74th Annual
James Steele Conference on Diseases in Nature Transmissible to Humans

Wednesday May 21, 2025 – Friday May 23, 2025

Westin San Antonio North,
San Antonio, Texas

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This Diseases in Nature Conference is sponsored by the Texas Department of State Health Services Zoonosis Control Branch with support provided by the Texas Health Institute. For more information about zoonoses in Texas, please visit the Zoonosis Control Branch's website at www.texaszoonosis.org. For more information about the Texas Health Institute, please visit www.texashealthinstitute.org.

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History of DIN

The James Steele Conference on Diseases in Nature Transmissible to Humans (formerly known as the Southwest Conference on Diseases in Nature Transmissible to Man) focuses on zoonoses and environmentally acquired infectious diseases of interest to health professionals. Participants include human medical providers, veterinarians, public health professionals, scientists, animal control officers, and others involved in the diagnosis, investigation, and prevention of zoonotic diseases.

The conference serves as a forum for the presentation of research, epidemiological data, and other aspects of emerging and current zoonoses and environmentally acquired infectious diseases. Papers outlining case studies, outbreak investigations, basic and applied research, and surveillance program reports are presented with the primary theme of the conference being the ecology and epidemiology of these diseases.

The Southwest Conference on Diseases in Nature Transmissible to Man had its first official meeting on June 2, 1951, but its origin was a decade earlier. In late January of 1941, J.V. Irons, Sidney Bohls (Associate Director and Director of the Texas Department of Health (TDH) Laboratories), and A. B. Rich (Director of Veterinary Public Health at TDH) put together a seminar in the old Norwood building in downtown Austin. The purpose of this seminar was to provide continuing education in the areas of clinical laboratory techniques and microbiology to local technicians.

The group from the Texas Department of Health continued these seminars throughout 1941, expanding to include speakers from the biology department at the University of Texas. By 1943, the meeting had grown both in size and scope and was given the name Conference on Diseases of Animals Transmissible to Man, and Texas A&M University was added to the list of sponsors.

At that time, Dr. James H. Steele was a veterinarian in the U.S. Public Health Service. Dr. Steele founded the first veterinary public health program at the U.S. Public Health Service, where he served for 26 years. Dr. Irons and Dr. Steele were close associates and good friends. Dr. Irons asked Dr. Steele to deliver many papers at the conference and Dr. Steele worked closely with the organizing committees, suggesting many subject areas to explore.

In 1949, Dr. Irons realized that the conference was getting a wide variety of papers from a growing contingent of researchers, physicians, veterinarians, and laboratorians. He proposed that the name be changed once again to the Conference on Diseases in Nature Transmissible to Man.

In 1950, the federal government, to increase knowledge and interest in biological warfare, proposed that 4 regional conferences be established as a venue for new and important papers to be given and discussed. Dr. Irons and Dr. Steele agreed that the existing Conference on Diseases

History of DIN (continued)

in Nature Transmissible to Man would fit neatly into this niche, and the Southwest Conference on Diseases in Nature Transmissible to Man was officially born.

In 1973, the conference keynote address was formally named the J.V. Irons Keynote Address to honor Dr. Irons' contributions to the conference. Dr. Jim Steele was the first J.V. Irons keynote speaker.

From 1951 through 2006, the conference met annually, becoming a premiere conference for the presentation of papers related to the emergence and re-emergence of zoonotic and environmentally acquired infectious diseases and biological warfare, now referred to as bioterrorism. At the business meeting at the end of the 2006 conference, the membership voted unanimously to change the name of the conference to the James H. Steele Conference on Diseases in Nature Transmissible to Humans to honor Dr. Steele's contributions to veterinary public health and to the creation and continued success of this conference.

Wednesday, May 21, 2025	
7:45	**Call to Order and Announcements** Bonny Mayes, MA, E-RYT 200, Department of State Health Services, Austin, TX Pamela Wilson, DrCH, MEd, LVT, MCHES, Department of State Health Services, Austin, TX
8:00-10:00	**Session I – Parasitic & Fungal Zoonoses** Moderator: Amanda J. Kieffer, DVM, MPH, DACVPM
8:00	**Heart Rate Variability Derangements in Dogs with Chagas Disease: A Potential Indicator of Autonomic and Cardiac Disruption** Roy Madigan, DVM, United Veterinary Care, Spring Branch, TX
8:30	**Neuroinflammatory Responses Induced by *Trypanosoma cruzi* in a Murine Model** Mariel Búrquez-Escobedo, DVM, Baylor College of Medicine, Houston, TX
9:00	**Natural Infections of Coccidioides in Captive Non-Human Primates: Pathological Findings, Zoonotic Implications, in an Endemic Region** Henry Jegede, DVM, MVSc, Texas Biomedical Research Institute/Southwest National Primate Center, San Antonio, TX
9:30	**Leishmaniasis in Texas: A Scoping Review Using a One Health Approach** Morgan Jibowu, PhD, MPH, Baylor College of Medicine, Houston, TX
10:00	**BREAK**
10:30-12:00	**Session II – Flea-Borne (Murine) Typhus** Moderator: Ronald D. Tyler Jr., DVM, MS
10:30	**Acute Cholecystitis in Murine Typhus: The Cholecystectomy That Was Not Meant to Be** Nicolas A. Melgarejo, MD, FACP, FIDSA, San Antonio Infectious Diseases Consultants, San Antonio, TX
11:00	**Fulminant Murine Typhus in a Pediatric Patient** Franz Puyol, MD, University of Texas Health Science Center, San Antonio, TX
11:30	**Characterizing Demographic Trends and Hospitalization Factors in Flea-Borne Typhus Patients in Southern Texas** Zoie Fan, BSA & Thomas Tran, BSA, University of Texas Health Science Center, San Antonio, TX
12:00-1:30	**LUNCH ON YOUR OWN**
1:30-3:00	**Session III – Tick-Borne Disease** Moderator: Brent L. Moore, DVM, MS, MPH, DACVPM
1:30	**Tick-Borne Relapsing Fever in the USA** Gregory M. Anstead, MD, PhD, South Texas Veterans Healthcare System, San Antonio, TX
2:00	**Spotted Fever Group Rickettsioses (SFGR) in South Texas** Omar Garcia, BSN, CHW, City of Laredo Public Health Department, Laredo, TX
2:30	**Exposure to a Spirochete-infected *Ornithodoros turicata* Collected from the Home of a Clinical Patient in Austin, Texas** Job Lopez, PhD, Baylor College of Medicine, Houston, TX Bonny Mayes, MA, E-RYT 200, Department of State Health Services, Austin, TX
3:00	**BREAK**
3:30-5:30	**Session IV – Surveillance** Moderator: Sarah Murphy Gunter, PhD, MPH
3:30	**Surveillance of Ticks in Harris County, Texas: Identifying Factors Influencing Tick Abundance** Michelle Downey, MS, Harris County Public Health, Houston, TX
4:00	**Neglected Tropical Diseases Surveillance in a Population of Mexican Americans in Starr County, Texas** Megan Duffey, MD, Baylor College of Medicine, Houston, TX Shynitha Pulluri, Baylor University, Waco, TX
4:30	**A Rare Fatal Case of West Nile Virus Reactivation in a Pediatric Patient with Acute Myeloid Leukemia, 2023** Kamesha Owens, MPH, Department of State Health Services, Austin, TX
5:00	**Building Networks with Wildlife Rehabilitation Facilities: SARS-CoV-2 Surveillance and Assessment of Biosecurity Practices** Hayley Yaglom, MS, MPH, Translational Genomics Research Institute, Flagstaff, AZ

Thursday, May 22, 2025	
7:55	**Call to Order and Announcements**
8:00-9:30	**Session V – H5N1 Influenza Virus I** Moderator: Cherissa Abdul Hamid, DVM, MPH
8:00	**Highly Pathogenic Avian Influenza and Wildlife** Sara Wyckoff, DVM, Texas Parks and Wildlife Department, Austin, TX
8:30	**Navigating Academic-Industry-Public Health Partnerships for Emerging Infectious Disease Events, such as H5N1, in the US** David Douphrate, PhD, MPT, MBA, CPE, CSP & Rebecca Fischer, PhD, MPH, DTM&H, Texas A&M University, College Station, TX
9:00	**Public Health Response to Highly Pathogenic Avian Influenza A (H5N1) Virus Detection at a Zoological Park in Maricopa County, Arizona, November 2024** Melissa Kretschmer, MA, CVT, CIC, Maricopa County Department of Public Health, Phoenix, AZ
9:30	**BREAK**
10:00-11:30	**Session VI – H5N1 Influenza Virus II** Moderator: Annajane (Aj) Marlar, DVM, MRCVS, DACVO
10:00	**Shedding of Influenza A Virus in Dairy Cattle** Jason Lombard, DVM, MS, Colorado State University, Fort Collins, CO
10:30	**Occupational Task Exposures Associated with Seropositivity of Highly Pathogenic Avian Influenza A (H5N1)** Anabel Rodriguez, PhD, MPH & Loni Taylor, DVM, PhD, MPH, Texas A&M University, College Station, TX
11:00	**Dairy H5N1: Insights from an Early Detection Study of Dairy Herds in California** Chloe Stenkamp-Strahm, DVM, PhD, Colorado State University, Fort Collins, CO
11:30-1:00	**LUNCH ON YOUR OWN**
1:00-2:30	**Session VII – Arboviral Diseases** Moderator: David Smonko, DVM
1:00	**Developing a Cross-Protective Flavivirus mRNA Vaccine** Jennifer Clinton, PhD, Baylor College of Medicine, Houston, TX
1:30	**Arbovirus-Associated Hospitalizations in Texas, 2008-2023 (DSHS Public Usage Data File)** Brian Reiber, BS, Texas A&M University, College Station, TX
2:00	**A Curious Case of West Nile Virus: Donor-Derived or Vector-borne?** Mattalin Vojacek, MPH, CIC, Brazoria County Health Department, Angleton, TX
2:30	**BREAK**
2:45-3:45	**Scientific Poster Session** Desserts Served
4:00-5:00	**J.V. Irons Keynote Lecture** Moderator: Bonny Mayes, MA, E-RYT 200
4:00-5:00	**From Bog to Bedside: How Phage Therapy is being Revitalized to Treat Multi-Drug Resistant Bacterial Infections** Steffanie Strathdee, PhD, UC San Diego, La Jolla, CA
5:00-6:30	**J.V. Irons Reception** Light Hors d'oeuvres & Drinks Served

Friday, May 23, 2025	
8:25	**Call to Order and Announcements**
8:30-10:00	**Session VIII – Bacterial Zoonoses** Moderator: Brendan Sullivan, DVM, MPH
8:30	**Brucellosis in the Lone Star State: Insights into Hospital-Associated Cases, 2006–2021** Andrew Lam, MPH, Texas A&M University School of Public Health, College Station, TX
9:00	**Fort Bend County Response to Low-risk Occupational Exposure to *Burkholderia pseudomallei* Bacteria** Catalina Lozano, Fort Bend County, Rosenberg, TX (Jesus-Aldana Barron, BS, Fort Bend County, Rosenberg, TX – backup presenter)
9:30	**Sporadic Tularemia Occurrence in Tennessee, 2014—2024: Illness Characteristics, Reported Exposures, and Investigation Timeliness** Kaitlin Thompson, BS, Tennessee Department of Health, Nashville, TN
10:00	**BREAK**
10:30-12:30	**Session IX – Viral Zoonoses** Moderator: Jeffrey Musser, DVM, PhD
10:30	**From Sample to Result: The DoD FADL's Approach to Rabies Testing - Challenges, Solutions, and Best Practices** Robert Fathke, DVM, PhD, MS, MPH, DACVPM & Kamarin Janelle Aragon, U.S. Army Department of Defense, San Antonio, TX
11:00	**Inter-Species Infection and Food Supply Risk Identification in the Setting of Suspected Cutaneous Anthrax, Secondary to Palmar Penetration by Bone and Inoculation with Contaminated Goat Meat in a Dallas County Food Handler** Gabriela Calvi, MPH, CHW, Texas Department of State Health Services, Austin, TX
11:30	**Encephalomyocarditis Virus: A Rodent-Borne Zoonosis with Non-Human Primate and Public Health Implications** Olga Gonzalez, DVM, DACVP, Texas Biomedical Research Institute, San Antonio, TX
12:00	**Evaluating Preventative Measures for the Zoonotic Transmission of Swine Influenza A Variant at Agricultural Fairs in the United States: A Mathematical Modeling Study** Dana Pittman Ratterree, MPH, Texas A&M University, College Station, TX
12:30	**ADJOURN**

Back-up Presentations:

A Cohort-Based Analysis of Flea-Borne Typhus: Correlating Risk Factors at the Census Tract Level in San Antonio, Texas
Zoie Fan, BSA, and Thomas Tran, BSA, University of Texas Health Science Center, San Antonio, TX

Indigenous Leishmaniasis in Texas, 2007-2022
Bonny Mayes, MA, E-RYT 200, Department of State Health Services, Austin, TX

Wednesday, May 21, 2025

8:00-10:00 Session I: Parasitic & Fungal Zoonoses

Moderator: Amanda J. Kieffer, DVM, MPH, DACVPM
Texas Department of State Health Services, San Antonio, TX

Source: https://ket.org/program/deep-look/how-a-kissing-bug-becomes-a-balloon-full-of-your-blood/

Heart Rate Variability Derangements in Dogs with Chagas Disease: A Potential Indicator of Autonomic and Cardiac Disruption

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Additional authors: Toby West; Luis C Ascanio; Juan D. Ramirez; Christopher McMahan; Alberto Paniz-Mondolfi

Our presentation will focus on how we assessed heart rate variability (HRV) as a marker of autonomic nervous system (ANS) disruption and its role in disease progression in dogs with Chagas disease (CD) and evaluated arrhythmias and conduction abnormalities in symptomatic and asymptomatic groups.

A prospective observational study on dogs treated at a small animal hospital in central Texas from August 2023 to December 2023, was conducted. Ambulatory 24-hour Holter monitoring was conducted to assess HRV metrics (pNN50 and rMSSD), arrhythmias, and conduction abnormalities. HRV parameters were categorized as high, normal, or low. Dogs were classified as symptomatic or asymptomatic based on clinical presentation and comparisons HRV and electrocardiographic findings between groups were performed.

One hundred twelve client-owned dogs with confirmed *Trypanosoma cruzi* infection, were included. Of the 112 dogs, 46 (41.1%) were symptomatic, and 66 (58.9%) were asymptomatic. HRV disruptions were observed in 63% of dogs, underscoring early and widespread autonomic dysregulation in *T. cruzi* infection. Symptomatic dogs had more arrhythmias (1.54 vs. 1.02, $p = 0.02$) and a higher prevalence of second-degree atrioventricular blocks (0.19 vs. 0.03, $p = 0.01$), but HRV abnormalities were similar between groups.

HRV abnormalities were prominent across all dogs with CD, regardless of symptoms, suggesting their utility as early markers of autonomic and cardiac dysfunction. These findings highlight HRV's potential for monitoring disease progression, particularly in asymptomatic dogs, supporting its inclusion in routine assessments for T. cruzi infections.

HRV analysis may enhance early detection and management of CD, an emerging One Health issue, by addressing underdiagnosed autonomic and cardiac dysfunction in dogs.

Neuroinflammatory Responses Induced by *Trypanosoma cruzi* in a Murine Model

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Trypanosoma cruzi (TC) is an intracellular parasite and etiological agent of Chagas disease (CD): a neglected illness that mainly affects developing countries. Chronic TC infections are associated with fatal cardiomyopathies and gastrointestinal disorders that develop due to the associated inflammatory response. The cytokines Interleukin-6 (IL-6) and tumor necrosis factor (TNF) have been detected in cardiac and gastrointestinal tissues, confirming inflammation as the parasite's strategy for causing damage in these organs. Clinical manifestations of central nervous system (CNS) damage such as meningoencephalitis and motor deficits have been reported during both acute and chronic CD. This is especially common in HIV-positive patients, where CD causes fatal encephalitis. Yet, CNS symptoms and their causes in immunocompetent patients have rarely been researched. It is unknown if these symptoms are associated with the parasite invading nervous tissue or if inflammatory mediators are penetrating the blood-brain barrier. Mechanisms used by the parasite to damage the CNS remain elusive and little is known about the interplay between the immune system and Chagas-affected brain tissue. A cell type that reacts to parasitic neurotropism are astrocytes, a parenchymal cell of the CNS that increases the inflammatory state of nervous tissue by releasing inflammatory chemokines. During astrogliosis, glial fibrillary acidic protein (GFAP) is released, indicating loss of astrocytic structure. IL-6 and TNF are expressed by reactive astrocytes and upregulated in other neurogenerative infections like *Trypanosoma brucei*, where elevated levels of both cytokines are associated with brain inflammation. Using an infected murine model, our results show increased levels of IL-6, TNF and inflammatory biomarker GFAP in brain tissue. Despite increased expression of IL-6, we did not detect parasite DNA in CNS tissue, leading us to believe that these cellular mediators are responsible for inflammation. Our study explores how CD induced expression of IL-6 and TNF leads to brain injury.

Natural Infections of Coccidioides in Captive Non-Human Primates: Pathological Findings, Zoonotic Implications, in an Endemic Region

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Additional authors: Olga D. Gonzalez, DVM, DACVP; Vinay Shivanna, DVM, PhD, DACVP, DACVM; Donna Perry, D.V.M., PhD; Edward Dick, Jr., DVM, DACVP

Coccidioidomycosis (Valley fever) is a fungal disease endemic to arid regions of the Americas, including the U.S.-Mexico border. While it is widely recognized in humans, natural infections in captive outdoor housed non-human primates (NHPs) remain poorly documented. This study investigates historical records of Coccidioides infections of apes and Old-World NHPs housed in a research facility at San Antonio, Texas, USA, providing critical insights into its impact on captive NHP populations and potential zoonotic risks.

Gross necropsy examinations, supplemented by histopathological analyses, were performed on affected NHPs. Clinical histories were reviewed, and fungal identification was confirmed via histology. Clinical manifestations varied but were primarily characterized by significant weight loss (10–35%), coughing, exercise intolerance, and occasional lameness. Radiographic findings included pulmonary consolidation and osteolytic lesions of the axial and appendicular skeleton, although few cases were diagnosed post-mortem as an incidental finding on histopathology. Disseminated disease involving thoracic and abdominal organs was frequently observed. The most common morphologic diagnoses included granulomatous lymphadenitis, pneumonia, splenitis, osteomyelitis, tracheitis, esophagitis, hepatitis, pleuritis, and nephritis. Granulomatous inflammation was characterized by abundant multinucleated giant cells with intracytoplasmic 16-30um spherules containing basophilic endospores rimmed by a 2-3µm wide negative staining capsule.

Two cases of human infection linked to animal exposure (cat bite and horse necropsy) have been reported historically, highlighting the occupational risks for facility personnel in endemic regions. Although no zoonotic cases were documented in this study, the detection of natural Coccidioides infections in a captive NHP outdoor facility underscores the intersection of environmental exposure and animal care. Given the potential for transmission through environmental contamination, occupational exposure, or incidental contact, Coccidioidomycosis should be regarded as a zoonotic disease. These findings emphasize the importance of proactive health monitoring and enhanced occupational safety protocols for veterinary and research personnel in endemic areas.

Leishmaniasis in Texas: A Scoping Review Using a One Health Approach

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Additional authors: Richard Chung; Nina Tang, BS; Sarah Guo; Leigh-Anne Lawton, MS; Brendan Sullivan, DVM, MPH; Dawn M. Wetzel, MD, PhD; Sarah M. Gunter, PhD, MPH

Leishmaniasis, caused by *Leishmania* spp., is an endemic vector-borne disease in Texas, yet its epidemiology and ecological drivers remain poorly characterized. Despite the increasing recognition of autochthonous cases, research gaps persist in understanding transmission dynamics, vector ecology, and the role of reservoir hosts.

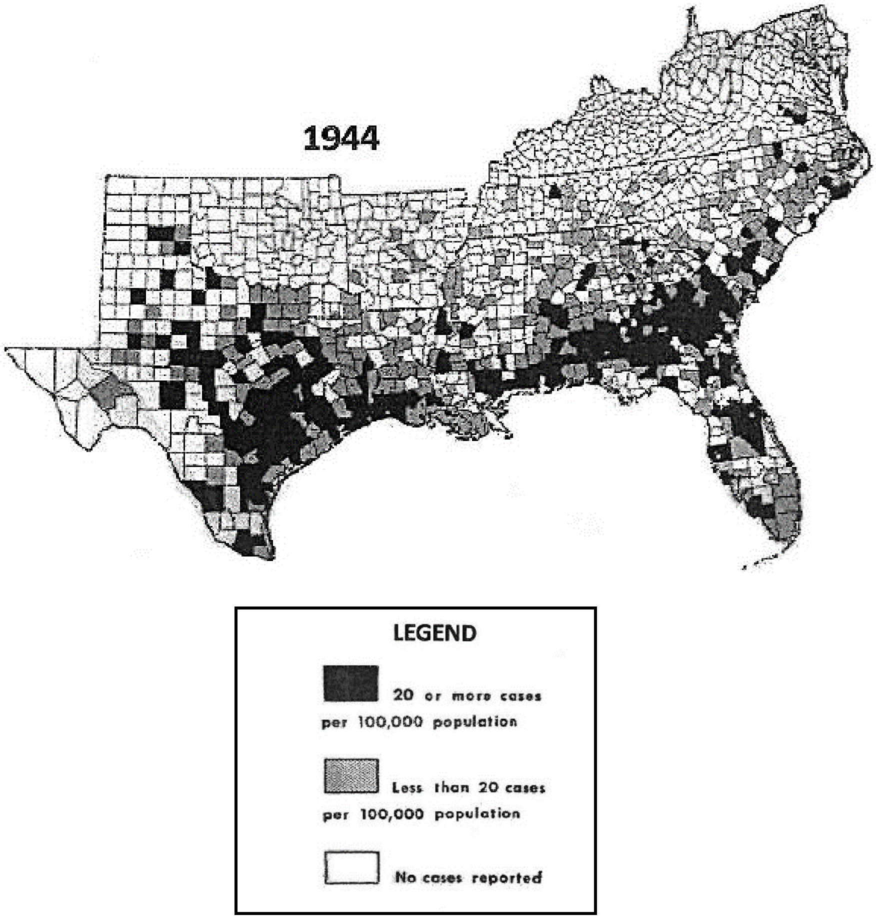
To address these gaps, we conducted a scoping literature review to systematically map existing research on *Leishmania* in Texas. Using a One Health framework, we examined studies on human cases, sand fly vectors, potential reservoir hosts, and environmental drivers of transmission. Our findings highlight the geographic expansion of leishmaniasis, particularly in regions experiencing urbanization and land-use change. While domestic animals, including dogs, have been implicated as potential reservoirs, their precise role in transmission within the state remains unclear. Additionally, unique genetic characteristics of *L. mexicana* in Texas suggest ongoing evolutionary selection pressures that may influence disease dynamics.

Surveillance and reporting remain significant challenges due to barriers such as limited clinical awareness, underdiagnosis, and inconsistent case reporting. Addressing these issues requires a multidisciplinary approach that integrates human, animal, and environmental health perspectives. This review underscores the increasing need for enhanced surveillance systems, expanded vector studies, and increased public health awareness to mitigate the spread of leishmaniasis in Texas. Strengthening interdisciplinary collaboration will be critical for developing effective prevention and control strategies to protect both human and animal populations in Texas.

Wednesday, May 21, 2025

<u>10:30-12:00 Session II: Flea-borne (Murine) Typhus</u>
Moderator: Ronald D. Tyler Jr., DVM, MS
Texas Department of State Health Services, Harlingen, TX

Incidence of Flea-borne Typhus in the Southeastern U.S., 1944



Source: Publ Hlth Rep 1952; 67: 1249-57; provided by Christopher Paddock, MD, MPHTM, CDC Rickettsial Zoonoses Branch

Acute Cholecystitis in Murine Typhus: The Cholecystectomy That Was Not Meant to Be

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A 36-year-old man with no significant medical history presented with a three-week history of headache, neck pain, fever, chills, generalized malaise, and hyporexia. He denied respiratory, urinary, gastrointestinal, or abdominal symptoms. The patient reported exposure to multiple pets, including cats, a dog, a turtle, a bearded dragon, and a pig, as well as feral cats around his property. On physical examination, he was afebrile, hemodynamically stable, and nontoxic appearing. The abdominal examination was unremarkable, with no tenderness or distension. Laboratory results showed elevated inflammatory markers (ESR 62, procalcitonin 2.67) and liver enzymes (ALT 103 U/L, AST 56 U/L, alkaline phosphatase 238 U/L) with normal white blood cell count and negative blood cultures. Imaging revealed gallbladder distention with cholelithiasis. A hepatobiliary iminodiacetic acid (HIDA) scan confirmed acute cholecystitis. Serologic testing showed positive typhus IgG and IgM titers (1:256), indicating a rickettsial infection. The patient was treated with a 7-day course of doxycycline, resulting in rapid symptom resolution. He was discharged without cholecystectomy.

Acute cholecystitis associated with murine typhus is rare, with only a few cases documented. A 2017 case report describes a 54-year-old male with acute acalculous cholecystitis during murine typhus, confirmed by serology and successfully treated with doxycycline. Additionally, a 2006 report details a traveler whose murine typhus infection mimicked acute cholecystitis, leading to diagnostic challenges. These cases highlight the need to consider murine typhus in the differential diagnosis of acute cholecystitis, especially in endemic areas or patients with relevant exposure. This case underscores the importance of zoonotic infections in patients with compatible exposure and systemic symptoms, emphasizing the diagnostic value of typhus serology in endemic regions.

Fulminant Murine Typhus in a Pediatric Patient

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Additional author: Theresa Barton, MD

A 17-year-old previously healthy female presents with 10 days of headache, malaise, dark urine and myalgias. She was tachycardic, hypotensive, thrombocytopenic, with elevated inflammatory markers, nitrites in her urinalysis, and significant elevation in serum creatinine. She had a rapid clinically deterioration with seizures, respiratory failure, vasopressor requirement, renal failure and bruising on venipuncture sites and right foot where she had a recent injury. A CT of her head revealed bilateral thalamic infarcts.

Initial differential included urosepsis given her positive nitrites, staphylococcus toxic shock syndrome related to her right foot injury, murine typhus as she has pet dogs in an endemic area, multi-system inflammatory syndrome in children due to COVID-19 infection a year prior, and hemophagocytic lymphohistiocytosis. On day three of hospitalization, she developed dry gangrene with ischemia of her left lower extremity and right toes that required a below knee amputation of the left and transmetatarsal amputation on the right. *Rickettsia typhi* IgM was positive, confirmed by Karius testing (detects pathogen DNA in the blood). On day 2 of hospitalization, she initiated a ten-day course of doxycycline. She required hemodialysis for a month prior to transitioning to inpatient rehabilitation where she was discharged after a nearly 2-month hospitalization.

Murine typhus is endemic to South Texas with rising incidence in the mid early-mid 2010s. Common exposures are fleas, dogs, cats, or urban wildlife, with most cases occurring in the summer. The treatment is doxycycline with clinical improvement usually within 3 days of initiation. The clinical course for most patients is uncomplicated; however, over 20% experience significant complications including septic shock and severe respiratory, neurologic, renal, hepatic, cardiac, and ocular manifestations.

This case highlights the need for a high index of suspicion given the potential for significant morbidity and clinical severity of murine typhus in an endemic region such as South Texas.

Characterizing Demographic Trends and Hospitalization Factors in Flea-Borne Typhus Patients in Southern Texas

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Flea-borne typhus (FBT), or murine typhus, is a rickettsial disease caused by *Rickettsia typhi* that commonly presents as a non-specific febrile illness. Though relatively uncommon, Texas reports the highest number of cases of FBT annually with most cases concentrated in the southern part of the state. The course of patients with FBT can range from mild and self-limited to severe. Over 60% of patients with reported FBT are admitted. Here, we aimed to characterize better the demographic features of patients who contract FBT. From an initial group of 1076 patients who have had *Rickettsia* serologies collected from January 2020 through October 2024 at University Hospital in San Antonio, TX, a cohort of 176 probable patients was formed from patients who had positive serologies for *Rickettsia typhi* (defined as IgM ≥ 1:256). Through chart reviews, demographic information such as age, gender, and geographic location were collected and analyzed along with other factors such as symptoms on presentation and length of hospital stay. This information provides an important foundation for future studies to identify possible demographic trends in patients with FBT and other indicators that could portend a worse prognosis or longer hospitalization.

Wednesday, May 21, 2025

1:30-3:00 Session III: Tick-Borne Disease
Moderator: Brent L. Moore, DVM, MS, MPH, DACVPM
Texas Department of State Health Services, Tyler, TX

Ornithodoros turicata

Source: Personal photo provided by Bonny Mayes; tick collected in Austin, TX.

Tick-Borne Relapsing Fever in the USA

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Tick-borne relapsing fever (TBRF) is caused by spirochetal bacteria of the genus *Borrelia* and is transmitted primarily by soft ticks of the genus *Ornithodoros*. In the USA, TBRF occurs primarily in the western states. Specific *Borrelia* species are transmitted by specific ticks; *B. hermsii*, *B. turicatae*, and *B. parkeri* are transmitted by *O. hermsi*, *O. turicata* and *O. parkeri*, respectively. After the tick bite, a small papule with a central eschar in a few days. After an incubation period of about 7 days, there is a sudden onset of fever. The first fever episode ends with rigors, tachycardia, and elevated blood pressure, soon followed by profuse diaphoresis, a drop in the body temperature, and hypotension. Death due to TBRF is most common at this point. Other common symptoms are headache, myalgias, chills, nausea, vomiting, and joint pain. Occasionally, patients may suffer meningoencephalitis, cranial neuritis, myelitis, and radiculopathy. Myocarditis may cause Adult Respiratory Distress Syndrome. TBRF during pregnancy may result in still birth; transplacental transmission has been reported. TBRF is diagnosed by the visualization of the spirochetes in the blood smear. Doxycycline is the treatment of choice. Cases in Texas have been decreasing since the 1930s for unclear reasons. In the 1930s, there were about 52 cases in Texas per year; now there is only about one case per year. Although TBRF has a low mortality rate, it is very unpleasant to the individual patient until they are properly diagnosed and treated. The understanding of TBRF in the first half-century of the 20th century in the USA required multiple tracts of inquiry: the human epidemiology and clinical aspects of the disease; the identification of the vectors and reservoirs; determining the relationship to specific species of ticks to specific *Borrelia* species; and determining the molecular basis of the relapsing nature of the infection.

Spotted Fever Group Rickettsioses (SFGR) in South Texas

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The finality of this presentation is to help public health/healthcare professionals identify clinical features, epidemiological data, and risk factors associated with Spotted Fever Group Rickettsioses (SFGR) in South Texas, as well as prevention and management strategies tailored to the region. The warm climate, environmental factors and the significant tick population in South Texas can contribute to the spread of SFGR in humans. Understanding infection rates, geographic distribution, and tick-host interactions in the South Texas region can aid in early detection, improve diagnostic efforts, and inform public health policies to reduce the risk of human infection. Additionally, raising awareness among healthcare providers and the public can lead to better disease management and prevention strategies.

Exposure to Spirochete-Infected *Ornithodoros turicata* Collected from the Home of a Clinical Patient in Austin, Texas

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The most common cause of tick-borne relapsing fever (TBRF) in the Southwestern United States is *Borrelia turicatae*, which is transmitted by *Ornithodoros turicata*. Historically, human cases of TBRF have been associated with caves and rural settings like rustic cabins and outbuildings frequented by peridomestic mammals. Recent reports suggest a change in vector ecology with spirochete-infected *O. turicata* identified in public parks and green spaces within sprawling urban centers in Texas.

On February 29, 2024, an individual was at home in Austin and found a tick engorging on his leg and sent it in to the Texas Department of State Health Services (DSHS) Zoonosis Control Branch (ZCB) for tick testing at the University of North Texas Health Science Center (UNTHSC). ZCB staff identified the tick as a soft tick, likely *O. turicata*, and called the individual to let him know the tick was a potential vector of TBRF and to ask if the tick could be sent to researchers at the Baylor College of Medicine (BCM) as opposed to UNTHSC. The individual agreed and proceeded to state that he was recently hospitalized and still suffering from Bell's palsy. He stated that he tested positive for Lyme disease but was told that it was a false positive. He also expressed interest in pursuing more testing, if possible, to determine the etiology of his illness.

Because Lyme disease and TBRF are reportable in Texas, ZCB staff obtained the individual's medical records and requested that a serum sample be forwarded for additional testing at CDC. The tick was shipped to BCM for identification and testing. The clinical course of individual's illness, lab results, tick testing results, and implications of the changes in vector ecology will be discussed.

Wednesday, May 21, 2025

3:30-5:30 Session IV: Surveillance

Moderator: Sarah Murphy Gunter, PhD, MPH
Baylor College of Medicine, Houston, TX

Source: Photo from Zoonosis Control Field Skills, 2024

Surveillance of Ticks in Harris County, Texas: Identifying Factors Influencing Tick Abundance

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In recent years, ticks, and the pathogens that they vector, have been of increasing importance to public health. In 2024, the human burden of tickborne disease in the United States was over 71,000 cases. Another cause for concern has been the expansion of the geographic ranges of tick vectors within North America. These observations highlight the need to understand the environmental and ecological factors that influence tick dispersal, abundance, and behavior. The Mosquito and Vector Control Division (MVCD) of Harris County Public Health has been conducting regular tick surveillance since 2017. Here we assess tick collection data in terms of temperature, humidity, habitat type, collection method, and time of year to identify patterns that may be useful in predicting where and when tick activity in our region occurs. Notably, different seasonal patterns are observed for the three primary tick species collected in Harris County (*Amblyomma americanum*, *A. maculatum*, and *Ixodes scapularis*). These tick species also exhibit different behaviors that may translate into different effective field collection methods. This information can be used to assess the risk of tick encounters and in educating the community to help prevent tickborne illnesses in people and pets.

Neglected Tropical Diseases Surveillance in a Population of Mexican Americans in Starr County, Texas

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Neglected tropical diseases (NTDs) are a major cause of morbidity in impoverished communities worldwide. Although these diseases were previously thought to be non-endemic in the United States, a growing body of evidence suggests they may be re-emerging in the US south. The Texas-Mexico border is at an elevated risk due to high poverty rate and areas lacking adequate municipal services and housing. Chagas disease has already been described in this area, and we hypothesized that other NTDs would be co-localized in this population. We conducted a cross-sectional investigation of 10 NTDs in a population of adults (n=616) and children (n=269) living in Starr County, Texas using stool real-time polymerase chain reaction (*Blastocystis* spp, *Giardia intestinalis*, *Cryptosporidium*, *Entamoeba histolytica, Strongyloides stercoralis, Ascaris lumbricoides, Trichuris trichiura, Ancylostoma duodenale*, and *Necator americanus*) and serological testing (*S. stercoralis* and *Taenia solium*). We conducted risk factor analyses using self-reported survey data and neighborhood-level variables. We found 13.37% (48/359) *Blastocystis* positivity, 0.84% (3/359) *Giardia* positivity, and 0.28% (1/359) *Strongyloides* positivity on stool testing in the adult cohort and 6.7% (18/269) *Blastocystis* positivity and 0.9% (2/227) *Giardia* positivity in the pediatric cohort. On serological testing for strongyloidiasis, we found a 3.3% (20/606) and a 1.7% (3/176) seropositivity in the adult and pediatric cohorts, respectively. Finally, we found an overall seropositivity to *T. solium* of 7.4% (45/605) in the adult cohort. We identified unique risk factors for soil transmitted helminth infection, strongyloidiasis, and cysticercosis. Although the clinical significance of *Blastocystis* positivity may be unknown, the presence of this and other NTDs in this population shows the need for more robust epidemiological investigations in south Texas.

A Rare Fatal Case of West Nile Virus Reactivation in a Pediatric Patient with Acute Myeloid Leukemia, 2023

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West Nile virus (WNV) is an endemic arbovirus transmitted by *Culex* species mosquitoes which clinically presents in humans as either neuroinvasive or non-neuroinvasive (febrile) disease. Most infected humans are asymptomatic but about one percent have neuroinvasive disease; this disproportionately affects individuals who are immunocompromised or those with significant co-morbidities.

In October 2022, the Texas Department of State Health Services (DSHS) received positive WNV lab results (PCR and serology) on a 14-year-old male. Follow-up by the local health department (LHD) revealed the patient received several blood product transfusions due to acute myeloid leukemia. The onset of neuroinvasive disease symptoms occurred multiple days after hospital admission for leukemia treatment; the patient was immunocompromised due to this treatment. The case was extensively investigated via multi-agency collaboration (Centers for Disease Control and Prevention [CDC], DSHS, and the LHD) to determine if the source of the WNV infection was due to recent and/or previous blood product transfusions. Tracebacks of blood products were inconclusive, and transmission mode of the WNV was deemed indeterminate.

In April 2023, DSHS received positive WNV PCR, WNV IgM and IgG commercial lab results on this same patient. The patient had experienced a new acute onset of neurologic symptoms consistent with WNV. Due to additional blood and bone marrow transfusions to treat the leukemia, both bloodborne and vector-borne exposures were considered once again. The blood transfusion traceback findings were unremarkable and the bone marrow donor was thoroughly tested for WNV infection prior to transplant. Unfortunately, the patient would later die almost two months after onset.

Additionally, determination of the possibility of WNV reinfection versus WNV reactivation from the previous infection was necessary. After all possible avenues of transmission were investigated, CDC and DSHS agreed there was not sufficient evidence to report the patient as a West Nile virus reinfection case. WNV reactivation is rarely reported in the literature but in severely immunocompromised patients such as this individual, the possibility of incomplete viral clearance and/or latency in the tissue can pose a risk of reactivation. More exploration on this topic is necessary as it may be more common than previously reported and represents an opportunity for public health intervention and education.

Building Networks with Wildlife Rehabilitation Facilities: SARS-CoV-2 Surveillance and Assessment of Biosecurity Practices

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Human-animal interactions at wildlife rehabilitation facilities, where ill or injured wildlife are temporarily housed in human care, are understudied and varied. It is well understood that animals infected with SARS-CoV-2 can infect other animals and humans in close contact. However, questions remain, regarding which wildlife species might be susceptible to SARS-CoV-2 infection and the best biosecurity practices at wildlife rehabilitation facilities to mitigate risk of disease transfer. In collaboration with USDA-APHIS and the University of Florida-Emerging Pathogens Institute (UF-EPI), we have built a network of more than 65 wildlife rehabilitation centers across 30 states to investigate species susceptibility, biosecurity practices, and epidemiologic risk factors.

Enrolled wildlife rehabilitation facilities are provided with project protocols and supplies to collect respiratory swabs, rectal or fecal swabs, and blood samples from arboreal, terrestrial, or aquatic mammals native to North America. Necessary permissions and permits are requested by UF-EPI from respective state entities. Samples are submitted to the TGen North laboratory and screened by RT-qPCR (viral detection) and viral neutralization assays (antibody detection). We are also assessing biosecurity policies and the use of the hierarchy of controls at wildlife rehabilitation facilities to identify best practices for disease prevention at this human-wildlife interface.

Since 2023, over 3,300 samples from 62 species including squirrels, rabbits, bats, raccoons, white-tailed deer, and opossums have been screened for SARS-CoV-2. These include >2400 swab samples and >950 blood samples. Virus was detected by RT-PCR in one eastern gray squirrel, and antibodies against SARS-CoV-2 were detected in 10 white-tailed deer fawns, a bobcat, and a beaver. This work sheds light on species susceptibility and demonstrates the importance of establishing One Health collaborative networks with the wildlife community.

Thursday, May 22, 2025

8:00-9:30 Session V: H5N1 Influenza Virus I

Moderator: Cherissa Abdul Hamid, DVM, MPH
Texas Department of State Health Services, Lubbock, TX

Source: Personal photo provided by Dr. Susan Rollo.

Highly Pathogenic Avian Influenza and Wildlife

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Highly pathogenic avian influenza (HPAI) is a zoonotic Alphainfluenzavirus that infects birds and mammals including humans. While HPAI historically has been a concern for domestic poultry, the recently circulating HPAI A(H5N1) clade 2.3.4.4b strain has established itself in wild bird populations since its introduction to the United States in early 2022. While both low pathogenic AI and highly pathogenic AI have been found in wild bird populations with minimal disruption, HPAI A(H5N1) 2.3.4.4b, hereafter referred to as H5N1, has been implicated in over 10,000 wild bird deaths since January 2022. Additionally, in two unprecedented moves, H5N1infections have been found in both terrestrial and marine wild mammals but also domestic dairy cattle with disease ranging from mild illness to death in mammals. The detection of H5N1 in wild mammals and dairy cattle serves as a reminder of HPAI's ability to spillover into new species and its potential to shift to a more virulent or transmissible disease in people. This presentation will discuss and compare the 2014 HPAI H5N2 and current HPAI H5N1 outbreaks in wildlife along with data from Texas regarding current detections in wildlife, the wildlife-dairy interface, plus surveillance and mitigation efforts by the Texas Parks and Wildlife Department.

Navigating Academic-Industry-Public Health Partnerships for Emerging Infectious Disease Events, such as H5N1, in the US

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Public health preparedness and response activities during emerging infectious disease events often require stakeholder engagement across various sectors of the community. The ongoing avian influenza virus (AIV) outbreaks in production animals and their farm workers presents unique challenges and underscores a need for collaboration, partnership, and intentional crosstalk for successful assessment and mitigation efforts. The current situation is not only a public health challenge. It is also an occupational health challenge that introduces a key stakeholder in its management. Producer owners and organizations play an essential role in protecting not only animals and their products so heavily depended on in the US, but also their workers, and thus should be engaged in discussions of realistic, feasible, and effective solutions. On the human public health side, affected populations are vulnerable and often lack access to testing, treatment, and other health resources. Protection in high-risk settings is imperative – yet there are cultural, linguistic, and social sensitivities to consider in these populations, and thoughtfulness about their general understanding of infectious diseases they may be exposed to, awareness about outbreaks, understanding factors that could protect them or leave them at risk, and hesitations to interact with health services, particularly public health agencies. Measures to protect workers and other high-risk populations, their families, production animals, production operations, and, ultimately, public health necessitate intentional crosstalk and thoughtful engagement. Academics can sometimes aid in bridging stakeholders but must operate with consideration to clinical, veterinary, and public health activities to identify and make progress toward common goals. They can also help bring awareness and insight to the scientific community, facilitate epidemiologic awareness, contribute unique expertise and perspective, and support initiatives and activities by veterinary & human public health. A team at the Texas A&M School of Public Health will share their perspectives, challenges, and successes from their ongoing investigation into AIV A(H5N1) among dairy farm workers in the US and share their vision for a national response network to future zoonotic disease events.

Public Health Response to Highly Pathogenic Avian Influenza A (H5N1) Virus Detection at a Zoological Park in Maricopa County, Arizona, November 2024

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Maricopa County Department of Public Health (MCDPH), Arizona Department of Health Services, and Arizona Department of Agriculture employ a One Health approach to monitor zoonotic diseases in Arizona. On December 6th, 2024, highly pathogenic avian influenza A(H5N1) virus was detected in two animals at a Maricopa County zoological park.

MCDPH obtained a list of all potentially exposed individuals (PEI) who had been on-site since November 21st. A risk assessment survey was distributed electronically to PEI; appropriate guidance was sent based on self-assessed risk level. Those with direct, close contact with infected/ill animals or environment without appropriate PPE were high-risk, enrolled in an automated daily symptom monitoring system, and advised for post-exposure prophylaxis (PEP). MCDPH staffed on-site PEP distribution and followed up with symptomatic high-risk PEI. Low-risk were those without a high-risk exposure; they were advised to self-monitor for symptoms. MCDPH collaborated with One Health partners to provide mitigation advisement. The risk to the general population was assessed as low; a joint media release notified the public.

MCDPH received a list of 201 PEI; 70% were staff, 30% were volunteers. Response rate for the risk assessment was 62%. Of 125 respondents, nineteen (15%) assessed themselves as high-risk, 104 (83%) as low-risk, and two (2%) as no-risk. Age was known for 114 PEI; the median age was 28 years (Q1–Q3: 22–50.5). When sex at birth was reported (n=117), most were female (68%). PEP was distributed to 32 PEI. MCDPH investigated 37 symptomatic PEI; none resulted in an influenza A(H5N1) diagnosis. The zoo modified interactive exhibits and implemented enhanced biosecurity.

We report influenza A(H5N1) detections at a zoo in Maricopa County. Response activities included mitigation guidance, symptom monitoring, and providing PEP. No human influenza A(H5N1) cases were identified. Pre-existing One Health partnerships and plans were essential to mount a coordinated response.

Thursday, May 22, 2025

10:00-11:30 Session VI: H5N1 Influenza Virus II

Moderator: Annajane (Aj) Marlar, DVM, MRCVS, DACVO
Texas Department of State Health Services, Arlington, TX

Source: www.aphis.usda.gov/livestock-poultry-disease/avian/avian-influenza/hpai-livestock/testing

Shedding of Influenza A Virus in Dairy Cattle

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Detection of Influenza A virus (IAV) H5N1 was made in dairy cattle in March 2024. The pathogenesis and shedding of the virus in different excretions of this novel host are not well understood, although early studies detected the virus in milk at high levels and in nasal excretions and urine at low levels.

Seven H5N1 affected dairy herds in CO and CA agreed to participate in serial sampling of cattle over a 10-week period. Nasal swabs, serum, and urine were collected once weekly, while milk samples were collected twice weekly. Multiple classes of cattle were sampled including replacement heifers and cows that were clinical, nonclinical, had recently calved, and were nonlactating. Samples were tested by Rt-PCR IAV at NAHLN laboratories, and IAV detections were classified as shedding events.

A total of 517 cattle were tested. The percentage of cattle shedding varied by sample type and cattle class, with some shedding via more than one route. A majority of clinically affected cows (52%) had PCR detection in at least one excretion; 96% shed in milk, 10% in urine, 8% in serum, and 3% in nasal excretions. Milk shedding was inconsistent and intermittent, with some cows shedding for more than 80 days. A minority of nonclinical cows (23%) had PCR detection: 80% shed in milk, 15% in urine, 15% in serum, and 10% in nasal excretions. Virus was detected in nasal excretions of 11% of replacement heifers. Less than 5% of nonlactating and recently calved cows had virus detected in collected samples. Understanding viral excretion routes and duration provides additional information critical to controlling disease spread.

Occupational Task Exposures Associated with Seropositivity of Highly Pathogenic Avian Influenza A (H5N1)

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U.S. agricultural operations are a vital economic contribution and source of food security. A threat to the future of agriculture, including the health, safety, and well-being of dairy farm workers, is a threat to national security. Dairy farm workers in the U.S. are predominantly immigrant, Hispanic males, of approximately 30 to 35 years of age with limited English proficiency, formal education, and living under the poverty level. Identifying occupational exposures, tasks, and sources of infectious diseases transmission is essential for interim control measures to protect workers and safeguard minimal disruption to production. We initiated a cross-sectional study among dairy farm workers in the US to estimate the cumulative incidence of exposure to Influenza A(H5N1) and to seek clarity on modifiable risk factors. We paired serologic and molecular testing with an interviewer-administered questionnaire, adapted and condensed from the CDC's Highly Pathogenic Avian Influenza A (H5N1) Exposure Questionnaire. Participants were asked about sociodemographic, occupational exposure measures (proximity, duration, frequency) to sick cattle, animal contact, use of personal protective equipment (PPE), and recent avian influenza outbreak awareness. Nasopharyngeal and conjunctival swabs were collected for molecular detection of Influenza A, and serum was obtained for antibody detection via hemagglutination inhibition (HI) to characterize prior exposure. Swab specimens testing positive for Influenza A on PCR were submitted for sequencing, and seropositive samples were submitted for testing by microneutralization assay. Serologic and molecular evidence from this vulnerable population indicate that robust active surveillance and continued monitoring of exposure and risk estimation are essential to public health awareness and epidemiologic intelligence, with respect to avian influenza. Findings from the investigation will further inform prevention, detection, and opportunities for health and occupational interventions for avian influenza as well as other zoonoses. In this presentation, we will share data available from our ongoing investigation in this dynamic epidemic landscape.

Dairy H5N1: Insights from an Early Detection Study of Dairy Herds in California

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Highly pathogenic avian influenza virus H5N1 (H5N1) infection causes non-pathognomonic clinical signs in dairy cattle: nasal discharge, lethargy, fever, a drop in rumination and milk production, and mastitis. Despite being a year since the first dairy cases, we do not understand how H5N1 is transmitted within herds. To better understand movement of this virus in cows, we conducted early surveillance of non-affected dairy herds (n = 19) in California using daily bulk tank milk (BTM) testing for H5N1 via Rt-PCR for Influenza A Virus. Once detected in the BTM of surveilled herds, sampling of pen-level daily milk (n = 5 herds) was initiated, and environment and air samples were collected (n = 7 herds) from locations on each farm. Detection of H5N1 in BTM samples occurred 4-9 days prior to the detection of clinical signs in cows of each herd, and the duration of H5N1 BTM detection varied by herd but continued for a minimum of one month. Pen-level sampling showed viral detection in the milk from all pens of cattle within one week of clinical signs. Environment and air samples were classified into 7 categories based on farm location collected. H5N1 was detected from milking equipment, parlor surfaces and flush water, with the highest proportion of detections from milking equipment. There were no H5N1 detections in samples taken from housing areas, feeders, waterers, non-milking equipment and office surfaces. On a single farm, H5N1was detected using two separate aerosol collection devices from four sampling locations, collected on a single day. Other airborne sampling strategies on farms were unable to detect H5N1 from aerosols. Our results show that H5N1 is present on farms before the identification of sick cattle, with the virus spreading quickly to all pens. Taken together, environmental detection and pen spread suggests that within-herd transmission of H5N1 likely occurs via multiple routes.

Thursday, May 22, 2025

1:00-2:30 Session VII: Arboviral Diseases

Moderator: David Smonko, DVM
Texas Department of State Health Services, Temple, TX

Source: www.cdc.gov/oropouche/outbreaks/2024/index.html

Developing a Cross-Protective Flavivirus mRNA Vaccine

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Flaviviruses including Zika (ZIKV), dengue, and West Nile are arthropod-borne viruses that cause >400 million infections annually, leading to significant morbidities such as birth defects and neurological deficits. Outbreaks occur seasonally and climate change is increasing vector distribution, disease spread, and outbreak potential. While vaccines against individual flaviviruses are in development, most are not approved for use. As prior studies indicated that ZIKV envelope (E) protein may provide cross-protection against related flaviviruses, this study aims to develop a pan-flavivirus mRNA vaccine targeting the highly conserved flavivirus E protein and assess initial immunogenicity in mice. Three mRNA candidate vaccines expressing ZIKV E protein and different signal sequences were formulated in lipid nanoparticles as individual singlevalent E constructs, or a multivalent vaccine with all three. C57BL/6 mice (n=6) received prime and boost immunizations of singlevalent, multivalent, or eGFP control vaccine 21 days apart, and sera was collected prior to each immunization. Sera and spleens were harvested 21 days after final immunizations and tested for neutralizing antibodies and T cell responses by plaque reduction neutralization tests (PRNTs) and flow cytometry, respectively. Cross-protection was evaluated against multiple flaviviruses by PRNTs for neutralizing antibodies in vitro. We have successfully generated ZIKV E mRNA constructs, confirmed their expression in vitro by immunofluorescence and western blotting, and completed mouse immunization regimens. As these studies are ongoing, we anticipate that the ZIKV E mRNA multivalent vaccine will be the most immunogenic by inducing high levels of CD8 T cells and effective neutralizing antibodies against related flaviviruses. If successful, this study highlights the potential for an effective cross-protective flavivirus mRNA vaccine. Future studies will assess protection against acute flavivirus infection and identify correlates of protection. The long-term goal of this work to generate an effective, safe, and broadly protective flavivirus vaccine that can be readily adaptable for outbreak mitigation.

Arbovirus-Associated Hospitalizations in Texas, 2008-2023

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Arboviruses are a significant threat to global public health, including in Texas. Over the past two decades, the incidence of infection has increased, driven by climate change and the expansion of suitable habitats for the main mosquito vectors *Aedes ageptyi* and *Culex quinquefasciatus*. Despite this global trend, the picture in Texas is less clear, and there is poor understanding of the potential impacts on local healthcare systems, communities, and individuals despite increasing infection rates suggested at the national level. To shed light on trends in severe arboviral disease, Hospitalization data from the Texas Department of State Health Services (DSHS) Public Usage Data Files (PUDF) from 2008 to 2023 were analyzed to identify epidemiological trends, demographic patterns, and regional variations in arbovirus cases requiring hospitalization. A retrospective cross-sectional analysis was conducted over 48 million hospital records, describing cases by age, sex, race-ethnicity, illness severity, geographic region (DSHS Public Health Regions), and examined whether cases presented classic arboviral symptoms. During the 15-year period under study, 4,387 hospital records referenced arboviral infections, including West Nile Virus (WNV), Dengue, Chikungunya, Yellow Fever, Zika, St Louis Encephalitis (STLE) and several equine encephalitis viruses (Western, Eastern, and Venezuelan), WNV accounted for the highest proportion (83.06%) of arbovirus hospitalizations, followed by Dengue (10.87%) and Zika (2.89%). Dengue (2.13) and Chikungunya (0.24) have statistically significant increases in cases throughout the time period (alpha < 0.05). Most hospitalized patients were aged 55–69 years (93.33%) or identified as non-Hispanic white (53.07%). The severity of the illness varied by virus, with WNV and STLE accounting for most severe infections with increased severity as age of hospitalization increased. These findings emphasize the growing impact of arboviral diseases in Texas, stressing the importance of improved clinical recognition of these important infections and public health strategies for surveillance, prevention, and vector control efforts to reduce and respond to outbreaks and to safeguard vulnerable populations.

A Curious Case of West Nile Virus: Donor-derived or Vector-borne?

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At the end of August, I received a phone call from a local hospital reporting a case of neuroinvasive West Nile Virus in a woman in her 50’s. Upon review of her medical record two things immediately stood out to me: 1) She had a kidney transplant only 3 weeks before her symptom onset, and 2) her address. Her home was located in close vicinity to a West Nile Virus positive mosquito pool that our local Mosquito Control Department had notified us of that same week. I notified my regional office of the situation, and they encouraged me to obtain samples from the organ donor and have them sent to DSHS so that we could rule out donor-derived transmission. This turned out to be quite the ordeal, but eventually I made contact with the organ donation organization. They sent me a copy of the donors negative West Nile Virus PCR screening with samples taken at the time of organ harvest and then also had their lab send the archived donor samples to DSHS who forwarded them to the CDC. While awaiting results, I was able to interview the cases daughter who confirmed that the case had no recent travel, didn’t spend much time outdoors, and kept her windows closed due to the heat but did also have appropriate window screens. She indicated that the case mostly was only outside to walk to and from the car. A few weeks later the lab report came in from the CDC. The organ donor was West Nile Virus PCR negative but also West Nile Virus IgM positive. The question remains: was this donor derived or vector borne transmission? Or, does this simply highlight the prevalence of West Nile Virus?

Thursday, May 22, 2025

Scientific Poster Session

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Thursday, May 23, 2025

4:00 – 6:30 J.V. Irons Keynote Lecture & Reception

Moderator: Bonny Mayes, MA, E-RYT 200
Texas Department of State Health Services, Austin, TX

The J.V Irons Keynote Lecture is named in honor of J.V. Irons, Sc.D., whose career with the Texas State Department of Health (now known as the Texas Department of State Health Services) spanned 41 years. Dr. Irons, who received his degree from the University of Indiana, served as Director of the Bureau of Laboratories for the last 25 years of his distinguished career. His leadership influenced and molded the laboratories' services more than that of any other individual.

Dr. Irons authored or co-authored more than 90 scientific or professional publications and contributed to 5 reference texts on microbiology and public health. He was an active member of many professional public health and scientific organizations, including the Pan American Sanitary Bureau in Lima, Peru, where he served as a temporary advisor. Dr. Irons received a citation from the Peruvian Department of Health for his contributions to that country's smallpox eradication program. He improved smallpox diagnosis in Peru by enhancing fertile egg membrane culture techniques.

Indiana State University presented Dr. Irons with the Distinguished Alumni Service Award in 1963 and he received the George Caldwell Award in Pathology from the Texas Society of Pathologists in 1968. In 1973, the keynote address of the Southwest Conference of Diseases in Nature Transmissible to Man (now known as the James Steele Conference on Diseases in Nature Transmissible to Humans) was named in his honor.

Thursday, May 22, 2025
4:00-5:00 pm
J.V. Irons Keynote Lecture

Steffanie Strathdee, PhD

Dr. Steffanie A. Strathdee is the Harold Simon Distinguished Professor in the Department of Medicine at the University of California San Diego School of Medicine. She co-directs UCSD's center for Innovative Phage Applications and Therapeutics (IPATH) which was the first center of its kind in North America. An infectious disease epidemiologist, she has spent the last two decades focusing on prevention of infectious diseases in marginalized populations. In 2019, she co-authored a memoir, *The Perfect Predator: A Scientist's Race to Save Her Husband from a Deadly Superbug*, that relays IPATH's first experience with phage therapy. In 2018, TIME magazine named her as one of 50 most influential people in health care for her work to revitalize phage therapy in the West.

From Bog to Bedside: How Phage Therapy is Being Revitalized to Treat Multi-Drug Resistant Bacterial Infections

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Friday, May 23, 2025

8:30-10:00 Session VIII: Bacterial Zoonoses

Moderator: Brendan Sullivan, DVM, MPH
Texas Department of State Health Services, Houston, TX

Source: www.aphis.usda.gov/operational-wildlife-activities/feral-swine/distribution

Brucellosis in the Lone Star State: Insights into Hospital-Associated Cases, 2006–2021

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Brucellosis is a substantial global public health concern, with over 500,000 human cases documented each year. In the US, human brucellosis is a relatively rare disease, with ~100 to 200 cases reported per year. Despite the sporadic nature of disease reports locally, some things remain unclear about its epidemiology in Texas. Texas's expansive agricultural sector presents an opportunity for zoonotic transmission, and understanding the epidemiologic context in the state could inform local public health, clinical practices, and education opportunities. Complementary to case reports, hospitalization records can be a source for valuable insight into the epidemiology of severe disease and serve as a surrogate for local epidemiologic dynamics. To this end, this study aimed to describe brucellosis-associated hospitalizations in Texas from 2006 to 2021, leveraging data from the Texas Inpatient Public Use Data File. During the 15-year study period, a total of 599 hospitalizations associated with *Brucella* infection were identified: 55.6% male, 50.3% Hispanic, and 55.6% ≥45 years of age. Notably, patients bear substantial clinical disease; half of patients had major (34.7%) or extreme (15.9%) disease severity, and many were classified as at major (23.0%) or extreme (9.7%) risk of mortality; hospital stays exceeded 5 days in 63.6% of these hospitalizations. Most severe illness occurred in the ≥45 age group, and only 1.7% of cases expired. Still, 14.5% of hospitalizations were children <15 years. ArcGIS Pro's optimal hotspot analysis identified a cluster of counties in Central Texas as significant hotspots with ≥90% confidence, where public health and clinical awareness campaigns may be helpful. Continued surveillance and analysis to further pinpoint risk factors for infection and severe disease will inform prevention and management strategies.

Fort Bend County Response to Low-risk Occupational Exposure to *Burkholderia pseudomallei* Bacteria

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Occupational exposures to melioidosis can occur in hospital laboratory environments when proper infection control and biohazard protocols are not followed. Melioidosis is caused by the bacterium *Burkholderia pseudomallei*, which spreads to humans and animals through direct contact. The infection can be contracted by inhaling contaminated dust or water droplets, as well as through contact with contaminated soil or water, particularly via skin breaks such as cuts or scrapes. Cases may increase following hurricanes, heavy rainfall, and other severe weather events, as the bacteria rise to the surface of the soil.

Fort Bend County received a report regarding occupational exposure at a hospital laboratory. The incident occurred when a laboratorian accidentally opened an agar plate outside of a biological safety cabinet to check for any bacterial growth from a patient blood sample which is considered low-risk exposure. After the incident, the exposed staff was notified that the sample tested positive for *B. pseudomallei*.

FBC, Texas DSHS, and CDC immediately started an inter-agency response and recommended serological monitoring. Blood samples were collected from the exposed individual on weeks four and six from the date of exposure and sent to the CDC for testing. An ELISA (enzyme-linked immunosorbent assay) based test was performed to detect antibodies against *B. pseudomallei* in the blood. Both tests resulted negative. In addition, post-exposure monitoring (PEM) was conducted for symptom identification and was logged in using a risk assessment form. Self-monitoring of temperature was recorded twice daily for 21 days after exposure. Identification, management, preventive measures, and timely response are crucial to minimizing the risk of occupational exposure, preventing infection, and ensuring the safety of laboratory personnel.

Sporadic Tularemia Occurrence in Tennessee, 2014—2024: Illness Characteristics, Reported Exposures, and Investigation Timeliness

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Francisella tularensis transmission to humans occurs sporadically through tick bites or contact with infected animals. Tularemia has differing clinical syndromes and is considered a bioterrorism concern due to aerosolization capability. We describe the clinical presentation of sporadic tularemia, reported exposures, and timeliness of investigation in Tennessee.

Tularemia cases during 2014–2024 were reviewed. Based on nationally notifiable case definitions, cases were classified as probable if serologic, molecular, or pathologic testing detected *F. tularensis* or confirmed if *F. tularensis* was cultured. In Tennessee, case investigations ascertain clinical presentation, healthcare encounters, and exposures (e.g., animal contact, occupation) for persons testing positive for tularemia. We describe illness characteristics and exposure information.

Thirty-nine tularemia cases were reported; 37 were probable and 2 were culture-confirmed. From illness onset, testing occurred after a median of 14 days (IQR=6–30), and public health investigation after a median of 24 days (IQR=15.5–46). Clinical information was available for 19 cases (49%), including 9 hospitalizations and 1 death. Reported symptoms included: fever, sweats, or chills (n=16), lethargy or fatigue (n=7), cough or shortness of breath (n=5), and sore throat (n=3). Clinical signs documented included peripheral lymphadenopathy (n=7), conjunctivitis (n=4), skin lesions (n=2), and tonsillitis or pharyngitis (n=1). "Syndrome" was specified for 12 (31%) cases and included pneumonic (n=3), typhoidal (n=3), glandular (n=3), ulceroglandular (n=1), oculoglandular/oropharyngeal (n=1), and intestinal (n=1). Reported risk factors among 17 (47%) cases included landscaping (n=5), tick bite (n=5), and contact with domestic dogs (n=5) or other animals (n=4). All cases appeared sporadic with no temporal or spatial clustering identified. The variety of clinical presentations for tularemia complicates diagnosis and timely reporting. Risk factors for tularemia were consistent with enzootic reservoirs and sporadic transmission to humans. To improve public health surveillance and bioterrorism response, we recommend increased timeliness of diagnosis, reporting, and assessment of risk factors.

Friday, May 23, 2025

10:30-12:30 Session IX: Viral Zoonoses

Moderator: Jeffrey Musser, DVM, PhD
Texas A&M University (Retired Professor), College Station, TX

Source: Digital poster submission for the Zoonosis Control Branch 2025 Rabies Awareness & Prevention Poster Contest.

From Sample to Result: The DoD FADL's Approach to Rabies Testing - Challenges, Solutions, and Best Practices

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The Department of Defense Food (DoD) Analysis and Diagnostic Laboratory (FADL) has a rich 80-year history of providing trusted expertise and technical knowledge to support critical missions. It comprises six sections: Cholinesterase Reference Laboratory, Chemistry, Microbiology, Diagnostic, Field Technical Services, and Quality Assurance. The Diagnostic Section is equipped to test for multiple vector-borne and zoonotic agents (e.g., Equine Infectious Anemia virus, *Borrelia burgdorferi*, *Trypanosoma cruzi*, *Leishmania infantum*, and Rabies virus). The Rabies Fluorescent Antibody Virus Neutralization (FAVN) test is the most requested test. Our FAVN results are used to validate vaccine efficacy against rabies for Military Working Dogs (MWDs) and Privately Owned Animals (POAs). The Section also performs Direct Fluorescent Antibody Testing (DFA) on postmortem animal brain tissue. This presentation highlights technical and operational support for FAVN and DFA testing. We also describe technical approaches, quality control, and operational workflow to maintain high sample capacity and customer satisfaction. From 2024 through January 2025, the Diagnostic laboratory analyzed over 10,000 FAVN serological samples and over 70 DFA brain tissue samples. We also trained over 40 Veterinary Corps Officers and staff globally, decreasing error rate and increasing productivity for operation workflow. These results are achieved through exceptional quality control from sample processing to resulting. This requires continuous and meticulous efforts from all team members. The FADL Diagnostic Section provides high-quality technical support, analyzing thousands of samples and supporting (DoD). With its expertise and capabilities, the FADL Diagnostic Section is a vital asset, contributing to the safety and well-being of animals and personnel, and achieving significant milestones in 2024 and 2025. Recent focus on process improvement enables FADL to effectively respond to evolving infectious disease landscape.

Inter-Species Infection and Food Supply Risk Identification in the Setting of Suspected Cutaneous Anthrax, Secondary to Palmar Penetration by Bone and Inoculation with Contaminated Goat Meat in a Dallas County Food Handler

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Dallas County Health and Human Services (DCHHS) fielded a hospital report of a patient with a blackened, involuted palmar hand wound suspected to be cutaneous anthrax after a penetrating injury in a food handler/restaurateur preparing goat meat. The patient was prescribed Augmentin at an urgent care. Two weeks later with worsening symptoms, doxycycline was initiated, and the wound was cleansed prior to sampling. Initial cultures had no growth, but this did not rule out an anthrax diagnosis, given prior antibiotics.

DCHHS performed chart abstraction and interviewed the patient with a translator, before enlisting the assistance of an interdisciplinary team. After an inspection of the patient's workplace revealed multiple restaurants using this unlicensed supplier, an Epidemiologist joined Texas Meat Safety Assurance inspectors to perform an inspection of the farm responsible for the meat processing and distribution.

CDC testing detected orf virus, also known as Ecthyma contagiosm, a member of the genus Parapoxvirus. Primarily affecting sheep and goats, orf virus can infect humans, particularly those who work with animals and process meat. Investigation uncovered an unlicensed farm operating under grossly unsanitary conditions with multiple goats exhibiting sores consistent with orf virus. The coordinated team effort resulted in closure of the index case's workplace, destruction of contaminated meat, and a temporary cessation of farm operations for the unlicensed distributor.

Food handlers and distributors can operate illegally under conditions that endanger the community. Differential diagnoses for animal-borne illnesses, including orf, should consider the presentation of compatible skin lesions and epidemiological risk factors—including occupational exposure—to aid in identifying similar illness clusters. Increasing orf familiarity could prevent unnecessary testing and reduce antibiotic misuse. Coordination with regulatory authorities can prevent contaminated livestock from entering our food supply. Infection Preventionists and Epidemiologists should consider negative results situationally and examine details such as antibiotic timing around cultured specimens when reviewing reports.

Encephalomyocarditis Virus: A Rodent-Borne Zoonosis with Non-Human Primate and Public Health Implications

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Encephalomyocarditis virus (EMCV) is non-enveloped and icosahedral with a single-stranded RNA genome (Cardiovirus, Picornaviridae). This ubiquitous rodent-borne virus infects a broad range of mammalian species, including humans. Following fecal-oral transmission, the virus exhibits myocardial and neural tropism, inducing cell lysis and tissue inflammation in the acute and chronic phases of the disease. Due to rat and mice infestations, epizootic EMCV outbreaks have been reported worldwide in zoological, research, and animal production facilities. Serological surveys have shown human exposure results in robust neutralizing antibody responses. The few confirmed human infections have been non-lethal and self-limiting, causing generalized malaise and fever. However, a plausible disease correlation was reported serologically in pediatric patients exhibiting meningitis and encephalitis in the 1940s, although virus isolation was not performed. In vitro studies have unequivocally demonstrated EMCV replication in human myocardial cell lines and brain tissue, indicating potential public health risks. At the Southwest National Primate Center (SNPRC), EMCV outbreaks in captive-bred, outdoor-housed baboons have caused significant mortality between 1987-1990 and 2019, with the most common clinical presentation being dyspnea, acute heart failure, and sudden unexpected death. Myocarditis was a histopathologic hallmark of baboons infected with EMCV. The epidemiology underlying the 20-year gap between epizootic events at SNPRC remains undetermined, providing an opportunity to study rodent-to-non-human primate transmission cycles in Texas. EMCV is an understudied zoonosis for which non-human primates are an ideal model for studying disease pathogenesis and countermeasure development.

Evaluating Preventative Measures for the Zoonotic Transmission of Swine Influenza A Variant at Agricultural Fairs in the United States: A Mathematical Modeling Study

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Agricultural fairs provide a unique interface between humans and swine. Utilizing epidemiological data from a 2011 H3N2 zoonotic influenza outbreak at a Pennsylvania agricultural county fair, we developed a mathematical model to estimate the risk of zoonotic transmissibility to exhibitors and attendees. Several data-driven scenarios of the swine-to-swine transmission and the number of infected pigs at the start of the exhibition. Additionally, we used our model to estimate the impact of control strategies to mitigate the risk of influenza A variant transmission from pigs to humans. We simulated preventative measures recommended by the Swine Exhibitions Zoonotic Influenza Working Group. Preventative measures simulated included shortening exhibition duration, improved biosecurity, pre-fair pig testing, and quarantining sick animals. Our model estimates the probability of swine-to-human H3N2v transmission per minute of swine contact, indicating significant variations in transmission risk between exhibitors and attendees, influenced by disease transmission among pigs. The effectiveness of control strategies was shown to vary substantially with the preventative measures. Fewer outbreaks of the virus were observed in the model when implementing pre-fair testing due to fewer pigs arriving at the fair infected. This approach generated the lowest prevalence of the disease in swine and humans. Shortening the exhibition to three days and enhancing biosecurity significantly reduced the risk and size of swine influenza outbreaks among pigs and humans during county fairs. However, quarantining sick pigs did not significantly reduce infection prevalence due to the majority of pigs experiencing asymptomatic infections. While individual fair attendees face a low infection risk per contact relative to exhibitors, the large annual attendee population increases the likelihood of zoonotic events and the emergence of potential pandemic influenza variants. Shortening the exhibition duration together with enhanced biosecurity measures emerges as the most effective method for preventing zoonotic transmission without requiring additional resources such as test kits.

POSTER

First Documented Detection of *Trypanosoma cruzi* in *Paratriatoma hirsute*

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We present the first documented detection of *Trypanosoma cruzi* in wild-caught *Paratriatoma hirsuta* collected on military installations in Imperial County, California and Yuma County, Arizona. We collected 20 adults and 63 nymphs from 15 wood rat nests as part of a broader Chagas disease surveillance effort. Initial *T. cruzi* PCR screen analysis identified six presumptive positive *T. cruzi* samples. These were re-analyzed using a novel kinetoplast PCR/Sanger sequencing assay based on published validated targets. Traditional PCR amplicon was submitted to an external laboratory for sequencing. Analysis of Sanger sequence data for a unique 20 base pair region confirmed *T. cruzi* identification in each *P. hirsuta* sample. This species has been experimentally infected with *T. cruzi* in the lab previously, but this is the first documented detection of natural *T. cruzi* infection in wild *P. hirsuta*. This finding informs Chagas disease surveillance and preventive measures in Sonoran and Mojave deserts where *P. hirsuta* may be serving as a secondary vector in sylvatic zoonotic disease cycles of *T. cruzi*.

POSTER

Innovating for a Safer Tomorrow: The DoD Food Analysis and Diagnostic Laboratory's Advances in Infectious Disease Testing and Diagnostics

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The Department of Defense (DoD) Food Analysis and Diagnostic Laboratory (FADL) protects U.S. Service Members and their Families through innovative, adaptive, timely and accurate testing of all food, water, and diagnostic submissions for DoD through a highly efficient and accredited institution now and in the future. The FADL contains four testing sections, including Cholinesterase Reference Laboratory, Chemistry, Microbiology, and Diagnostic. This presentation highlights the FADL Diagnostic Section's unique capabilities in both immunodiagnostic and molecular techniques and describes future directions as the Section supports military working dogs (MWDs), privately owned animals (POAs) and their owners, government and owned equids, government employees with potential occupational exposure to rabies (e.g., Veterinarians, Researchers, MWD handlers), public health and entomology departments. The Section contributes to animal and human health by testing animal, arthropod, human, environmental, and food samples for a variety of infectious agents. The Section performs testing for diseases of zoonotic and military significance in humans and animals. The most frequently performed test is the Rabies Fluorescent Antibody Virus Neutralization (FAVN) for MWDs and POAs of authorized DoD beneficiaries. The Section performs the Rapid Fluorescent Focus Inhibition Test (RFFIT) for rabies-vaccinated government personnel with occupational exposure to the rabies virus, ensuring adequate protection in high-risk environments. The Section also conducts the rabies Direct Fluorescent Antibody Test (DFA). The laboratory also maintains the MWD Serum Repository and supports DoD-approved research projects with these samples. Molecular efforts include vector-borne surveillance for various emerging infectious diseases, including Chagas Disease and Leishmaniasis. The Section is conducting targeted SARS-CoV-2 wastewater biosurveillance and analyzing the need to include other pathogens. The Section is committed to expanding and refining capabilities and collaborative, One Health contributions.

POSTER

Spatial Patterns of *Aedes* Mosquito Abundance in Harris County, Texas: Implications for Targeted Control Strategies

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Mosquito-borne diseases pose significant public health challenges, necessitating innovative approaches for effective management and control. This study examines spatial and temporal trends in the abundance and distribution of *Ae. aegypti* and *Ae. albopictus* using surveillance data from Harris County Public Health Mosquito and Vector Control from 2021 to 2022. We observed that *Ae. aegypti* populations peak in urban centers during the summer months, while *Ae. albopictus* exhibits a more consistent year-round abundance with less distinct spatial patterns. By integrating mosquito surveillance data with spatial analyses of built environment factors—including land use, land cover, census demographics, and municipal data—we identified non-random patterns shaping mosquito distribution. Our findings reveal a strong association between *Ae. aegypti* abundance, older housing, and the proportion of residents living below the federal poverty line. In contrast, *Ae. albopictus* was linked to socioeconomic disparities but not housing age. These insights enhance predictive modeling for medically important mosquito populations, providing critical guidance for targeted prevention and control efforts in Harris County communities most vulnerable to mosquito-borne disease.

POSTER

Statewide Tick Surveillance through Community Engagement and Citizen Science

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Tick-borne diseases are both a persistent and growing public health concern worldwide. The geographic range of established tick species has broadened, and new invasive tick species have emerged over the past decade. To better understand the epidemiology and risks of tick-borne diseases in Texas, we have established a state-wide citizen science-based tick surveillance and testing program. This initiative uses advanced molecular epidemiology techniques to analyze submitted ticks from across the state. This study functions as a community resource, offering free tick identification and pathogen testing for individuals and empowers residents to contribute valuable data, improving our understanding of tick distribution, risk factors, and the spread of tick-borne diseases. We have collaborated with 18 (36%; 18/50) of the Texas Wildlife Management Areas run by Texas Parks and Wildlife to obtain ticks collected from hunter-harvested animals. Additionally, we have solicited ticks from the public using a website and targeted social media advertisements. A total of 556 ticks have been submitted for analysis. These samples are comprised of 10 species submitted from 254 counties. Pathogen testing has identified 38% (215/556) of ticks as *Rickettsia* positive, 4% (24/556) as *Ehrlichia* positive, and no samples have tested positive for *Borrelia*. By implementing such a citizen-driven initiative, we can improve early detection, and public health responses, and mitigate the impact of these diseases across the state.

POSTER

Salmonellosis in Texas: Hospitalization Trends from 2008 to 2023

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Annually, 48 million people in the United States get ill due to foodborne illness. Out of these, 128,000 get hospitalized and 3,000 die. Non-typhoidal *Salmonella* is the leading cause of hospitalization (35%) and death (28%) resulting from foodborne illness. Salmonellosis is a reportable condition yet there are few descriptive epidemiological studies available that describe hospitalization trends associated with it in Texas. We aim to describe the annual hospitalization trend and interplay of sociodemographic factors in acquiring *Salmonella* in Texas over the period of 16 years (2008 to 2023). A descriptive study based on the hospitalized dataset; Public Use Data File provided by Texas Department of State Health Service was performed. Chi-square analysis followed by multinomial logistic regression was utilized to better understand the association between illness severity, mortality risk, and length of hospital stay with socio-demographic factors. We identified a total of 18,368 cases and noticed an increasing hospitalization trend of Salmonellosis over the period of 16 years with maximum incidence being 5.51 per 100,000 population in 2023. Hot spot analysis revealed diffuse distribution of cases around south-east, central and northern Texas. Salmonellosis was more common in the elderly population (65 years and above, 32.72%) with equal distribution in both sexes. It was more common in Non-Hispanic White (49.74%) followed by Hispanics and Non-Hispanic Black. The length of hospital stays in most cases was 5 or less days (66%) and the majority of them were admitted to an acute care unit (51.61%). Non-Hispanic Black (RRR=2.80, P= <0.001, 95% CI= 2.33, 3.77), and elderly population (RRR= 15.77, P= <0.001, 95%CI= 12.32, 20.19) were at increased risk to have severe illness. This study provides valuable insight into distribution patterns of hospitalization associated with salmonellosis in Texas.

POSTER

Investigating the Impact of Climate on the Propagation of Infectious Diseases in Hidalgo County

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The Texas Rio Grande Valley (RGV) is characterized by a subtropical climate, which, coupled with its seasonal precipitation, creates a conducive environment for both beneficial and detrimental biological activity. While the climate is favorable for agricultural productivity, it concurrently facilitates the proliferation of various infectious diseases. Recurrent seasonal events, such as cyclosporiasis and mosquito seasons, underscore the significant influence of climatic conditions on both human and animal health within the region.

This study aims to examine the correlation between climate variables and the incidence of infectious diseases in Hidalgo County. Weather datasets encompassing temperature, humidity, and precipitation metrics for the year 2022 were analyzed alongside infectious disease records to identify potential correlations.

A subset of this investigation focused on murine typhus, utilizing a dataset of reported cases to assess the relationship between weather patterns and disease symptom onset. In 2022, Hidalgo County reported a total of 80 murine typhus cases, with the highest incidence (16.25%) occurring in June. Analysis revealed that June was the hottest month of the year, with an average temperature of 87°F and an average humidity of 70%—conditions conducive to flea proliferation. This methodological framework, which contrasts weather conditions with the onset of disease symptoms, could be extended to a broader spectrum of zoonotic and other infectious diseases reported in Hidalgo County. Understanding these climate-disease interactions can inform the development of predictive models and intervention strategies, ultimately contributing to a reduction in the prevalence of infectious diseases within the region.

POSTER

A Cohort-Based Analysis of Flea-Borne Typhus: Correlating Risk Factors at the Census Tract Level in San Antonio

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Flea-borne typhus, caused by *Rickettsia typhi*, is a vector-borne infectious disease transmitted through fleas that infest rodents. Outbreaks are common in areas with poor sanitation, overcrowded housing, and limited healthcare access. This study investigates the relationship between socioeconomic, environmental, and health-related factors and the prevalence of flea-borne typhus at the neighborhood level in San Antonio, Texas. Using data aggregated at the census tract scale, key indicators such as poverty, housing density, educational attainment, urban crowding, urban heat effect, and sanitation infrastructure are analyzed. The Area Deprivation Index (ADI) and Social Vulnerability Index (SVI) are used to measure socioeconomic disadvantage. Additionally, American Community Survey (ACS) data on housing conditions, crime rates, and healthcare access are included to assess their role in disease transmission.

A cohort of 176 seropositive cases (IgM titer ≥ 1:256) from University Hospital is used to explore the association between these factors and the incidence of flea-borne typhus. Preliminary findings indicate that higher poverty levels, inadequate housing quality, and limited healthcare access are correlated with increased risk of flea-borne typhus in vulnerable neighborhoods.

This study highlights the importance of addressing socioeconomic and environmental factors—such as overcrowded housing and poor sanitation—in preventing flea-borne typhus outbreaks. The findings provide insights into how targeted public health interventions can mitigate health disparities and reduce the risk of disease transmission in at-risk communities.

Disclosure to the Learner

Requirement of Learner

Participants requesting continuing education (CE) credits/contact hours or a certificate of attendance for this conference need to complete registration; sign the sign-in sheets for sessions every day; attend sessions for which credit is sought (credit awarded commensurate with participation); complete, sign, and submit an Attendance Verification Form; and complete and submit the participant evaluation.

Before leaving the conference, submit the completed and signed Attendance Verification Form at the registration desk.

After the conference concludes, the evaluation will be accessible at the conference website (www.diseasesinnature.com) and must be completed and submitted by midnight Friday, May 30, 2025, to receive a certificate.

Please note: Veterinarians, Licensed Veterinary Technicians, and animal control officers will acquire their certificates when submitting their Attendance Verification Form before leaving the conference. All other professionals seeking CE or those just seeking a certificate of attendance will not receive a certificate until after a completed evaluation is received by 5-30-25 via the link provided on the conference website.

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This event received no commercial support.

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Registered Sanitarians:

The Texas Department of State Health Services Continuing Education Program is a sponsor of continuing education for Registered Sanitarians according to the Texas Administrative Code Rule §119.27 (d).
The Texas Department of State Health Services Continuing Education Program has designated a maximum of 16.00 contact hours for Registered Sanitarians.

Social Workers:

The Texas Department of State Health Services Continuing Education Program has designated a maximum of 16.00 contact hours for Social Workers.

Certificate of Attendance:

The Texas Department of State Health Services Continuing Education Program has designated a maximum of 16.00 hours for attendance.

Animal Control Officer (ACO):

A maximum of 16 continuing education hours are available for ACOs to use toward their Texas Health and Safety Code, Ch. 829, training requirements.

Veterinarians and Licensed Veterinary Technicians (LVTs):

The Texas Board of Veterinary Medical Examiners (TBVME) has approved a maximum of 16 CE hours in the clinical category for full attendance for veterinarians and for LVTs.

Conference Objectives

Upon completion of this activity, participants should be able to:

1. Session I – Parasitic and Fungal Zoonoses
describe the effects of *Trypanosoma cruzi* infection on heart rate variability and cardiac conduction in the dog; identify the cytokines that play a key role in *T. cruzi* neuroinflammation in an immunocompetent murine model; a**ssess** the clinical and pathological findings of coccidioides infections in captive non-human primates and evaluate their zoonotic and occupational health implications in endemic regions; and describe the contemporary epidemiology and ecology of *Leishmania mexicana* in Texas using a One Health perspective.

2. Session II – Flea-Borne (Murine) Typhus
distinguish acute acalculous cholecystitis as an uncommon clinical presentation of *Rickettsia typhi* infection; identify and describe the extent of critical illness from infection with murine typhus; and describe the demographic characteristics and clinical presentations of patients diagnosed with flea-borne typhus (FBT) in South Texas, including factors associated with disease severity and hospitalization duration.

3. Session III – Tick-Borne Disease
describe the signs and symptoms, discovery process, and current epidemiology of tick-borne relapsing fever (TBRF) and distinguish between signs and symptoms of TBRF and other tick-borne diseases; and identify clinical features, epidemiology, and risk factors associated with spotted fever group rickettsioses in South Texas, as well as evaluate prevention and management strategies tailored to the region.

4. Session IV – Surveillance
compare tick distribution among different habitats and environmental gradients in southeast Texas (Harris County, Texas); describe the prevalence and list risk factors for strongyloidiasis and other neglected tropical diseases in Starr Country, Texas; describe differences between West Nile virus neuroinvasive and non-neuroinvasive disease, plus West Nile virus reactivation in immunocompromised individuals; and identify the importance of collaborative networks with wildlife rehabilitation facilities to conduct SARS-CoV-2 surveillance in native US mammals.

5. Session V – H5N1 Influenza Virus I
compare and contrast previous strains of highly pathogenic avian influenza (HPAI) (i.e. H5N2) in wildlife against the current H5N1 strain; interpret cross-sector conversations and challenges among entities involved in public health events, unique challenges of assessing the human impact of avian influenza among livestock workers, and how an academic-industry-public health model can be utilized to address challenges, specifically with respect to health among agriculture workers during an outbreak of avian influenza; and describe public health response regarding potentially exposed individuals after a HPAI detection at a zoological park.

6. Session VI – H5N1 Influenza Virus II
compare H5N1 viral excretion routes in cattle and estimate duration of shedding via these routes; describe the methods used to identify occupational exposures, tasks, and sources of infectious disease transmission among dairy farm workers and evaluate the significance of serologic and molecular testing in estimating the cumulative incidence of exposure to Influenza A (H5N1), plus identify modifiable risk factors; and assess bulk tank milk surveillance data from farms affected with H5N1 and use this to distinguish where farms may be in their outbreak course.

Conference Objectives (continued)

7. Session VII – Arboviral Diseases
evaluate the safety profile of a pan-flavivirus mRNA vaccine and assess humoral and cellular immune responses associated with vaccination; analyze trends, demographic patterns, and regional variations in severe arboviral diseases in Texas using hospitalization data from 2008 to 2023, plus discuss improved clinical recognition, surveillance, prevention strategies, and vector control to protect vulnerable populations; and describe the key objectives and components of an arboviral case investigation.

8. JV Irons Keynote Session
compare and contrast the advantages and disadvantages of bacteriophage therapy versus antibiotics.

9. Session VIII – Bacterial Zoonoses
describe trends in brucellosis-associated hospitalizations in Texas from 2006 to 2021, identifying key demographic and geographic risk factors; apply the discussed guidance to assess and manage low-risk occupational exposure **to** *Burkholderia pseudomallei; and* identify symptoms, syndromes, and potential risk factors of tularemia**.**

10. Session IX – Viral Zoonoses
distinguish the Department of Defense Food Analysis and Diagnostic Laboratory's technical and operational processes required to produce accurate and reliable results for the rabies fluorescent antibody virus neutralization assay and direct fluorescent antibody; differentiate a suspect anthrax case versus an orf virus; distinguish transmission and host range of encephalomyocarditis virus (EMCV), recognize and interpret disease manifestation in non-human primates and humans, examine potential public health implications, and identify research gaps and potential use of non-human primates as animal models for EMCV; and appraise preventative measures for the zoonotic transmission of swine influenza at agricultural fairs in the United States using mathematical models.

Backup Presentation – A Cohort-Based Analysis of Flea-Borne Typhus: Correlating Risk Factors at the Census Tract Level in San Antonio, Texas (only presented if there is a cancellation in the scheduled agenda)
assess the relationship between socioeconomic, environmental, and health-related factors and the prevalence of flea-borne typhus at the neighborhood level in San Antonio.

Backup Presentation – Indigenous Leishmaniasis in Texas, 2007-2022 (only presented if there is a cancellation in the scheduled agenda)
describe clinical information of human leishmaniasis cases and the process of reporting to public health.