) can also transmit rabies virus (RABV), which is endemic in bats in Indiana. Indiana does not regulate the private ownership of NHPs. In July 2018, the Indiana State Department of Health (ISDH) was notified that a privately owned macaque had escaped from its outdoor enclosure and bitten a child.

METHODS: The macaque owner declined humane euthanasia at an exotic animal veterinary clinic and elected instead to dispatch the macaque himself via gunshot to the left lateral chest wall. No veterinary diagnostic laboratories in Indiana accept NHPs, so the cadaver was shipped to a neighboring state for necropsy and pathogen testing. Brain tissue specimens were tested for evidence of RABV and B virus infection by direct fluorescent antibody (DFA) test and polymerase chain reaction (PCR), respectively. Risk assessments were conducted for all potentially exposed persons. Medical records for the bite victim were reviewed. Serum specimens from the bite victim were tested for evidence of B virus infection by Western blot at the National B Virus Resource Center.

RESULTS: The macaque necropsy revealed no gross or microscopic evidence of infectious disease; no evidence of RABV or B virus infection was found. Both the bite victim and the macaque owner received recommendations to complete antiviral prophylaxis and undergo testing for evidence of B virus infection. The owner declined both. The bite victim completed antiviral prophylaxis and also received a course of antibiotics. Serum specimens collected from the bite victim 3 days and 25 days after the bite had no detectable B virus antibodies.

CONCLUSIONS: Privately owned macaques and other NHPs can pose serious health risks to their communities. Injuries inflicted by NHPs therefore require a prompt public health response. Public health and veterinary diagnostic laboratories that routinely test for RABV may not accept or be equipped to test specimens from NHPs due to human health risks. Private owners of NHPs may be reluctant to comply with public health recommendations. Health departments should be prepared for these challenges when responding to bites inflicted by NHPs.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; One Health; Veterinary Public Health
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11742
Abstract Type	Quick
Abstract Title	Lyme Disease Cases Acquired in Europe Reported to the Florida Department of Health, 2009–2018

Abstract

BACKGROUND: The majority of Lyme disease cases reported to the Florida Department of Health (Florida Health) are acquired outside the state. This includes cases acquired abroad. Lyme disease outside North America is caused by different serotypes or genospecies. Differences in testing and lack of awareness of Lyme disease among travelers abroad may lead to under-reporting of internationally acquired cases. Multiple health agencies in Europe have reported increased geographical distribution of tick vectors and a rise in incidence of cases being reported. This study analyzes Lyme disease cases with exposure in Europe.

METHODS: Probable and confirmed cases of Lyme disease were classified per the Council of State and Territorial Epidemiologists' national case definition. Cases investigated and reported to Florida Health between January 1, 2009, through December 31, 2018, (as of January 2, 2019) were reviewed and sorted according to import status of acquired outside of the U.S. and origin of exposure in Europe or a European country. Lyme disease incidences in European countries were obtained from data reported by European Centre for Disease Prevention and Control (ECDC) and the World Health Organization.

RESULTS: Twenty-eight cases of Lyme disease with exposure in Europe were reported, with an average of three cases and range of one to five cases per year. Countries of exposure included Austria, Belgium, Czech Republic (3), Denmark, Finland (2), France (3), Germany (5), Hungary, Netherlands, Poland, Scotland, Sweden (2), Switzerland (2), Ukraine, and unspecified European countries (3). Sixteen cases (57%) reported known tick bites abroad, with an additional six (21%) reporting exposure to tick habitats. The majority of cases reported exposure in central Europe, which the ECDC recognizes as the highest area for Lyme disease infection rates on the continent.

CONCLUSIONS: The ECDC currently provides specific Lyme disease educational materials for travelers to Europe. Centers for Disease Control and Prevention has online resources where travelers can search disease information by country of destination, but these resources do not include information on Lyme or other tick-borne diseases by location of travel. Including tick-borne disease risk information in the destination query would be helpful for both travelers and their health care providers. Florida Health is adding information on international tick-borne disease risks to existing resources. A protocol was also created for county epidemiology staff to use when investigating Lyme disease cases with exposure in other countries, as the current Lyme disease case definition only references exposure in high and low incidence U.S. states.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	International Health; Infectious Diseases; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Affiliation	State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Monitoring Bat Rabies in the United States: Considerations for Improved Species Identification and Virus Characterization.

Abstract

BACKGROUND: Species identification and virus characterization data for rabid bats in the United States is limited. Given the implications that bat rabies virus (RABV) variants have for human health, understanding the transmission dynamics of RABV variants within and between bat species is crucial. To date, there has been limited systematic evaluation of virus characterization data of bats submitted to the U.S. national animal rabies surveillance system.

METHODS: The authors evaluated submitted specimens and selected those that merit prioritization for virus characterization. These samples of epizootiological importance (SEI), were selected based on characteristics that would improve detection of sentinel events in disease dissemination. National animal rabies surveillance data, years 2010–2015, were analyzed and the total number of positive samples obtained for each SEI category across the six-year time span was used to calculate the estimated number of samples and confidence intervals that public health laboratories could expect if all SEI underwent RABV characterization. Additionally, we evaluated the number of bats submitted for rabies testing in which species was identified.

RESULTS: The SEI were defined as: rabid non-indigenous bats; rabid bats in southern U.S. border states, Florida, Puerto Rico and the U.S. Virgin Islands; and rabid bats not commonly found to be infected with RABV. During 2010–2015, there were 160,017 bats submitted for testing, including 74,928 (47%) where bats were identified by species. Among the bats with species information included, 33,882 (45%) were defined as SEI. Annually, 692 (95% CI, 600–784) SEI were rabid and 295 (95% CI, 148–442) underwent virus characterization. Performing virus characterization of SEI would result in 387 (95% CI, 287–506) samples each year. In total, 9,552 rabid bats were identified over the six year period, and 2,029 (21.2%) underwent virus characterization.

CONCLUSIONS: Increased RABV characterization of SEI and identification of bat species would help inform our understanding of RABV epizootiology in bat species, some of which have frequent human contact. Laboratory testing of SEI should be evaluated by each public health laboratory to ensure testing does not strain routine diagnostic laboratory capacity.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Epidemiology; Sustainability
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10857
Abstract Type	Quick
Abstract Title	Potential for Zoonotic Parasitic Transmission in Dog Parks in the Birmingham- Alabama Metropolitan Area

Abstract

BACKGROUND: Visiting dog parks and dog-friendly parks is a popular activity among dog owners. With the rise in the popularity of dog park visits in the Birmingham metropolitan area, the risk of transmission of parasitic infections might be a concern. The objective of this pilot study was to assess the prevalence of parasites in dog stools from dog parks in the Birmingham metro area.

METHODS: In this study, dog fecal samples were collected from dog parks and dog-friendly parks around the Birmingham metro area in two different years (2016 and 2018) and tested for intestinal parasites. Stool sedimentation technique was used and samples were examined microscopically for parasites.

RESULTS: Ten percent of dog fecal samples collected in 2016 were found to be positive (3/30) for larvae and hookworm eggs that may be transmitted to humans. Only one (out of 40) of the samples that were tested in 2018 (2.5%), tested positive for hookworm eggs. The overall percent of specimens positive for parasites in dog feces from the dog parks surveyed was 5.71% (4/70) when using the traditional parasitological method (low sensitivity).

CONCLUSIONS: Even though the overall prevalence of positive dog stool samples and the worm burden were low, this findings indicates that there is a potential risk of zoonotic infection transmission while visiting dog parks and dog friendly parks. Users of parks should be informed and educated on the risk of infection and how to prevent and lower the risk of infection. Specimens from 2018 will be tested using molecular techniques (PCR) next in order to get a better picture of the prevalence of parasites of zoonotic importance in dog feces from dog parks in Birmingham.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Veterinary Public Health; Disease Prevention; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10950
Abstract Type	Quick
Abstract Title	Quantifying Vector Control Response to Human Arboviral Disease

Abstract

BACKGROUND: In New Jersey, vector-borne disease surveillance/control is coordinated between state and local public health and vector control agencies. The New Jersey Department of Health (NJDOH) shares information on human cases of mosquito-borne disease with vector control partners for timely surveillance and control. Although there has been anecdotal evidence on actions taken in response to human case notifications, these actions have not been documented. In 2018, NJDOH implemented a survey to document these efforts.

METHODS: NJDOH designed an online survey (NoviSurvey) that collected information about vector control response, including site visits, public education, surveillance and pathogen testing, and control. After receiving acute arboviral disease laboratory reports, NJDOH notified the New Jersey Department of Environmental Protection (NJDEP), providing the disease, patient address, and date of specimen collection. NJDEP provided this information to the appropriate county mosquito control agency (CMCA) and sent a survey link to the CMCA to complete for each notification. At the end of the season, the data was exported into Excel for analysis.

RESULTS: There were 121 human arboviral notifications between 6/5/18 and 11/18/18. 92 surveys were completed, for a 76% response rate. After human case notification, 39% CMCA's made a home visit and 83% visited the patient's neighborhood. Visits were conducted more often for West Nile virus (WNV) and CA serogroup virus (1 case) and less often for travel associated diseases. Visits were conducted a median of 1 day after notification. Findings included stagnant water, containers or plants holding water, and tires/tire swings. When speaking with homeowners (42%) and neighborhood residents (31%), educational topics included habitat reduction/eliminating standing water, mosquito repellents, and residential spraying. None educated homeowners to treat clothing/gear, or to avoid mosquito bites 3 weeks after travel. CMCA's set mosquito traps during 39% of home visits and 49% of neighborhood visits. When visits were made in response to a WNV human case, 36-38% of sample submissions were positive for WNV. Mosquito control measures included larviciding, adulticiding, and environmental remediation. Control measures were implemented a median of the same day as the visit and 1 day after notification.

CONCLUSIONS: CMCA's provided timely response and control measures after 85% of human arboviral disease notifications. Several CMCA's reported strong collaboration with local health departments to coordinate response and implementation of additional area-wide surveillance and control measures. CMCA response included mosquito control, environmental remediation, and community education. Opportunities exist to improve educational messaging, particularly for travel-associated diseases.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases; Vectorborne Disease
Consider for Different Presentation?	Yes
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Affiliation	State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11167
Abstract Type	Quick
Abstract Title	Rabies Post-Exposure Prophylaxis of Veterinarians and Veterinary Staff Following Contact with Rabid Animals, Kansas 2013 – 2017

Abstract

BACKGROUND: The Advisory Committee on Immunization Practices (ACIP) classifies veterinarians and veterinary staff (VS) at frequent risk for rabies exposure. The most common route of rabies exposure is from a bite; however, non-bite exposures, which rarely cause rabies in the United States (US), should be evaluated on a case-by-case basis. In Kansas, local health departments (LHDs) perform rabies exposure risk assessments and provide rabies post-exposure prophylaxis (PEP) recommendations per ACIP guidelines. Rabies surveillance data was evaluated to characterize veterinarians and VS rabies exposures and to determine if ACIP PEP recommendations were followed.

METHODS: All rabies diagnostic test results were submitted to the Kansas Department of Health and Environment daily from the Kansas State University Rabies Laboratory. Rabies-positive animals were entered into Kansas' electronic disease surveillance system and assigned to the LHD in the county where the animal resided or was found. A standardized rabies risk assessment form, based on ACIP guidelines, was utilized for investigation. LHD investigation included evaluation of all veterinarians and VS in contact with the rabid animal. PEP was recommended based on ACIP exposure risk. From 2013 – 2017 veterinarians and VS contacts of rabies-positive animals were evaluated for: 1) exposure status, 2) PEP recommendation, and 3) compliance with PEP recommendation.

RESULTS: There were 324/5515 rabies-positive animals; 76% wildlife and 24% domestic. Cattle (n=32) and cats (n=28) were the most frequent rabid domestic animals. Sixty-one veterinarians and VS were evaluated; 52 for exposure to livestock and 9 for exposure to small animals. PEP was recommended for 16/52 veterinarians and VS exposed to livestock of which 63% (10/16) were non-bite exposures. Eleven veterinarians and VS considered not exposed and 23 with unknown exposure to rabid livestock received PEP outside of ACIP recommendations. Nine of sixty-one veterinarians and VS were potentially exposed to a rabid small animal. PEP was recommended for 56% (5/9); all for non-bite exposures. No additional veterinarians or VS received PEP due to a small animal exposure.

CONCLUSIONS: To our knowledge, this is the first evaluation of PEP recommendations and compliance of veterinarians and VS in the US. Despite ACIP recommendations for PEP based on exposure risk, veterinarians and VS received PEP outside of ACIP guidelines. Veterinarians and VS should adhere to veterinary standard precautions to reduce potential non-bite exposures. It is crucial that veterinarians and VS understand ACIP recommendations to make informed decisions regarding PEP and to provide accurate information to clients with rabid animals.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Occupational Health; One Health; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11125
Abstract Type	Quick
Abstract Title	Raccoons, Cats, and the Odd Otter, Oh My! - Rabies Virus Surveillance, Identification, and Prevention in Miami-Dade County, 2018

Abstract

BACKGROUND: In Florida, it is estimated that at least 60,000 residents and visitors are bitten each year by a domestic or wild animal. A *rabies virus exposure* is any bite, scratch, or other contact in which saliva or nervous tissue of a suspect or known rabid animal enters an open or fresh wound or encounters mucous membranes by entering the eye, mouth, or nose of another animal or person.

METHODS: The Florida Department of Health in Miami-Dade County (DOH Miami-Dade) monitors possible animal-to-human rabies transmission through the investigation of all individuals exposed to a suspected rabid animal and/or those that receive or are recommended to receive post-exposure prophylaxis (PEP). Data for animal bites/exposures and animals sent for rabies virus testing between January 1 and December 31, 2018 were abstracted from Merlin, the Florida Department of Health Surveillance System and analyzed using SAS v9.4.

RESULTS: Between January 1 and December 31, 2018, DOH Miami-Dade received 2,094 reports of animal bites/exposures among Miami-Dade County residents, of which 449 (21.4%) met case definition as a possible exposure. Among these, 249 (55.5%) occurred among women, and 266 (59.2%) occurred among individuals of Hispanic ethnicity. Median age was 33 (range 0 to 99). The vast majority (426, 94.9%) of exposures were bites with most individuals sustaining a single bite/wound in a specific area (351, 78.2%). Among individuals with a single exposure site, exposures to the arm or hand were most frequently reported (197, 56.1%). High priority exposures, defined as those occurring to the head or neck, occurred in 7.3% of all reports, regardless of if the individual sustained bites/wounds in a single area or multiple areas. Among the 449 individuals who met case definition as a possible exposure, 336 (74.8%) were recommended PEP of whom 166 (49.4%) initiated treatment; 160 (47.6%) were lost to follow-up. Among all reported animals involved in potential exposures, dogs accounted for the majority of events (301, 67.0%) followed by cats (108, 24.1%) and other wild animals, including raccoons, monkeys, rats, and bats (21, 4.7%). Of 195 animals sent for rabies virus testing, 11 (5.6%) were positive, a nine-fold increase from the previous three-year average.

CONCLUSIONS: In 2018, Miami-Dade County saw a significant increase in rabies positive animal identification. Although human rabies is rare, the potential risk of transmission from animals and humans remains. Enhanced surveillance is necessary to ensure that individuals potentially exposed to rabies virus undertake the proper preventative measures to mitigate infection.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Surveillance; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11653
Abstract Type	Quick
Abstract Title	Raising the Standard: Reviewing Positive Predictive Values of Spotted Fever Rickettsiosis Titers and Assessing Surveillance in the Context of the Current National Case Definition -- Georgia, 2018

Abstract

BACKGROUND: Spotted fever rickettsioses (SFR) are tickborne bacterial diseases caused by pathogens in the genus *Rickettsia*. The indirect immunofluorescence assay (IFA) is the most common reference test for laboratory identification of SFR. The current national case definition for a confirmed case of SFR (2010) requires clinically compatible symptoms and an IFA immunoglobulin G (IgG)-specific antibody titer of at least 1:64 drawn in the first week of illness, with a fourfold change in convalescent titer drawn 2-4 weeks later. This study reviews positive predictive values of SFR titers and assesses SFR surveillance in Georgia in the context of the current national case definition.

METHODS: The Georgia Department of Public Health receives electronic and paper reports of SFR via notifiable disease reporting. Suspect case-patient data are uploaded to the State Electronic National Disease Surveillance System (SendSS). Epidemiologic, clinical, and IFA IgG laboratory testing data from 2018 were analyzed and characterized according to the SFR national case definitions and positive predictive values (PPV) for different titer levels were calculated. This analysis was restricted to suspect-cases with laboratory draw dates in 2018 and investigations completed by December 18th, 2018.

RESULTS: IFA IgG results were analyzed from 478 suspect SFR case-patients. Sixty eight percent (326) of these reports were fully investigated, of which 18% (58) were found to meet clinical criteria for a case, with one confirmed SFR case in 2018. The PPV was 0.15 for an initial titer of 1:64, 0.20 for an initial titer of 1:128, and 0.20 for an initial titer of 1:256 or greater. Only 7% (33) of cases reported a convalescent draw, with 1% (5) during the appropriate time frame to meet the case definition. Eleven percent (55) of investigations had a date of onset that differed from the date their lab was drawn.

CONCLUSIONS: Cases with an initial titer of 1:64 had the lowest PPV but none were greater than 0.20, demonstrating a high background of SFR seroprevalence in Georgia. Many cases who met clinical criteria remained classified as probable because they lacked a convalescent titer in the appropriate time period. Additionally, as the lab date is often used as the default date of onset, it is difficult to determine how long after onset of symptoms a patient is tested. These limitations question the accuracy of diagnosis of SFR in Georgia and highlight sensitivity flaws with the most commonly reported form of SFR laboratory testing.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Local Epidemiology; Surveillance; Vectorborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11208
Abstract Type	Quick
Abstract Title	Record Number of Malaria Cases Imported into the United States, 2016

Abstract

BACKGROUND: Malaria is a potentially life-threatening disease caused by *Plasmodium* parasites, transmitted through infective mosquitos. Typically, malaria infections in the United States (U.S.) are imported among persons who traveled to regions with ongoing malaria transmission. Rarely, malaria is acquired within the U.S. through exposure to contaminated blood products, congenital transmission, nosocomial exposure, or local mosquito-borne transmission.

METHODS: Confirmed malaria cases diagnosed by microscopy and polymerase chain reaction (PCR) were reported to health departments, who conducted case investigations. Case reports were transmitted to CDC through the National Malaria Surveillance System, the National Notifiable Diseases Surveillance System, or direct CDC consultations.

RESULTS: In 2016, CDC received 2,078 confirmed malaria case reports, including two congenital cases, three cryptic cases, and one case acquired through blood transfusion. This is the highest number of imported malaria cases in the U.S. since 1972. Compared to recent years, the number of cases reported in 2016 is an 18% increase from the 2010 – 2014 average (1,754 cases annually), and a 36% increase from 2015 (1,524 cases). Note that in 2015, coinciding with the Ebola virus disease (Ebola) outbreak in West Africa, the associated health notices and post-travel monitoring, there was an 11.6% decrease in malaria cases (1,524 cases), compared to 2014 (1,725 cases). In 2016, approximately 80% of cases originated from Africa, and more than 60% of these were from West Africa. In 2016, *P. falciparum* accounted for more than two-thirds of the infections, followed by *P. vivax* (12%), fewer than 5% of cases were infected with *P. ovale* , *P. malariae* , or mixed species infections; the species was not known for approximately 10% of cases. PCR testing confirmed approximately one-third of cases. Approximately 15% of patients had severe malaria, and seven people died. Of the U.S. resident patients who reported purpose of travel, approximately 70% were visiting friends or relatives. Among U.S residents, 94% of patients with malaria did not adhere to, or take a CDC-recommended chemoprophylaxis regimen.

CONCLUSIONS: After the U.S. observed a decrease in imported malaria cases in 2015, likely associated with the Ebola outbreak, cases rebounded from West Africa and across Africa, and a record number of malaria cases were imported in 2016. Since the early 2000s, there has been worldwide success to reduce the malaria disease burden, although progress has plateaued in recent years and malaria remains endemic in many regions, and the use of appropriate chemoprophylaxis medications by travelers is inadequate.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11798
Abstract Type	Quick
Abstract Title	Selected Cardiac Abnormalities in Trypanosoma Cruzi Serologically Positive, Discordant, and Negative Government Working Dogs

Abstract

BACKGROUND: Chagas disease is increasingly recognized in the southern U.S., where triatomine vectors transmit *Trypanosoma cruzi* among wildlife and domestic dogs with occasional vector spillover to humans. Clinical outcome in canines is variable ranging from asymptomatic infections to chronic heart disease to acute death. In order to characterize cardiac manifestations of *T. cruzi* infections, we tracked a cohort of naturally-infected government working dogs and a matched cohort of uninfected dogs. We hypothesized that selected measures of cardiac disease (abnormal rate, abnormal rhythm, and elevated cardiac troponin I (cTnI; a biomarker of cardiac injury)) would occur more commonly in infected than uninfected dogs matched by age, breed sex and location.

METHODS: We placed an ambulatory ECG monitor (Holter) on 41 dogs including 17 *T. cruzi*-infected, 18 uninfected dogs and 6 dogs with discordant results as measured by three independent serological tests.

RESULTS: The presence of ECG abnormalities varied by *T. cruzi* infection status ($p=0.006$), where 76.5% of positive, 100 % of discordant, and 33.3% of negative dogs showed ≥ 1 abnormality. The most common cardiac abnormalities included supraventricular and ventricular arrhythmias and atrioventricular block. Infected dogs had more distinct types of ECG abnormalities than uninfected dogs, with discordant dogs not different from either group ($(2) = 7.95$, $p=0.019$). Infected dogs had higher serum concentrations of cTnI than both uninfected dogs ($p=0.044$) and discordant dogs ($p=0.06$). Based on dog handler reports, nearly all (4/5; 80%) dogs with reported performance decline or fatigue were infected dogs.

CONCLUSIONS: Understanding the cardiac manifestations of natural *T. cruzi* infections in dogs is critical for prognostication and to establish a baseline for interpreting data from intervention studies. The cardiac manifestations of Chagas disease in these highly valued working dogs is likely associated with a yet- unquantified impact on their ability to work, economic and security consequences.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Affiliation	Academic Institution

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Tick-Borne Relapsing Fever in an Area with a Previous Known Cluster

Abstract

BACKGROUND: In September 2018, the National Park Service (NPS) Office of Public Health (OPH) learned of a confirmed Tick Borne Relapsing Fever (TBRF) case in an NPS employee who lived in a group of cabins where there had been a cluster of at least four TBRF cases two years prior. Because the development of a new case suggested ongoing exposure risk, we investigated in order to identify areas for potential improvement in communication and education, integrated pest management (IPM), and illness recognition and reporting.

METHODS: The NPS OPH led a collaborative effort with the park, the NPS IPM, and the California Department of Public Health that included a site visit. Prior to the visit, we distributed a survey to employees aimed at better understanding current thoughts and practices related to TBRF and other rodent-associated diseases. During and prior to the visit, the team met with various work groups in the park, as well as a physician who lived at the site and was instrumental in diagnosing the most recent case. The team also toured park cabins and facilities to help identify areas of rodent ingress and offer recommendations for rodent exclusion.

RESULTS: The majority of the 62 park employees who completed the pre-visit survey identified rodent-related concerns in their home or workplace. Barriers to removing/excluding rodents included the high numbers of rodents in the areas, difficulty excluding them, limited resources for maintenance work, and lack of information on best practices. During the building inspections, we noted areas of potential rodent inclusion. In response to these findings, the team developed an integrative, multi-faceted approach aimed at empowering employees. This approach included education about rodent-exclusion techniques, suggestions for and some provision of materials, including copper mesh, snap traps, spray foam, and hardware cloth, suggestions for enhancing integrated pest management within the park, and information for employees to help them seek medical care when appropriate. Tools developed included an internal employee web page on preventing rodent-associated diseases, a rodent-exclusion supply list, a reporting scheme for employee illness, an employee handout on diseases encountered in a wilderness setting designed them to recognize possible exposures and symptoms, and an employee wallet card to present to healthcare providers when seeking medical care.

CONCLUSIONS: A case of TBRF in a National Park site where there had been a previous cluster demonstrated the need for ongoing efforts to prevent rodent-associated disease. XX

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Disease Prevention; Infectious Diseases; Vectorborne Disease
Consider for Different Presentation?	Yes
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Affiliation	Federal Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Understanding the Burden of Typhus Group Rickettsioses in the United States Using a Large, Insurance Claims Database

Abstract

BACKGROUND: Typhus group rickettsioses (TGR) are vector-borne diseases that include *Rickettsia typhi* (murine typhus) and *R. prowazekii* (epidemic typhus). Improvements in pest management, hygiene, and sanitation led to dramatic decreases in disease incidence during the 20th century. While both diseases are still present in the United States, little is known about their national prevalence, as neither is nationally notifiable. In order to understand the TGR burden in the United States, we summarized nationally representative administrative claims data from a large, commercially insured population.

METHODS: We conducted a descriptive retrospective analysis using the 2003–2016 Truven Health MarketScan® Commercial Claims and Encounters databases. We included any individual <65 years of age with an inpatient admission or outpatient visit with a TGR code from the International Classification of Diseases, Ninth or Tenth Revisions, Clinical Modification (ICD-9/10-CM). The first record with TGR was considered the incident diagnosis. Epidemiologic characteristics associated with the incident diagnosis were summarized for all individuals, and changes in disease patterns during the study period were evaluated.

RESULTS: From 2003–2016, we identified 1,799 unique patients with an ICD-9/10-CM code for a TGR. Average annual incidence was 4.5 patients per 1,000,000 person-years (range: 2.3–5.8/1,000,000 person-years). Epidemic typhus was the most common typhus group rickettsiosis diagnosed among 931 patients (51.8%), followed by murine typhus (n = 722; 40.1%). Recrudescence infection with *R. prowazekii*, known as Brill-Zinsser disease, occurred in 146 patients (8.1%). The majority of patients diagnosed with a TGR were female (n = 1019; 56.6%) and the median age was 42 years (range: 0–64 years). Most patients resided in the Northeast (n=695; 38.6%) and South (n=661; 36.7%) regions, though the incidence rate was almost three times higher in the Northeast (11.6/1,000,000 person-years) compared to the South (4.1/1,000,000 person-years). Hospitalizations were rare (n=74; 4.1%).

CONCLUSIONS: TGR are rarely diagnosed diseases among the U.S. commercially-insured population. More patients were diagnosed with epidemic typhus than murine typhus, even though *R. prowazekii* transmission requires body louse or flying squirrel exposure. Patients from all geographic regions were diagnosed with murine typhus and epidemic typhus, despite both diseases having limited geographical ranges. Insurance claims data do not incorporate symptoms or diagnostic information making validation of cases impossible. The misalignment of the epidemiology of insurance claims data versus historic, published TGR data suggests more studies are needed to determine the true burden of TGR in United States.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	ICD; Vectorborne Disease; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10605
Abstract Type	Quick
Abstract Title	Using Citizen Science to Enhance Surveillance of the Mosquito Vector <i>Aedes Aegypti</i> in Arizona, 2015–2017

Abstract

BACKGROUND: Vector surveillance is an essential component of vector-borne disease prevention, however, some communities lack resources to support extensive mosquito surveillance. *Aedes aegypti* mosquitoes have an established presence in Arizona and are one of the primary vectors of the arboviruses Zika, dengue, and chikungunya, remaining a threat for local disease transmission. To better describe *Ae. aegypti* distribution statewide, the Great Arizona Mosquito Hunt (GAMH) was launched during 2015–2017 in a collaboration between the Arizona Department of Health Services and other public health and academic partners. We aimed to assess the utility and feasibility of enlisting citizen scientists (general citizens who contribute their knowledge, tools, or resources) to add to *Ae. aegypti* surveillance efforts with a focus to enhance surveillance capacity in more rural Arizona regions.

METHODS: In August 2015, all 415 Arizona high schools were automatically enrolled using an introductory email unless they specifically opted out. We sent participating schools and youth organizations instructions and oviposition trap (ovitrap) kits which collect only mosquito eggs. They then conducted ovitrapping for 1–4 weeks during peak *Ae. aegypti* season in Arizona and returned the egg sheets to collaborating entomologists for identification. In 2016 and 2017, all schools that returned egg sheets the previous year were automatically enrolled. Schools who did not participate in the previous year(s) were invited to register to participate using an online enrollment form.

RESULTS: During the three years of the GAMH, 120 different schools or youth organizations participated. A total of 879 egg sheets were received and checked for *Aedes* eggs; during 2015–2017, respectively, 51%, 67%, and 48% of respondents indicated they believed they caught eggs. In contrast, relatively few participants had confirmed positive egg sheets (4%, 38%, 13% respectively). Three new areas in Arizona were identified that were not previously reported to have presence of *Ae. aegypti*. In 2017, 95% of respondents indicated that GAMH increased student engagement in classroom science.

CONCLUSIONS: Overall, the GAMH successfully engaged Arizona schools in mosquito surveillance, created hands-on educational opportunities in classrooms, and documented *Ae. aegypti* populations within Arizona from several areas that were not identified by routine mosquito surveillance during previous years. Our results suggest this youth-based citizen science approach could be a useful tool; collaborations between public health officials and the general public can improve the public's knowledge of mosquito-borne disease while providing valuable information for public health response planning and increasing overall preparedness to meet emerging arboviral threats.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Collaboration; Vectorborne Disease; Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11351
Abstract Type	Quick
Abstract Title	West Nile Virus Disease Burden in the City of Houston, 2014-2018

Abstract

BACKGROUND: West Nile Viral disease (WNV) is a vector-borne condition that is transmitted through an infected mosquito. It is considered the leading cause of domestically acquired arboviral disease in the United States. In general, majority of the cases are asymptomatic. One in five people who are infected will display mild symptoms like fever, headache, body ache, nausea and vomiting. Only about 1 in 150 infected people will develop serious neurologic complications such as encephalitis and meningitis. According to CDC, in 2017, in the State of Texas, there were total of 133 confirmed cases including 5 deaths and 14 presumptive blood donors. Out of the confirmed cases, there were 85 neuroinvasive and 48 non-neuroinvasive cases. The purpose of this study is to present and summarize the epidemiologic and clinical distribution of confirmed West Nile cases in Houston, Texas, from 2014-2018.

METHODS: Data were extracted from Houston's Electronic Disease Surveillance System (HEDSS) from January 1, 2014 to December 31, 2018. A total of 130 confirmed cases were analyzed to examine the epidemiologic and clinical characteristics of confirmed WNV cases. SAS statistical software was used to conduct statistical analyses. Case severity was determined (West Nile neuroinvasive disease [WNNND] and West Nile fever [WNF]) according to CDC's criteria, 2014.

RESULTS: During 2014-2018, a total of 531 human WNV cases were reported to Houston Health Department (HHD). 130 cases were confirmed, including 98 (75%) WNNV, (25%) WNF and 4 deaths. Males accounted for 68% of cases. About 60% of all cases occurred in persons aged 50-79. Whites (42%) had the highest number of confirmed cases followed by Hispanics (26%). Approximately 87% of the cases resulted in hospitalization. WNF cases mostly presented with fever (92%), headache (67%) followed by chills (62%). WNNV cases showed up with altered mental status (47%), stiff neck (37%), Ataxia (8%), and seizure (8%).

CONCLUSIONS: WNV is mostly prevalent in males, White adults over 60 years of age, with majority of cases has common neuroinvasive symptoms like altered mental status, stiff necks, Ataxia. For non-neuroinvasive cases has clinical symptoms like fever, headache, and chills and rigors. WNV infection is a markedly underreported disease as most of the infected people do not seek medical care due to mild or no symptoms. Currently there are no specific treatment available. Thus, continued monitoring and surveillance activities are warranted for prevention and control of WNV complications as well as decreasing the risk of infection.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases; Surveillance; Waterborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11721
Abstract Type	Quick
Abstract Title	Why Should We Do PCR? Assessment of Clinician Acute Arboviruses Test Ordering Practices

Abstract

BACKGROUND: Zika (ZIK) and dengue (DEN) viruses are flaviviruses with similar geographic distributions and clinical presentations and can be cross-reactive on antibody testing. Polymerase chain reaction (PCR) testing can detect viral ribonucleic acid (RNA) in acute infections and is available commercially. Additionally, secondary DEN infections may result in a low immunoglobulin (Ig)M antibody titer and early IgG elevation, making PCR the best way to confirm an acute DEN infection. Understanding provider test ordering practices can help inform clinician outreach and improve public health surveillance.

METHODS: Florida Department of Health epidemiologists work with commercial laboratories to forward select flavivirus positive samples to the state public health laboratories (SPHL) for confirmatory testing. Obtaining acute symptom onset date, required symptoms, recent travel history, and sample collection dates are pivotal to the laboratory testing algorithm. SPHL relies on state and county epidemiologists to acquire this information before assigning testing, if samples arrive without appropriate paperwork. Epidemiologists confirm and evaluate other epidemiologic information from providers to request additional arboviral testing from SPHL and to obtain convalescent samples as needed. SPHL and commercial laboratory results from confirmed and probable DEN and ZIK cases with symptom onset between January 1, 2016, and December 18, 2018, were reviewed to assess gaps in testing requested by providers.

RESULTS: Of the 70 PCR-positive DEN cases at SPHL, only one had provider-ordered PCR testing. Sixty-seven of these had DEN serology ordered commercially; thirteen had only significantly elevated IgG, which does not meet national DEN case definition criteria. Two additional cases had only ZIK or chikungunya commercial testing ordered. Among the 76 PCR-positive ZIK cases at SPHL, 51 had provider-ordered PCR and nine had only ZIK serology ordered. Commercial DEN serology was ordered for 62 of the ZIK cases.

CONCLUSIONS: Thirteen DEN and sixteen ZIK cases were identified that likely would not have been reported due to initial testing selection. Arboviral disease reporting helps drive mosquito control activity in Florida. In addition, molecular testing provides more disease-specific testing, which is particularly relevant for ZIK-linked birth defects. PCR serotyping of acute DEN cases also provides important epidemiologic information. The Centers for Disease Control and Prevention recommends both DEN and ZIK PCR when either is suspected as an acute illness; relying exclusively on IgM testing is not recommended. Health care providers should be encouraged to order PCR testing for suspected acute flavivirus patients and consider all clinically similar arboviruses endemic to the exposure location.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Epidemiology; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11530
Abstract Type	Quick
Abstract Title	Zika Virus — U.S. Virgin Islands, January 2016–January 2018

Abstract

BACKGROUND: Zika virus (ZIKV) is a mosquito-borne flavivirus that can cause asymptomatic infection, or fever, rash, and congenital malformation, including microcephaly. In the U.S. Virgin Islands (USVI), *Aedes aegypti*, the primary ZIKV vector, caused prior arbovirus epidemics, including the 2014 chikungunya virus epidemic that ceased after ~1 year. ZIKV emerged from Brazil and rapidly spread during 2015–2016 throughout the Americas. USVI consists of 3 main islands, including St. John (population ~4,000), St. Thomas (population ~52,000), and St. Croix (population ~51,000). We describe the epidemiology of the USVI ZIKV outbreak.

METHODS: ZIKV confirmed disease was defined according to the CSTE case definition. During January 2016–December 2018, serum samples and case-report forms were obtained from all pregnant women seeking prenatal care and persons who sought health care in USVI with ≥ 2 of the following clinical signs: fever, rash, arthralgia, conjunctivitis, or myalgia. ZIKV immunoglobulin M antibody, polymerase chain reaction, and plaque reduction neutralization testing were used to confirm ZIKV infection.

RESULTS: In total, 1,031 clinical cases were detected during January 3, 2016–January 24, 2018 (no additional cases have been detected as of January 3rd, 2019), with 919 (89%) detected during July–December 2016. Of those with data, patients' median age was 37 years (range: 0–84 years); 680/1028 (66%) were female, including 136 pregnant women. Rash (763/1030; 74%) and arthralgia (647/1030; 63%) were the most commonly reported clinical signs. ZIKV rates were higher on St. John (89 cases; 2225 cases/100,000 persons) and St. Thomas (685 cases; 1317 cases/100,000 persons), compared with St. Croix (257 cases; 504 cases/100,000 persons).

CONCLUSIONS: ZIKV affected populations throughout USVI. The majority of transmission occurred during July–December 2016 and ceased in January 2018, possibly because of herd immunity, environmental factors, or declining circulation of ZIKV in the Americas.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Epidemiology; Outbreaks
Consider for Different Presentation?	Yes
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