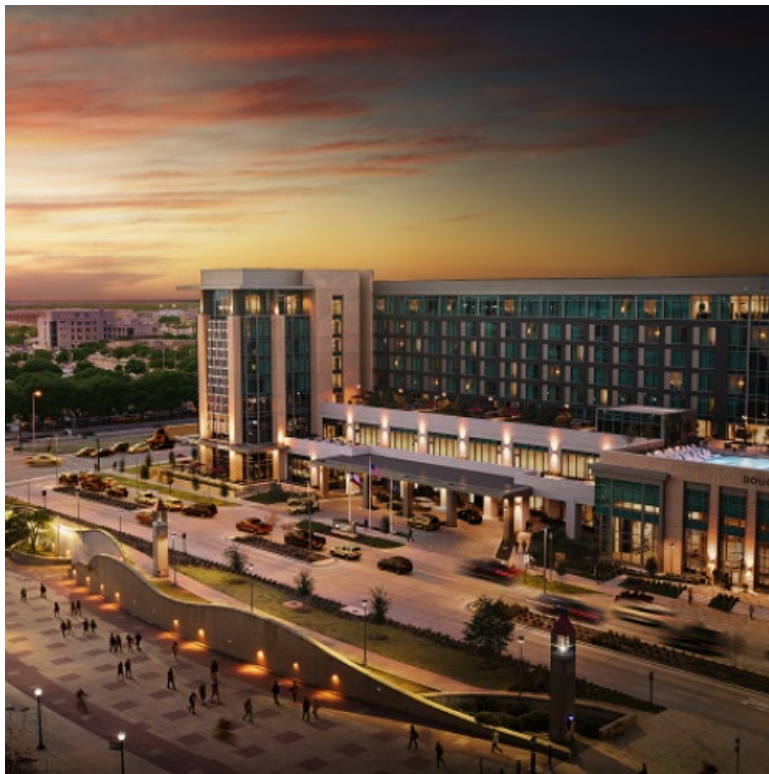




75th Annual James Steele Conference on Diseases in Nature Transmissible to Humans

Wednesday July 8, 2026 – Friday July 10, 2026

**Texas A&M Hotel and Conference Center,
College Station, 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, July 8, 2026	
7:45	CALL TO ORDER AND ANNOUNCEMENTS
8:00-10:00	Session I – Rickettsial Disease Moderator: Ronald D. Tyler Jr., DVM, MS
8:00	The Opossum as a Potential Reservoir for Flea-Borne Typhus Gregory M. Anstead, MD, PhD, South Texas Veterans Healthcare System, San Antonio, TX
8:30	Determination of Risk Factors for Typhus Group Rickettsiosis (Murine Typhus), in Galveston County Lucas S. Blanton, MD, University of Texas Medical Branch, Galveston, TX
9:00	Analysis of Four Mortality Cases in a Cohort of Probable Flea-Borne Typhus at University Hospital, San Antonio (January 2020 - October 2024) Christopher Dayton, MD, UT Health San Antonio, San Antonio, TX
9:30	Healthcare Provider Training to Reduce Morbidity and Mortality Attributable to Rocky Mountain Spotted Fever and Flea-borne Typhus in the U.S.-Mexico Border Region Christina Nelson, MD, MPH, Centers for Disease Control and Prevention, Fort Collins, CO
10:00	BREAK
10:30-12:00	Session II – Rabies Moderator: David Smonko, DVM
10:30	A Review of Kentucky Human Rabies Deaths: 1936-2024 Kelly H. Giesbrecht, DVM, MPH, Kentucky Department for Public Health, Frankfort, KY
11:00	Fox Rabies Variants: The Potential for Introduction, Re-emergence, and Host Shift Events in Texas Kathy Parker, MPH, Department of State Health Services, Austin, TX
11:30	The History of Rabies in Texas: Tales, Trivia, and Teasers Pamela J. Wilson, DrCH, MED, LVT, MCHES, Department of State Health Services (Retired), Austin, TX
12:00-1:30	LUNCH ON YOUR OWN
1:30-3:00	Session III – Chagas Disease Moderator: Susan Schaff, DVM, MPH
1:30	Initial Outcomes of Modified Benznidazole Treatment in Dogs Across Different Stages of Chagas Disease Rachel Busselman, DVM, PhD, Texas A&M University, College Station, TX
2:00	Acute Autochthonous Chagas Myocarditis in a Texas Infant Chia-Chi Angela Fu, MD, CTropMed, Baylor College of Medicine, Houston, TX
2:30	Veterinary <i>Trypanosoma cruzi</i> Infections: From Animals at the Home of a Recent Human Chagas Disease Case to Government Working Dogs in Texas Sarah Hamer, MS, PhD, DVM, DACVPM, Texas A&M University, College Station, TX
3:00	BREAK
3:30-5:30	Session IV – Surveillance Moderator: Paul E. Grunenwald, DVM, MS, DACVPM
3:30	Tick Surveillance Leading to Identification of <i>Amblyomma hebraeum</i> Containing <i>Rickettsia africae</i> , But Negative for <i>Ehrlichia ruminantium</i> in a Texas Resident Returning from International Travel Brent Moore, DVM, MS, MPH, DACVPM, Department of State Health Services, Tyler, TX Michael Allen, PhD, UNT Health, Fort Worth, TX
4:00	Occupational Risk Factors for Latent Tuberculosis Among Dairy Farm Workers in Texas, 2025 Anabel Rodriguez, PhD, MPH, Texas A&M University, College Station, TX Loni Taylor, DVM, PhD, MPH, Texas A&M University, College Station, TX
4:30	Identifying Drivers of Medically Important Mosquito Populations through Drone-acquired Imagery Analysis Following Hurricane Beryl in 2024 in Harris County, Texas Angela A. Zieba, MPH, Baylor College of Medicine, Houston, TX
5:00	Strengthening Tick and Tick-Borne Pathogen Surveillance through Animal Shelter Collaborations in Harris County, TX Brianna Weber, BS, Harris County Public Health, Houston, TX

Thursday, July 9, 2026	
7:50	CALL TO ORDER AND ANNOUNCEMENTS
8:00-9:30	Session V – Parasitic Zoonoses Moderator: Brendan Sullivan, DVM, MPH, DACVPM
8:00	Leishmaniasis in Animals: Epidemiology, Pathogenesis, Diagnosis, and Management Capt. Gina D’Addario, VMD, OIC, Naval Air Station Corpus Christi (CCNAS), Corpus Christi, TX
8:30	The Curious Case of the Neuro “Sister Psychosis” Christi Olszewski, LVT, Department of State Health Services, Lubbock, TX
9:00	The Resurgence of New World Screwworm and the Impact to Texas Sonja L. Swiger, PhD, MS, Texas A&M AgriLife Extension, Stephenville, TX
9:30	BREAK
10:00-11:30	Session VI – Vaccine-based Interventions Moderator: Amanda J. Kieffer, DVM, MPH, DACVPM
10:00	Conserved Tick Cement Proteins as Universal Antigens for Multi-Species Vaccine Development Jacquie Berry, BS, Texas A&M University, College Station, TX
10:30	Developing an Immunogenic and Cross-Protective Flavivirus mRNA Vaccine Megan Nicole Carey, MD, CTropMed, Baylor College of Medicine, Houston, TX
11:00	Within-Herd Transmission Dynamics of Highly Pathogenic Avian Influenza H5N1 in U.S. Dairy Cattle: A Modeling Approach Dana Pittman Ratterree, MPH, Texas A&M University, College Station, TX
11:30-1:00	LUNCH ON YOUR OWN
1:00-3:00	Session VII – Infectious Disease Testing and Diagnostics Moderator: Cherissa Abdul Hamid, DVM, MPH, DACVPM
1:00	A Metatranscriptomics Approach for Monitoring Arthropod-Borne Pathogens in Texas Alexander Arrow, BS, Baylor College of Medicine, Houston, TX
1:30	The Defense Food Analysis and Diagnostic Laboratory’s Advances in Infectious Disease Testing and Diagnostics Robert Fathke, DVM, PhD, MS, MPH, DACVPM, U.S. Army, San Antonio, TX Charles Hart, PhD, U.S. Army, San Antonio, TX
2:00	Rapid Detection of blaCTX-M ESBL-Producing Enterobacterales in Canine Urine Sara Lawhon, DVM, PhD, DACVM, Texas A&M University, College Station, TX
2:30	Metatranscriptomic Survey of <i>Ornithodoros turicata</i> Soft Ticks in Texas Reveals New Vector-Microbe Associations Alexander Kneubehl, PhD, Baylor College of Medicine, Houston, TX
3:00-4:00	SCIENTIFIC POSTER SESSION
4:00-5:00	Session VIII – One Health Moderator: Kelly Broussard, MPH
4:00-4:30	The Role of a Medical Entomologist in One Health Nina Dacko, MS, Texas A&M University & Gulf South VECTOR, Dallas, TX
4:30-5:00	To Be Determined
5:00-7:00	J.V. Irons Keynote Lecture & Reception Moderator: Bonny Mayes, MA, E-RYT 200, YACEP
5:00-6:00	Chagas Disease in Texas and Beyond Caryn Bern, MD, University of California, San Francisco, CA
6:00-7:00	RECEPTION

Friday, July 10, 2026	
7:50	CALL TO ORDER AND ANNOUNCEMENTS
8:00-10:00	Session IX – Case Reports Moderator: Briana O’Sullivan, MPH
8:00	Chronic Loiasis Presenting as a Migratory Conjunctival Worm Years After Exposure Divya Pillendla, MPH, Harris County Public Health, Houston, TX
8:30	Hantavirus, or Something Like it, in Travis County, Texas 2025 Anne Hanley, BSN, RN, Austin Public Health, Austin, TX
9:00	Novicidemia vs. Tularemia Revisited: A Suspected Novicidemia in an 8-Year-Old Female James Mobley, MD, MPH, San Patricio County Local Health Authority (Ret), Sinton, Texas
9:30	Soil, Spores, and Surprise: Travel-Associated Cutaneous Anthrax with Livestock Exposure Abisola Oladimeji, MD, MPH, Houston Health Department, Houston, TX
10:00	BREAK
10:30-12:00	Session X – Tickborne Disease Moderator: Sarah Murphy Gunter, PhD, MPH
10:30	Did the Prairie Dogs Volunteer as Tribute? Cherissa Abdul Hamid, DVM, MPH, DACVPM, Texas Department of State Health Services, Lubbock, TX
11:00	Addressing Challenges in Molecular Surveillance: Examining the Influence of Tick and Spirochete Biology on Relapsing Fever Spirochete Detection Job Lopez, PhD, Baylor College of Medicine, Houston, TX
11:30	The Dynamics and Epidemiological Implications of Vertical Transmission of <i>Borrelia turicatae</i> from the Argasid Vector, <i>Ornithodoros turicata</i> Brittany Armstrong, PhD, Baylor College of Medicine, Houston, TX
12:00	CONCLUSION

Backup Presentations:

Strongyloidiasis Epidemiology and Diagnostic Gaps in a Southern U.S. Safety-Net Health System	Megan Duffey, MD, Baylor College of Medicine, Houston, TX
Arbovirus Surveillance in Equines Using Diagnostic Testing from a Medical Diagnostic Laboratory	Laura Hopkins, MPH, Texas A&M University, College Station, TX

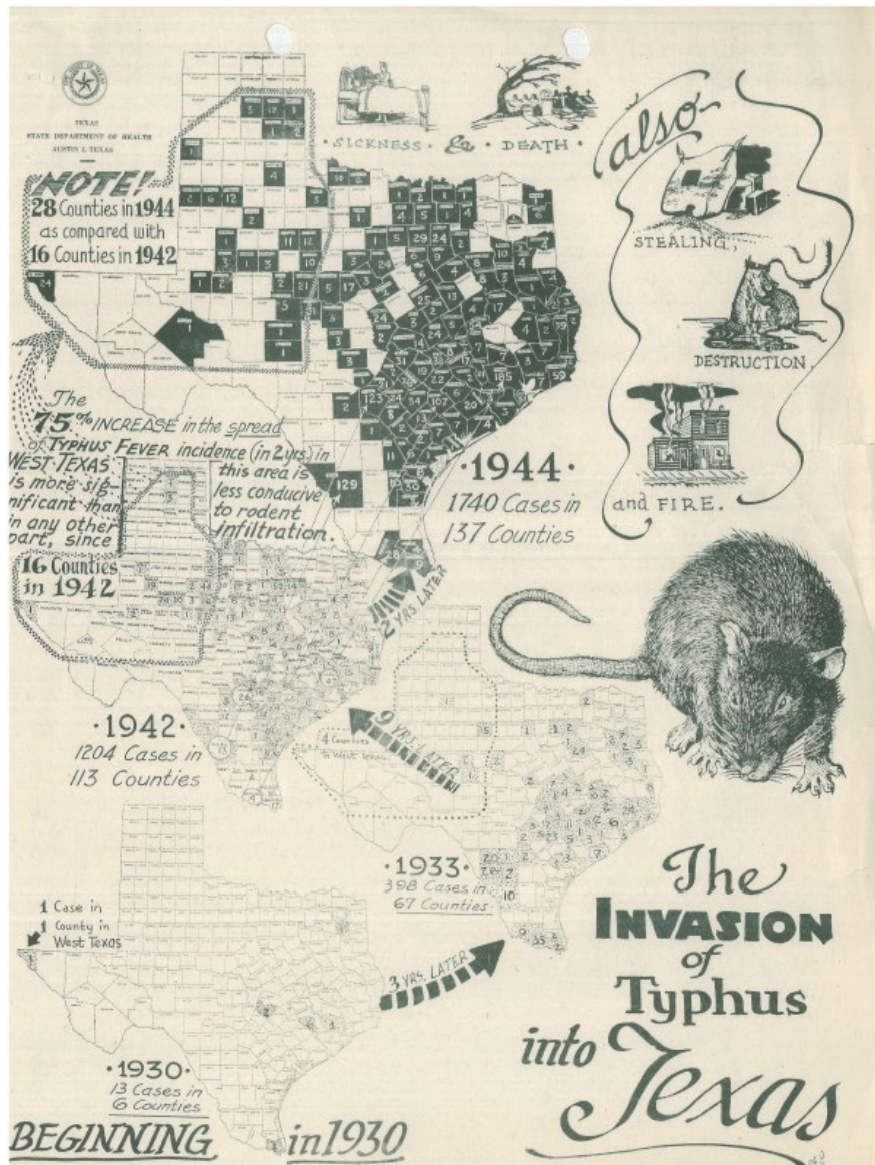


Wednesday, July 8, 2026

8:00-10:00 Session I: Rickettsial Disease

Moderator: Ronald D. Tyler Jr., DVM, MS

Texas Department of State Health Services, Harlingen, TX



1944 Texas Department of Health Flyer
Source: Zoonosis Control Branch



The Opossum as a Potential Reservoir for Flea-Borne Typhus

Gregory M. Anstead, MD, PhD

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Flea-borne typhus (FBT) is an infection caused by the bacteria *Rickettsia typhi*. It is typically an acute undifferentiated febrile illness, but about one-quarter of patients suffer respiratory, neurologic, renal, hepatic, cardiac, ocular, or other complications. The infection is typically transmitted to humans by the inoculation of a bite site, a skin abrasion, or mucous membranes with feces from fleas infected with these rickettsiae. Since the dawn of the new millennium, the incidence of FBT has dramatically increased in both Texas and California. The Virginia opossum *Didelphis virginiana* has been a suspected reservoir for the rickettsial organisms causing flea-borne typhus since the 1940s.

For this presentation, the literature from the 1940s to the present was reviewed to determine the reservoir role of the opossum, based on epidemiologic associations, serologic determinations, and the harboring of *Rickettsia*-infected fleas. The emergence of the opossum as a high-density mesopredator in the urban environment is also considered. Opossums are known to host more cat fleas than cats and other urban wildlife. The role of the opossum as a "vector amplifier" is interpreted with respect to its life history and compared to the domestic cat.



Determination of Risk Factors for Typhus Group Rickettsiosis (Murine Typhus), in Galveston County

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Additional author: Baraa Saad

Murine typhus is a flea-borne infection caused by *Rickettsia typhi*. In the United States, the contemporary transmission cycle involves opossums (*Didelphis virginiana*) as the reservoir and cat fleas (*Ctenocephalides felis*) as the vector. It is unclear if cats and dogs (also hosts for *C. felis*) play a role in human infection. The risk factors associated with acquiring *R. typhi* remain poorly understood. We hypothesize that those working in professions exposed to fleas are at greater risk for murine typhus. We performed a cross-sectional study comparing *R. typhi* serostatus of those working in veterinary clinics (animal care workers [ACWs]) to a control group (human healthcare workers [HCWs]). Serum was tested for antibodies against *R. typhi*, and participants answered a short questionnaire to assess exposures. We recruited 58 ACWs and 110 HCWs. *Rickettsia typhi* seropositivity was found in 11 (19.0%) ACWs versus 9 (8.2%) HCWs ($p = 0.048$). Reciprocal titers ranged from 128 – 2048 (geometric mean 397.9) in the ACW group versus 256 – 512 (geometric mean 348.4) in the HCW group ($p = 0.95$). Of the potential risk factors assessed by questionnaire, having a history of recognizing flea bites was associated with *R. typhi* seropositivity ($p = 0.016$). As expected, a self-reported history of previously being diagnosed with murine typhus was associated with *R. typhi* seropositivity ($p = 0.038$). There was no association between seropositivity and cat or dog ownership. There was also no association between seropositivity and the use of flea medications on companion animals, recognizing opossums around dwellings, or having a febrile illness in the prior year. In summary, those exposed to a high burden of fleas are at higher risk of *R. typhi* infection. Knowledge of those at risk for acquiring murine typhus may inform the development and implementation of prevention strategies targeting high-risk populations.



Analysis of Four Mortality Cases in a Cohort of Probable Flea-Borne Typhus at University Hospital, San Antonio (January 2020 - October 2024)

Christopher Dayton, MD

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Additional authors: Gregory Anstead; Zoie Fan

Flea-borne typhus, an infection caused by *Rickettsia typhi*, poses significant health risks in our region. This presentation reviews four mortality cases from a cohort of 176 patients diagnosed with probable flea-borne typhus at University Hospital in San Antonio from January 2020 to October 2024. Our analysis focuses on the clinical circumstances surrounding each mortality case, examining patient demographics, clinical presentations, underlying health conditions, treatment responses, and timing of medical intervention. The cohort exhibited a range of presentations. Each case was meticulously reviewed to understand the factors contributing to mortality. While timely diagnosis and treatment with doxycycline are critical, these cases highlight the challenges in managing advanced disease, particularly in patients with pre-existing conditions. The findings from this analysis underscore the urgent need for targeted public health initiatives aimed at increasing awareness of flea-borne typhus, especially in at-risk communities. Enhanced surveillance and prompt recognition of symptoms can facilitate earlier treatment and potentially reduce mortality rates. This presentation will discuss the specific circumstances of each mortality case, emphasizing the implications for clinical practice, public health policy, and future research in managing flea-borne typhus.



Healthcare Provider Training to Reduce Morbidity and Mortality Attributable to Rocky Mountain Spotted Fever and Flea-borne Typhus in the U.S.-Mexico Border Region

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Additional authors: Maureen K. Brophy; Marissa L. Taylor; Christopher D. Paddock; Johanna S. Salzer

Rocky Mountain spotted fever (RMSF), caused by *Rickettsia rickettsii*, is a deadly tick-borne disease emerging along the U.S.-Mexico border. From 2009-2023, 4,373 RMSF cases including 1,345 deaths (30.8% case fatality rate) were reported in northern Mexico. In 2023, an RMSF outbreak including three fatalities was reported in people seeking healthcare in the U.S. after travel to Mexico. Similarly, case counts of flea-borne typhus (FBT), a potentially severe infection caused by *R. typhi*, are also rising steadily in Texas, California, and other states. Preventing treatment delay-related death from RMSF and FBT relies on healthcare provider (HCP) awareness.

CDC's Rickettsial Zoonoses Branch partnered with state and local health departments to create and implement the Border "Training on Rickettsioses to Educate Clinicians" (TREC). Border TREC enhanced awareness of RMSF and educated HCPs on risk factors, clinical features, and treatment through comprehensive, in-person HCP trainings in the border region. CDC also created a free bilingual online RMSF training module to ensure broader access to Border TREC materials.

From May-December 2024, we delivered training to 450 HCPs and 100 public health officials across California, Arizona, and Texas, five tribal nations, and Tecate, Mexico. CDC and health departments are developing FBT training material for future collaborative implementation where FBT is emerging. Additional in-person Border TREC trainings are planned for 2026, which will include FBT and target the Mexico-Texas border region.

The RMSF case fatality rate in northern Mexico has highlighted gaps in HCP knowledge. Moreover, the recent emergence and shifting ecology of FBT is a growing public health concern. The Border TREC intervention has trained HCPs to recognize, diagnose, and treat RMSF promptly, and is an adaptable model for FBT. By building local capacity, we aim to reduce the impact of both RMSF and FBT on both sides of the border.



Wednesday, July 8, 2026

10:30-12:00 Session II: Rabies

Moderator: David Smonko, DVM

Texas Department of State Health Services, Temple, TX

RABIES: Know the Risk



Rabies is almost always **fatal**.
Prevention saves **lives**.

2026 Rabies Awareness & Prevention Poster Contest Winner (hand drawn – high school)



A Review of Kentucky Human Rabies Deaths: 1936-2024

Kelly H. Giesbrecht, DVM, MPH

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kelly.giesbrecht@ky.gov

Human rabies deaths in the United States have declined significantly due to laws requiring rabies vaccination of dogs and cats, along with stray animal control, and spay and neuter recommendations. As the new Kentucky State Public Health Veterinarian in 2017, I found only one slide showing five past human deaths in the state. Moving offices several years later, I came across old files and records of rabies deaths. Information was spotty, with news reports, and some medical reports. Reviewing this information creates documentation of past human rabies deaths in Kentucky. It also serves as a reminder why we have rabies laws and honors the victims.

A fourth year Lincoln Memorial Veterinary student intern's project was to review this information, create a Redcap project and enter the data. The information was reviewed by year, county, age, and type of animal bite. Some records lacked information.

A total of 39 cases were entered. Two were from states other than Kentucky and not included, leaving 37 Kentucky human rabies deaths. Date range is 1936-2024. Ages ranged from 1-80 years old. There were 10 females and 27 Males. Results included 14 dog cases, two fox bites, one mule, one cat, two bats, 14 unknown and three with no animal information. An Epi Curve with year and species over time shows deaths from dogs are early in the 1900's and deaths from bats occur later.

As expected, before pet vaccination laws and programs, dog bites were responsible for many human rabies deaths. Fewer deaths overall and deaths from bat rabies were recognized later in the 1900's. This data is incomplete, with species information unknown for many deaths. It chronicles what we have for Kentucky human rabies deaths and is a reminder why we need vaccination laws and programs.



Fox Rabies Variants: The Potential for Introduction, Re-emergence, and Host Shift Events in Texas

Kathy Parker, MPH

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kathy.parker@dshs.texas.gov

In 2013 the last case of Texas Fox (TF) variant rabies was reported from Concho County. There has not been another TF variant case of rabies reported in Texas since that date. However, there are legitimate threats for the re-introduction of the TF variant from Mexico and the introduction of the Arizona fox (AZ) variant from New Mexico. Additionally, a South Central Skunk (SCS) rabies outbreak among foxes is currently occurring in Central Texas, with probable fox-to-fox transmission and changes in monoclonal antibody patterns among some of the positive samples. Is this a host-shift or a complicated spillover event?

The Texas Department of State Health Services (DSHS) Zoonosis Control Program continues enhanced rabies surveillance in counties of interest and is evaluating genetic data from positive rabies specimens collected over the past five years by working with the DSHS Rabies Lab and the Centers for Disease Control and Prevention (CDC). We hope to determine the needs for future Oral Rabies Vaccination Program actions, increased public rabies education, and improving enhanced wildlife surveillance tools in Texas. There are three large Central Texas communities facing rabies risks from the fox outbreak and we will need to continue developing tools to monitor, evaluate, and respond to any fox driven rabies outbreaks in Texas.



The History of Rabies in Texas: Tales, Trivia, and Teasers

Pamela J. Wilson, DrCH, MEd, LVT, MCHES

Department of State Health Services (Retired), Austin, TX

pamjwil57@gmail.com

Additional authors: Rodney E. Rohde; Michael J. Bodenchuk

This historical journey of rabies, a viral zoonotic disease, begins with references from the 1800s, including reports from cowboys of “phoby cats” (skunks) and of how bitten individuals would ride horseback across Texas seeking a prevention lore called madstones. In Texas, rabies is enzootic in skunks and bats; rabies in bats motivated novel research projects. Rabies epizootics in coyotes and gray foxes stimulated the development of Texas’ Oral Rabies Vaccination Program (ORVP) by Zoonosis Control (ZC) at the Texas Department of Health (TDH), now referred to as the Department of State Health Services. With the 1994 declaration of rabies being a state health emergency, studies were directed toward establishing an effective dose of oral rabies vaccine and appealing bait for coyotes and gray foxes, plus defining the distribution area of the vaccine/bait units. The TDH Bureau of Laboratories Rabies-Arbovirus Section perfected testing for rabies virus variants in rabies specimens to determine where the domestic dog-coyote (DDC) and Texas fox (TF) variants were located. A plethora of agencies and individuals accomplished the effective launching of the ORVP for coyotes in 1995 in South Texas and for gray foxes in 1996 in West-Central Texas. TDH incorporated into state law an innovative protocol for rabies postexposure prophylaxis for unvaccinated domestic animals exposed to rabies, which has been noted nationally. State law mandates that an animal in this exposure category immediately be vaccinated against rabies and placed in confinement for 90 days with booster vaccines administered during the third and eighth weeks of confinement; alternatively, the animal may be euthanatized. Statewide ZC personnel created a unique Animal Control Officer Training Program, which has been conducted for decades. Other distinctive Texas rabies educational endeavors have included the Conference on Diseases in Nature Transmissible to Humans and the Rabies Awareness and Prevention Poster Contest.

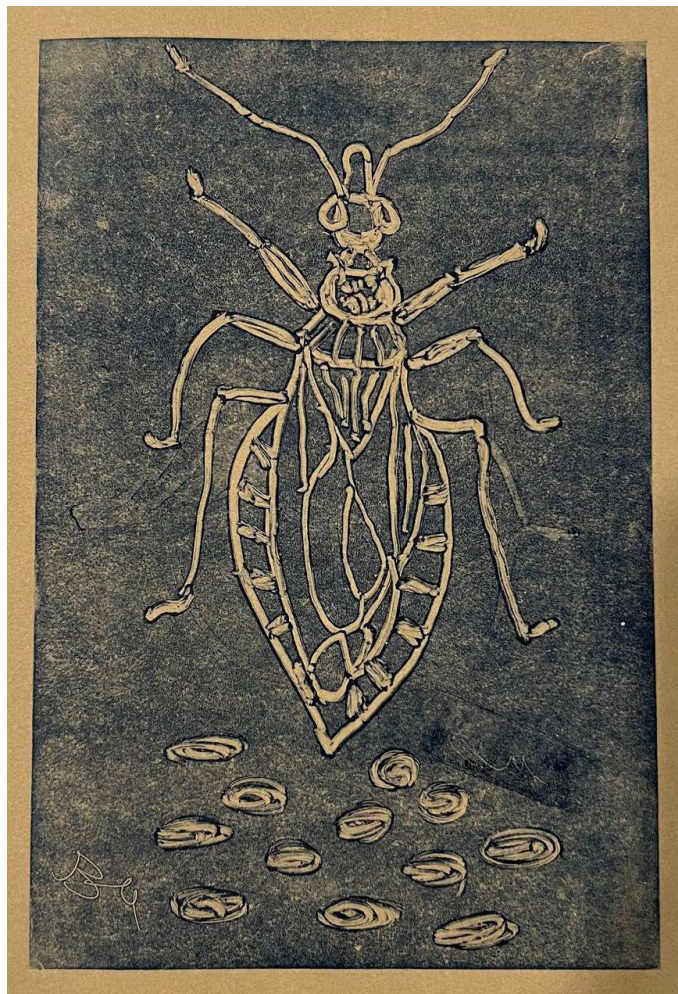


Wednesday, July 8, 2026

1:30-3:00 Session III: Chagas Disease

Moderator: Susan Schaff, DVM, MPH

Texas Department of State Health Services, El Paso, TX



Triatoma sp. Monprint by Bonny Mayes



Initial Outcomes of Modified Benznidazole Treatment in Dogs Across Different Stages of Chagas Disease

Rachel Busselman, DVM, PhD

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Additional authors: Jake Dunham, Sukjung Lim; Ashley B Saunders; Sarah A. Hamer

Chagas disease – caused by the parasite *Trypanosoma cruzi* – is characterized by cardiac disease in infected humans and dogs, ranging from mild subclinical arrhythmias to severe cardiomyopathy and death. In dogs, the effect of antiparasitic treatment on clinical disease progression during acute or chronic disease is unknown. Our objective is to identify a set of pet dogs with a recent positive Chagas diagnostic test and various clinical signs associated with Chagas disease and treat these dogs using a modified dosing regimen of benznidazole. We hypothesize that treated dogs will have limited progression of clinical cardiac disease during and after treatment, and the subset of dogs with detectable circulating parasite before treatment will have no detectable parasite after treatment. We are performing cardiac diagnostics (ECG, echocardiograms, Holter monitors, and cardiac troponin I) and testing for evidence of parasite (new highly sensitive *T. cruzi* qPCR and serologic assays) in each dog before, during and after the 6-month course of treatment, while obtaining weekly dog health surveys from owners. With a goal of treating 50 dogs, thus far we have enrolled 47 dogs, with 23 that will have completed their treatment by mid-June 2026. Initial clinical findings of enrolled dogs included dogs with varied *T. cruzi* IFA antibody results (1:20 – 1:163,840), cardiac troponin I (<20 – 2408.5 pg/mL [reference range 20-168 pg/mL]), and clinical findings (e.g., right sided cardiomyopathy, supraventricular and/or ventricular arrhythmias, apparently healthy). Several dogs were found to have comorbidities, emphasizing that other etiologies may contribute to the clinical status of Chagas-positive dogs. Temporary mild decreased appetite and lethargy have been reported in some dogs during treatment. Repeated diagnostics will inform the efficacy of this benznidazole dosing protocol for *T. cruzi* in dogs and reveal the potential protective effects of treatment on cardiac disease progression.



Acute Autochthonous Chagas Myocarditis in a Texas Infant

Chia-Chi Angela Fu, MD, CTropMed

Baylor College of Medicine, Houston, TX

Additional authors: Diana Nguyen, DO; Bonny Mayes, MA; Susan P. Montgomery, DVM, MPH; Caryn Bern, MD; Jaime Altcheh, MD; Eva H. Clark, MD, PhD; Jaime Fergie, MD

A 10-month-old unvaccinated boy presented to a Corpus Christi hospital with fatigue, emesis, and decreased oral intake. He had normal vital signs but was irritable and dehydrated. Initial labs showed leukocytosis, transaminitis, and pyuria. Despite intravenous fluids and empiric antibiotics, he developed worsening tachypnea and tachycardia. Cardiomegaly noted on x-ray prompted echocardiogram which revealed biventricular dysfunction and left ventricular apical thrombus. The patient was transferred to the intensive care unit and required intubation and Veno-Arterial Extracorporeal Membrane Oxygenation (VA-ECMO). Work-up demonstrated trypomastigotes on blood smear on hospital day (HD) 5, positive *Trypanosoma cruzi* molecular testing (quantitative polymerase chain reaction [qPCR] and next-generation metagenomic sequencing), and positive *T. cruzi* serology. His parents reported he had never traveled outside of Texas, but they had seen triatomines in the home on multiple occasions; both parents had negative *T. cruzi* serology. The patient began anti-trypanosomal therapy and transferred to a quaternary center for advanced cardiac support. Repeat echocardiogram demonstrated worsening ejection fraction (8%). He was eventually weaned off VA-ECMO and extubated by HD 19 and 22, respectively. He was monitored twice weekly via *T. cruzi* qPCR, which remained positive even after completing 60 days of anti-trypanosomal therapy (nifurtimox). Thus, he was started on a second course of anti-trypanosomal therapy (benznidazole) on HD 110. *T. cruzi* qPCR was first negative on HD 116, and he discharged on HD 117. Chagas disease is a vector-borne infection caused by the parasite *T. cruzi*. Transmission typically occurs through exposure to feces of the triatomine vector, directly or via contaminated food or beverages. The acute phase can present asymptotically, as self-limited febrile illness, or, rarely, as life-threatening myocarditis. The chronic phase can lead to long-term sequelae, namely cardiac and gastrointestinal complications. Early recognition and diagnostic testing are important as anti-trypanosomal therapy provides cure for most children with Chagas disease.



Veterinary *Trypanosoma cruzi* Infections: From Animals at the Home of a Recent Human Chagas Disease Case to Government Working Dogs in Texas

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Long established in transmission cycles between triatomine insects and animal reservoirs across the southern United States, the protozoan parasite *Trypanosoma cruzi* is increasingly detected in dogs in Texas. Identifying infected dogs allows for supportive and antiparasitic treatments to improve dog health. Additionally, in some cases, knowledge of infected animals may signal areas where humans are at risk of vector and parasite exposure. In response to a recent acute Chagas disease pediatric case in Live Oak County, TX, we investigated the peridomestic environment at the baby's home in October 2025. In one afternoon, twenty live and dead triatomines of *Triatoma gerstaeckeri* and *Paratriatoma lecticularia* were collected from peridomestic sites. Of 13 tested triatomines, 8 (61.5%) were *T. cruzi* qPCR-positive. Twenty-one domestic/peridomestic mammals (dogs, cats, mini horses, donkey, goats, rabbit) were sampled; 3 of 21 (14.3%) were *T. cruzi* qPCR-positive, and 6 of 9 (66.7%) animals able to be tested using serologic tests were seropositive. Our broader canine Chagas disease research program includes a study of the government working dogs that operate in Customs and Border Protection and Transportation Security Administration. We aim to quantify infections, characterize cardiac status, treat dogs, and recommend enhanced approaches for detecting and managing infected dogs. After collection of samples from these working dogs in San Antonio and the Rio Grande Valley of south Texas in fall 2025, we found 15/262 (5.7%) dogs had antibodies to *T. cruzi*, of which 7 (2.7%) had parasite DNA in the blood; this latter group of actively infected dogs are undergoing cardiac evaluations as candidates for antiparasitic treatment as we expand the study to working dogs across the country. Given the broad geographic areas to which these working dogs are deployed, enhanced screening and treatment protocols may be useful to prolong their working life across the country.



Wednesday, July 8, 2026

3:30-5:30 Session IV: Surveillance

Moderator: Paul E. Grunenwald, DVM, MS, DACVPM
Texas Department of State Health Services, Austin, TX



Photo source: <https://www.nhpr.org/2024-06-28/climate-change-more-ticks-tick-borne-disease>



Tick Surveillance Leading to Identification of *Amblyomma hebraeum* Containing *Rickettsia africae*, But Negative for *Ehrlichia ruminantium* in a Texas Resident Returning from International Travel

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African tick bite fever (ATBF), caused by *Rickettsia africae*, is a common travel-associated rickettsial infection acquired predominantly in sub-Saharan Africa through the bite of *Amblyomma* spp. ticks. This presentation describes the investigation of ticks submitted by a U.S. traveler following recent travel to an endemic region as well as a brief description of the patient.

As part of passive tick surveillance, the tick was morphologically and molecularly identified as *Amblyomma hebraeum*, a primary vector of *R. africae* in southern Africa. PCR testing confirmed the presence of *R. africae* in the specimens, supporting potential exposure to the agent of ATBF. Notably, the tick tested negative for *Ehrlichia ruminantium*, the causative agent of heartwater disease. This finding carries substantial One Health and regulatory importance.

Like other Spotted Fever Rickettsiosis (SFR), ATBF leads to typical signs and symptoms, including fever, headache, rash, and muscle aches. With ATBF, there is often an eschar in addition to a delayed seroconversion of 28 days, which makes serologic testing more tricky than common SFR that are native to the United States.

Travelers both from Sub-Saharan Africa to the United States as well as from the United States to Sub-Saharan African countries number in the hundreds of thousands, leading to substantial risks of these ticks reaching U.S. soil. This investigation underscores the value of integrated human–animal–vector surveillance systems in preventing the introduction of exotic pathogens. Timely laboratory characterization of traveler-associated specimens provides critical information for individual patient management while simultaneously supporting national biosecurity and foreign animal disease preparedness.



Occupational Risk Factors for Latent Tuberculosis Among Dairy Farm Workers in Texas, 2025

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Dairy farm workers face unique occupational health risks. One critical occupational concern is zoonotic exposure to *Mycobacterium tuberculosis* complex (MTBC). Despite the high global burden of tuberculosis (TB), the occupational risk factors and prevalence of TB among dairy farm workers in the United States (US) remain poorly understood.

Here, we conducted a cross-sectional study in 2025 to assess MTBC exposure and active infection among dairy farm workers (n=100) in two Texas farms—one with active cattle bovine tuberculosis (bTB) and the other with a history of bTB. We assessed prior exposure using serum interferon- γ release assays (IGRA) and screened for active infections via PCR of sputum samples, followed by whole genome sequencing of positive isolates.

We identified 12.0% of participants were positive for MTBC antibodies. Predictors of positive MTBC antibodies included working in an enclosed or poorly ventilated area of the farm (OR = 6.6, 95%CI: 1.5-29.2, $p < 0.01$), reporting not being able to take time off from work to seek medical care as a barrier to health access (OR = 8.0, 95%CI: 1.7-38.1, $p < 0.01$), and living with other dairy farm workers (OR = 8.7, 95%CI: 1.4-55.5, $p < 0.05$).

Our findings inform underrecognized occupational health risks and underscore the need for integrated surveillance at the human-animal intersection. Research-to-practice implications highlight several points of intervention, including improving ventilation systems [when appropriate], personal protective equipment (PPE) training and adherence, mitigation of crowded housing, and equitable sick-leave policies.



Identifying Drivers of Medically Important Mosquito Populations through Drone-acquired Imagery Analysis Following Hurricane Beryl in 2024 in Harris County, Texas

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Hurricane Beryl hit the greater Houston area in July 2024. This storm caused major rainfall and significant wind throughout the city, resulting in damage to the built environment. It occurred during peak mosquito season with active West Nile Virus transmission. There is currently limited knowledge on post-disaster drivers of medically important mosquitoes, and we believe this event provided an ideal opportunity to evaluate the impact of disaster related environmental changes on mosquito ecology. Using drone-acquired imagery post-disaster, we investigated the correlation between types of debris and mosquito composition and abundance across the City of Houston. Each location was surveyed once weekly over four weeks post-Hurricane Beryl and then monthly for 5 months. For each drone image, trap data was summarized and graphically represented pre- and post-storm event. Drone images were evaluated to characterize built environment and storm related debris. An analysis was conducted to determine drivers of medically important mosquito abundance. We identified non-organic debris, specifically children's pools and tires, as significant drivers of medically important mosquitoes. We believe this study represents a proof-of-concept for using remote sensing to inform community-level abatement efforts to protect public health post-natural disaster.



Strengthening Tick and Tick-Borne Pathogen Surveillance through Animal Shelter Collaborations in Harris County, TX

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Over recent decades, tickborne diseases have been of increasing concern to public health officials as the number of human cases has risen steadily. One way to better understand the risk of tickborne disease is to utilize the principles of One Health. The One Health Perspective describes disease risk in terms of the relationship among the environment, people, and animals. Tickborne disease diagnoses in animals (for example, in pets from veterinary clinics) may serve as an indicator of potential risk to human health. Clinics and animal shelters can be a source of vector samples recovered from animals, that can then be tested for pathogens. Harris County Public Health Mosquito and Vector Control Division (MVCD) is a long-standing mosquito and vector control program that utilizes integrated vector management principles in all aspects of its operations, including surveillance and pathogen testing, education, and outreach. In 2017, MVCD established a non-mosquito arthropod vector surveillance section, including regular field surveillance for ticks and tickborne pathogens. In addition to field collected samples, MVCD partners with Harris County Veterinary Public Health (Harris County Pets) to obtain ectoparasites such as fleas and ticks brought in with animals surrendered to the shelter or picked up as strays in the community. Here we present testing results from this work, as well as from our collaboration with Baylor College of Medicine, highlighting the different pathogens discovered in ticks found on shelter animals. Increased partnerships between Public Health officials and animal shelters and veterinary clinics can expand capabilities to identify risks to the community for vector-borne disease. The One Health Perspective complements an Integrated Vector Management program by emphasizing outreach and education in the intervention strategy.



Thursday, July 9, 2026

8:00-9:30 Session V: Parasitic Zoonoses

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



Detail of NWS larva showing the mouth hooks they use to eat living flesh. Image source: <https://www.cdc.gov/new-world-screwworm/situation-summary/index.html>



Leishmaniasis in Animals: Epidemiology, Pathogenesis, Diagnosis, and Management

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Leishmaniasis is a globally significant vector-borne disease caused by protozoan parasites of the genus *Leishmania*, transmitted primarily by phlebotomine sand flies, including the species of *Phlebotomus spp.* and *Lutzomyia spp.* The disease affects a wide range of mammalian hosts, with domestic dogs serving as the principal reservoir for zoonotic visceral leishmaniasis caused by *Leishmania infantum*. The parasite exists as extracellular promastigotes within the sand fly vector (infective form) and intracellular amastigotes within macrophages of the vertebrate host (diagnostic form).

Geographically, leishmaniasis is endemic in regions of the Mediterranean basin, Latin America, the Middle East, and parts of Asia, with emerging cases reported in North America (Southeast). In dogs, infection may manifest as cutaneous, mucocutaneous, or visceral forms, with the latter being most common and clinically significant. Transmission occurs primarily through sand fly bites (vector-borne), though vertical, venereal, and blood transfusion–associated transmissions are documented.

Clinical signs in dogs are variable and may include lymphadenomegaly, weight loss, cutaneous lesions (exfoliative dermatitis, ulcerations), lethargy, epistaxis, ocular inflammation, and renal disease secondary to immune complex deposition. Clinicopathologic abnormalities commonly include hyperglobulinemia, hypoalbuminemia, mild nonregenerative anemia, thrombocytopenia, and proteinuria. Renal failure due to glomerulonephritis is the leading cause of death. Histopathology typically reveals granulomatous inflammation with intracytoplasmic amastigotes within macrophages.

Diagnosis relies on a combination of serologic assays (e.g., IFA, ELISA), PCR testing, cytology, and histopathology. Treatment options often include allopurinol in combination with meglumine antimoniate, miltefosine, or amphotericin B. Preventive strategies include vector control (insecticide-impregnated collars, topical repellents) and blood donor testing. There are no vaccines available in the United States.

Case studies highlight a common presentation in military working dogs and underscore the importance of early recognition, comprehensive diagnostics, and prevention techniques in endemic regions.



The Curious Case of the Neuro “Sister Psychosis”

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Cysticercosis is an infection caused by the larva of the tapeworm parasite *Taenia solium*. The eggs of the tapeworm are shed in fecal material of infected humans and are ingested in contaminated food, water sources, or contact surfaces. Once ingested, the eggs hatch releasing the larva in the small intestine. The larva penetrates the intestinal wall and enters the blood stream. From there, the larva can migrate to any organ system in the body. Cysts are most frequently found in the skin, skeletal muscle, heart, eye, and central nervous system (brain and spinal cord). Cyst formation in the brain can result in neurocysticercosis, a neurologic manifestation of the larval infection. This manifestation depends on where and how many cysts are present. Although headaches and seizures are the most common clinical signs, a person may also suffer from confusion, altered mental status, ataxia, and hydrocephalus.

A 2025 case investigated by DSHS PHR 1 describes a 69-year-old-male from Mexico with repeated positive cysticercosis antibody test results dating back to 2021. This investigation reveals why early detection, treatment, and management of neurocysticercosis is pertinent to minimizing the long-term clinical signs associated with the disease.



The Resurgence of New World Screwworms and the Impact to Texas

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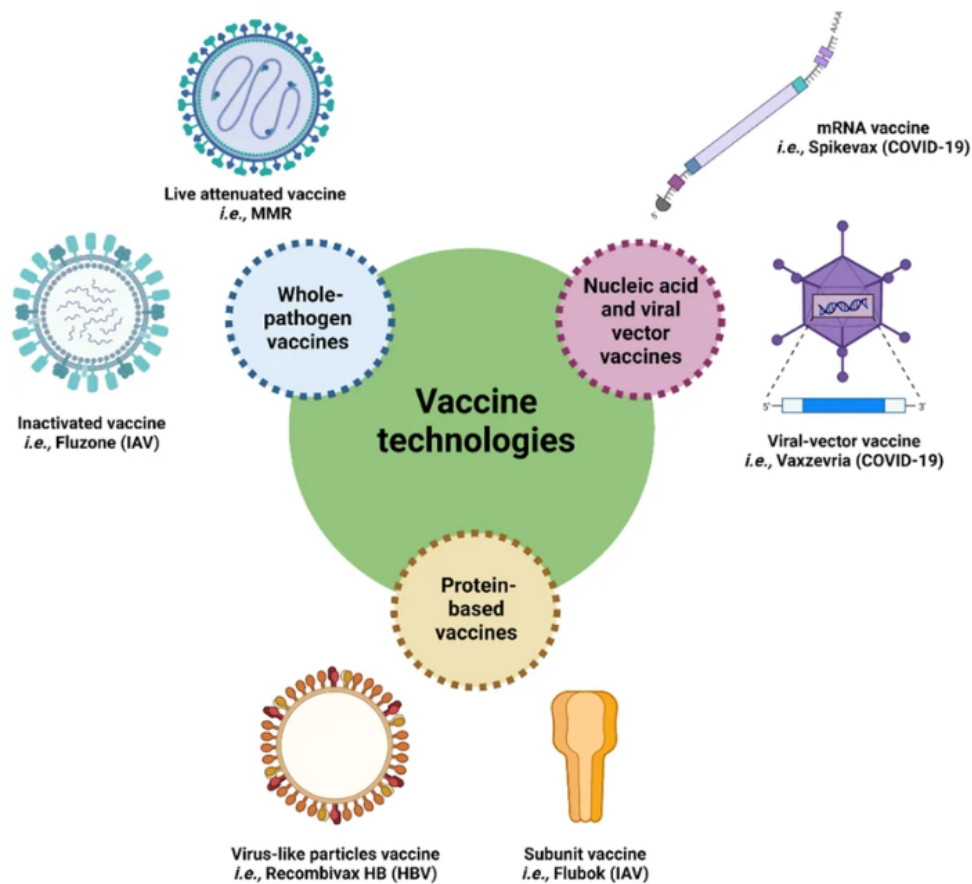
The New World screwworm is a parasitic blow fly that opportunistically takes advantage of warm-blooded animals for egg laying and larval feeding and development. Due to the severity of this fly, it was eradicated from North America and Central America from the 1950s until the early 2000's. Unfortunately, recent events have led to the expansion of this devastating fly and with it severe challenges that Texas must prepare for. The New World screwworm females lay their eggs on openings in the skin of animals and humans, and the ensuing larvae will feed on the living flesh of that host. The feeding from the larvae will lead to death of the animal within 7-14 days if the infestation is not tended to. With the resurgence of the New World screwworm in Central America and into Mexico, Texas lays on the forefront of potential cases and significant impact to our animals and economy. Texas is currently on high alert and working closely with USDA-APHIS to monitor the northward movement of this fly since the projected impact of this fly to Texas would cost \$2 billion annually to the Texas economy.



Thursday, July 9, 2026

10:00-11:30 Session VI: Vaccine-base Interventions

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



Schematic representation of vaccine technologies and examples of commercialized vaccines for human use.
HBV: hepatitis B virus; IAV: influenza A virus; MMR: measles, mumps, and rubella.

Source of image: https://www.researchgate.net/figure/Schematic-representation-of-vaccine-technologies-and-examples-of-commercialized-vaccines_fig2_365394324



Conserved Tick Cement Proteins as Universal Antigens for Multi-Species Vaccine Development

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Hard ticks in the United States are the leading cause of vector-borne diseases in the country, affecting millions of people annually. While there are 90 species of hard tick in the US, there are two species most associated with tick-borne disease (TBD) transmission: the Black-legged tick, *Ixodes scapularis*, and the Lone star tick, *Amblyomma americanum*. Collectively, these ticks can spread 11 different pathogens, occasionally transmitting multiple pathogens simultaneously. In conjunction with climate change, human development and animal movement, these ticks are rapidly spreading across the US. With current TBD preventions limited to acaricides and personal protection, the need for a comprehensive, multi-species anti-tick vaccine is paramount. Both tick species are considered long-term feeders, needing days or weeks to feed completely. This long-term feeding is facilitated by tick cement which is a protein-rich bioadhesive that is secreted into the skin where it hardens into a strong but malleable glue. This cement anchors the ticks' mouthparts within the skin, preventing them from being dislodged by host movement or grooming. Without the successful formation of cement, tick attachment and feeding is disrupted, preventing pathogen transmission. For this reason, we have done a comparative analysis of cement from both species of tick (*I. scapularis* and *A. americanum*) to identify protein similarities and potential vaccine candidates. Tick cement was collected from both species before and after feeding, from male, female, and nymphal ticks, and submitted for LC-MS/MS analysis. The proteomic profile of all collected samples was then analyzed bioinformatically through an in-house pipeline. From this comparison, we have identified multiple groups of proteins that are shared among both species of tick across all collections. These groups of proteins could have the potential to serve as anti-tick vaccine candidates, offering protection from multiple tick species and therefore multiple pathogens.



Developing an Immunogenic and Cross-Protective Flavivirus mRNA Vaccine

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Flaviviruses cause >400 million infections annually and can cause significant birth defects and neurological disability. Climate change is increasing flavivirus outbreak potential, and while vaccines against individual flaviviruses are in development, most are not approved, and none offer cross-protection against viruses with overlapping endemicity. Prior studies indicate that ZIKV envelope (E) protein may protect against related flaviviruses. This study aims to develop a cross-protective flavivirus mRNA vaccine targeting the highly conserved flavivirus E protein and assess immunogenicity in mice. Three ZIKV E mRNA candidate vaccines were generated with secreted, membrane-bound, or ubiquitin signal sequences to direct differential localization or processing. In vitro expression was confirmed by immunofluorescence and Western blotting. Vaccines were formulated in lipid nanoparticles as monovalent or multivalent constructs. C57BL/6 mice (n=12) received prime and boost immunizations of E constructs or eGFP controls 21 days apart. Sera were collected prior to each immunization. Sera and spleens were harvested 21 days post-boost. Splenocytes were stimulated with E peptide pools and T-cells were quantified by flow cytometry. Total ZIKV E-specific IgG antibodies were quantified by ELISA. Splenocytes from the secreted and membrane-bound E vaccine groups generated significantly higher antigen-specific Th1 CD8+ T-cell responses compared to controls. The same constructs elicited 3-fold higher total E-specific IgG titers compared to controls ($p < 0.05$), while the ubiquitinated construct was not statistically different from controls. Ongoing work is characterizing neutralizing antibody titers against ZIKV and other flaviviruses by plaque reduction neutralization tests as a measure of cross-protective potential. Results indicate that our ZIKV E protein mRNA vaccine elicits robust cell-mediated and humoral immunity in mice. Future studies will assess protection against ZIKV, dengue, and West Nile virus infections and identify correlates of protection. The goal of this work to generate an effective, safe, cross-protective flavivirus vaccine that can be readily adaptable for outbreaks.



Within-Herd Transmission Dynamics of Highly Pathogenic Avian Influenza H5N1 in U.S. Dairy Cattle: A Modeling Approach

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While H5N1 has historically been characterized by sporadic avian-to-mammal spillover, its recent establishment in dairy cattle suggests a shift toward sustained, high-intensity intra-herd transmission. Hypothesized transmission routes include the mechanical transfer of contaminated milk via milking equipment, environmental exposure to aerosols, and behavioral "mouth-to-teat" cycles. We developed a mathematical model of within-herd transmission of H5N1 in dairy cattle. We calibrated our model to data from a prospective cohort study of a large commercial dairy farm in Ohio using a Bayesian inference method. We then extended the model to understand the individual contributions of lactation-related and non-lactation-related transmission. Lastly, we adapted the model to evaluate the impact of intervention measures such as increased biosafety and a potential vaccine. Model calibration estimated a basic reproduction number (R_0) of 18.2 (95% CrI: 5.05–44.35). The median attack rate for all transmission routes combined was 99.87% (95% CrI: 98.74%–99.94%). Notably, the lactation route alone showed an attack rate of 99.86% (95% CrI: 95.80%–99.94%), compared to 41.02% (95% CrI: 18.51%–76.09%) for non-lactation routes. Our analysis indicated that an 80% efficacious vaccine alone would reduce the median attack rate by only 15.2% (95% CrI: 0.2%–99.8%). However, combining vaccination with biosafety measures that reduce transmission by 50% resulted in a 95.0% (95% CrI: 8.1%–99.9%) reduction. Because the attack rate for the virus is high, our analysis shows that vaccination alone may not be sufficient to mitigate the spread of the virus and will need to be combined with targeted biosecurity and biosafety measures. Identification of the transmission route for lactating cows is a priority to develop targeted biosecurity measures.



Thursday, July 9, 2026

1:00-3:00 Session VII: Infectious Disease Testing and Diagnostics

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



Source of image: <https://www.massgeneral.org/assets/MGH/images/pathology/lab-test-image-1.jpg>



A Metatranscriptomics Approach for Monitoring Arthropod-Borne Pathogens in Texas

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Surveillance functions as an early warning system for pathogen introduction and circulation, enabling timely mitigation by public health agencies. Current vector surveillance and clinical diagnostic strategies rely heavily on pathogen-specific assays, limiting detection capabilities. Unscreened, novel, and emerging pathogens are underreported or entirely missed. This study sought to define circulating viruses across South-Central Texas. Mosquito specimens (N=207) collected between 2021 and 2025 from Harris, Hays, Travis, Comal, and Fayette counties in Texas were analyzed using a metatranscriptomic viral discovery pipeline. Nucleic acid was extracted from specimens, and high-throughput Illumina RNA sequencing was performed. Reads underwent taxonomic classification using Kraken2, followed by assembly into contigs and scaffolds. Translated open reading frames were aligned against the NCBI Clustered Non-Redundant protein database using DIAMOND. Sequences were categorized based on similarity metrics into high-confidence known viruses, putative novel viruses, and unclassified sequences. A curated dataset was generated of assembled sequences representing the viruses present in the tested mosquito specimens. Samples from Hays, Travis, Comal, and Fayette counties are undergoing analysis for temporal and geographic variation in mosquito viromes. Our analysis of Harris County samples determined distinct viromes in *Culex quinquefasciatus* and *Aedes aegypti* collected at the same location, and that the virome within species changes over the course of the season, supporting the need for longitudinal mosquito collection for surveillance efforts. In addition to detecting common regional pathogens, such as West Nile virus, we detected emerging viruses with unknown pathogenic potential, including a suspected equine pathogen, *Alphamesonivirus cavallyense*. We are generating a pure viral isolate of *A. cavallyense* for additional testing. Integrating metatranscriptomics into mosquito surveillance advances a One Health framework by defining and characterizing the ecology of arthropod-borne pathogens affecting humans, wildlife, and livestock. Expanding surveillance beyond pathogen-specific assays strengthens early detection capacity and improves regional preparedness for emerging vector-borne disease threats.



The Defense Food Analysis and Diagnostic Laboratory's Advances in Infectious Disease Testing and Diagnostics

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The Defense Food Analysis and Diagnostic Laboratory (FADL) protect U.S. Service Members and their Families through innovative, adaptive, timely and accurate testing of all food, water, and diagnostic submissions for DoW 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 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 DoW-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.



Rapid Detection of blaCTX-M ESBL-Producing Enterobacterales in Canine Urine

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Lower urinary tract infections (UTI) are a common reason for presentation of dogs and cats for veterinary care. Zoonotic transmission of Enterobacterales, such as *E. coli*, from dogs to humans has been documented, making detection of antimicrobial resistant Enterobacterales, including both extended-spectrum beta-lactamase (ESBL) producing Enterobacterales (ESBLs) or carbapenemase producing Enterobacterales (CPE), in veterinary patients important for human health. Rapid detection of ESBLs from urine of veterinary patients has implications for antimicrobial drug selection and interventions to prevent zoonotic transmission. Residual urine specimens from dogs presented to a veterinary teaching hospital between March 18, 2024, and November 30, 2025, were used to compare the results of bacterial culture with a lateral flow device (LFD) for detection of blaCTX-M ESBLs in canine urine. A total of 146 urine samples met the inclusion criteria of presence of leukocytes on urinalysis and were tested. Of these, nine tested positive for the blaCTX-M enzyme using the LFD, while 13 were considered ESBL-positive using culture. The four specimens with discordant results had less than 10,000 cfu/mL (three samples) or were determined to carry blaCMY-2 but not blaCTX-M and were therefore not ESBL-positive. The prevalence of blaCTX-M ESBL-positive samples in this study was estimated at 8.2% (95% CI: 4.3 – 13.9%). The sensitivity of the LFD was estimated at 75% (95% CI: 42.8% to 94.5%) while the specificity of the LFD was estimated at 100.0% (95% CI: 97.3% to 100.0%). At the prevalence levels present in this study, the predictive value of a positive test was 100% (95% CI: 66.4% to 100%) while the predictive value of a negative test was 97.8% (95% CI: 93.7% to 99.5%). An advantage of the LFD was that it could be performed at point-of-care, and results were available three days earlier than culture.



Metatranscriptomic Survey of *Ornithodoros turicata* Soft Ticks in Texas Reveals New Vector-Microbe Associations

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Ornithodoros turicata is a medically important soft tick that transmits human relapsing fever and could vector African swine fever virus in Texas. Once considered primarily rural or peridomestic, *O. turicata* is increasingly found in dense urban settings in the southwestern United States and Mexico, elevating its public health significance. Despite its recognized role in relapsing fever transmission, the broader pathogen landscape of *O. turicata* remains largely unexplored, especially given that other argasid ticks can transmit viruses and parasites. To characterize microbial associations beyond relapsing fever spirochetes, we performed total RNA sequencing of 144 *O. turicata* ticks from seven Texas populations and used a metatranscriptomics analysis pipeline capable of detecting bacteria, viruses, and eukaryotic parasites. Viral diversity was limited; however, a novel rhabdovirus was detected at five sites, with prevalences ranging from 20–95%. Phylogenetic analysis indicated that this virus is related to alpharicinrhaviruses described in hard ticks. *Trypanosoma cruzi* was identified at three sites (15–55% prevalence) and were classified as discrete typing unit TcI. A novel Onchocercidae filarial organism was detected at four sites (10–65% prevalence), and further taxonomic characterization is ongoing. Despite successfully isolating the relapsing fever spirochete, *Borrelia turicatae*, from three of seven tick populations, we did not detect relapsing fever *Borrelia* by sequencing. These findings expand our understanding of microbial associations with *O. turicata*, including the first report of *T. cruzi* in field-collected ticks, a novel rhabdovirus, and a novel Onchocercidae organism. Ongoing studies are evaluating the ability of *O. turicata* to transmit these microbes to mammalian hosts and the sensitivity of metatranscriptomics for detecting relapsing fever *Borrelia* in soft ticks. By characterizing the microbes associated with *O. turicata* and clarifying the vector's role in their maintenance and transmission, we can more accurately assess the public health risk *O. turicata* poses to humans and animals.



Thursday, July 9, 2026

**Scientific Poster Session
3:00-4:00**

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Thursday, July 9, 2026

4:00-5:00 Session VIII: One Health

Moderator: Kelly Broussard, MPH

Texas Department of State Health Services, Austin, TX

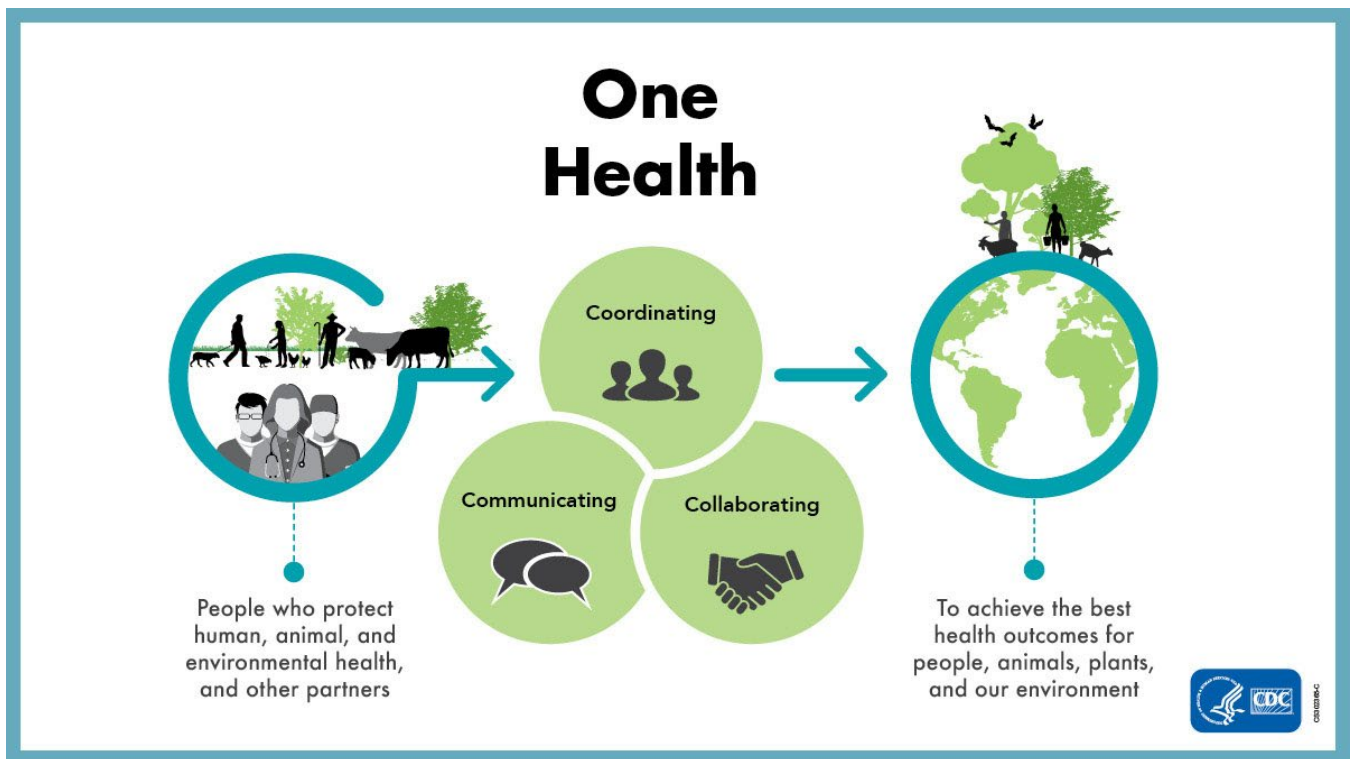


Image source: <https://www.cdc.gov/one-health/about/index.html>



The Role of a Medical Entomologist in One Health

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One Health describes the interdisciplinary collaboration of individuals involved in public, animal, ecological and environmental health. Somewhere within these disciplines falls the role of medical entomology. While it seems medical entomologists easily fit into the public health realm of this paradigm due to the nature of zoonotic vector-borne diseases, they may also be intertwined in disciplines outside of public health. Sustainability of vector control programs relies heavily on the cross-over between medical and urban pest entomology concepts. This presentation will cover the crossovers of medical entomology, pest control, human health, and comfort, economic impacts, and policy planning at local, state, and national levels.



One Health Topic (To Be Determined)



Thursday, July 9, 2026

5:00 – 7:00 J.V. Irons Keynote Lecture & Reception

Moderator: Bonny Mayes, MA, E-RYT 200, YACEP

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, July 9, 2026

J.V. Irons Keynote Lecture



Caryn Bern, MD

Dr. Bern has worked on Chagas disease since 2003, focusing on epidemiology, diagnostics and clinical management in the United States and Latin America. In Peru and Bolivia, she participated in field and hospital-based studies on Chagas disease diagnosis, epidemiology, congenital Chagas disease, vector control and evaluation of potential cardiac biomarkers. In the U.S., her work has focused on recommendations for diagnosis and management of chronic *T. cruzi* infection, Chagas cardiomyopathy, congenital Chagas disease and infection in the immunocompromised host, aimed at improving the knowledge base of U.S. clinicians, as well as mapping and disease burden estimates. She has co-authored more than 50 articles on Chagas disease including publications in JAMA, Clinical Microbiology Reviews, Clinical Infectious Diseases, Emerging Infectious Diseases and Journal of Infectious Diseases.



KEYNOTE ADDRESS: Chagas Disease in Texas and Beyond

Caryn Bern, MD

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Description of Content:

- *Trypanosoma cruzi* transmission dynamics are complex and show a high degree of geographic variability.
- Rational design of interventions to decrease transmission requires knowledge of local vector ecology, infection reservoirs, and routes of transmission to humans.
- Targeted screening based on known risk factors can enable earlier antiparasitic treatment and better management of Chagas disease sequelae.



Friday, July 10, 2026

8:00-10:00 Session IX: Case Reports

Moderator: Briana O'Sullivan, MPH

Texas Department of State Health Services, Austin, TX



Source of image: <https://www.highyieldmed.org/how-to-write-a-case-report/>



Chronic Loiasis Presenting as a Migratory Conjunctival Worm Years After Exposure

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Loiasis, caused by *Loa loa*, is endemic to West and Central Africa. Adult worm migration across the conjunctiva is a hallmark but is rarely observed outside endemic regions, and delayed manifestations can complicate diagnosis and management. A 19-year-old woman from Equatorial Guinea presented to the emergency department in December 2025 with complaints of an “eye worm” and intermittent ocular irritation and pain, with similar recurrent episodes since age five. She was admitted for two days. Ophthalmologic examination revealed a motile worm beneath the right upper eyelid; extraction was unsuccessful due to migration. Laboratory evaluation demonstrated eosinophilia and microcytic anemia. Blood tests suggested *Loa loa* infection, and a thick blood smear confirmed microfilariae. Serologic testing at the National Institutes of Health was positive for *Loa loa*-specific IgG and IgG4 antibodies. Due to the risk of severe inflammatory reactions with high microfilarial loads, antiparasitic therapy was deferred pending quantification by experts at Baylor College of Medicine and NIH. Microfilarial load was below high-risk thresholds, and treatment with ivermectin and albendazole for 21 days was initiated in January 2026. At follow-up in February 2026, symptoms were resolved completely. Initial misidentification of microfilariae as *Plasmodium* species delayed diagnosis, confirmatory evaluation, and initiation of appropriate treatment, a challenge in malaria-endemic settings due to laboratory misinterpretation and high prevalence of empiric malaria treatment. Although loiasis is not a reportable condition in Texas, this case underscores the potential for chronic infection decades after exposure and highlights how routine malaria testing practices can obscure filarial infections. Confirmatory parasitology evaluation, multidisciplinary coordination, and continued vigilance are essential for individuals from endemic regions, even after long-term residence in non-endemic areas.



Hantavirus, or Something Like it, in Travis County, Texas 2025

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Hantaviruses (genus *Orthohantavirus*; family *Hantaviridae*) are transmitted from infected rodent's saliva, feces and urine to humans. While certain strains cause severe diseases such as hantavirus pulmonary syndrome (HPS) or hemorrhagic fever with renal syndrome (HFRS), mild infections may be underreported due to nonspecific symptoms. Travis County has had only one confirmed case since 2004, and it was associated with out-of-area exposure. The majority of reported cases occur in the western United States. Nationally, 864 HV disease cases have been reported from 1993 to 2022.

On November 13, 2025, Austin Public Health (APH) was notified of a positive hantavirus IgM in a 29-year-old female presenting with fatigue, eye irritation, and mild cough following occupational exposure to rodent droppings at a workplace experiencing active rat infestation. APH coordinated with the Texas Department of State Health Services, the Centers for Disease Control and Prevention, the New Mexico Department of Health, and the University of New Mexico to guide clinical management and guidance for those affected by the infestation. Public health actions included a building inspection with City Code Enforcement, distribution of symptom surveys, and targeted education for employers.

The patient recovered without developing severe disease. Three individuals underwent hantavirus serologic testing; only the index patient had a positive IgM. No confirmed cases were identified, and the index case did not meet case definition. The rodent infestation was remediated by licensed pest control services and employers demonstrated high engagement with public health recommendations.

This investigation highlights the potential for hantavirus exposure in regions where it is considered uncommon, and the challenges of case ascertainment. Limited certified testing availability and lack of standardized case identification processes exposed gaps in current procedures. Interdepartmental collaboration, provider education, and community outreach regarding rodent exposure prevention are critical to improving identification and assessment of hantavirus risk in Travis County.



Novicidemia vs. Tularemia Revisited: A Suspected Novicidemia in an 8-Year-Old Female

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An 8-year-old female presented with 2-weeks history of persistent fever/chills, accompanying headache, severe malaise, anorexia & weight loss, nausea/vomiting, axillary lymphadenopathy and productive cough. The patient was hospitalized at a local children's hospital for 4 days while the illness was worked up. Thoracic radiography revealed mild perihilar bronchovascular prominence consistent with infectious bronchiolitis or reactive airways disease. The patient lives on a farm with horses, cows, goats, chickens, pigs, dogs, cats and a gecko. There was no travel outside the patient's local area in Texas and no contact with wild animals, tick attachments or fly bites. Patient's mother advised they have an above ground pool and that it is chlorinated but that the patient swam in it when it was not being chlorinated and was not being properly taken care of and was 'dirty'. A whole blood sample submitted to commercial laboratory for analysis was reported to the Local Health Department (LHD) with a result of microbial cell-free DNA detection for *Francisella tularensis*. Follow-up discussion with the commercial lab revealed the sample had only 22 microbial cell-free DNA fragments (i.e., not much). The commercial lab further advised that given the limited DNA in the sample, they could not confirm the *subspecies*, but their analysts advised the observed sequences appeared more consistent with subsp. *novicida* than the other subspecies (i.e., *tularensis*, *holarctica* and *mediasiatica*). With the absence of exposure history and an [appropriate lab test](#), the LHD closed the investigation as "not a case" and recommend the healthcare provider follow-up with *F. tularensis* serology. The patient responded positively with doxycycline and no additional diagnostic were shared. This case represents challenges assessing newer diagnostics techniques, environmental bacteria and immediately reportable conditions.



Soil, Spores, and Surprise: Travel-Associated Cutaneous Anthrax with Livestock Exposure

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Anthrax is a rare zoonotic disease primarily caused by *Bacillus anthracis* and, less commonly, by other toxin-producing *Bacillus* species. These spore-forming organisms persist in soil worldwide and typically infect livestock and wildlife; humans acquire infection through contact with contaminated animals, animal products, and environmental reservoir. In September 2025, Texas Children's Hospital (TCH) reported a suspected case of cutaneous anthrax to Houston Health Department (HHD), prompting a multi-agency epidemiologic investigation to confirm diagnosis, identify risk factors, and prevent secondary transmission. HHD epidemiology team conducted detailed caregiver interviews to assess travel and exposure history. Clinical data was abstracted from medical records. In collaboration with HHD laboratory, TCH, Texas Department of State Health Services (DSHS), and CDC, affected tissue underwent phenotypic and molecular testing. Skin biopsy specimen was forwarded to CDC for confirmatory immunohistochemical analysis. Previously healthy two-year-old female traveled to Mexico two weeks prior to presentation; played with livestock. She sustained a superficial abrasion to the right lateral knee after falling on concrete. No direct soil exposure, handling of animal hides/carcasses, or contact with sick livestock was reported. Five days post-injury, she developed fever (103°F), localized swelling, erythema, and progressive ulceration with central dark discoloration and increased joint swelling. The patient was hospitalized, treated with antibiotics, and discharged after four days. Molecular testing identified toxin-producing bacteria in *B. cereus* group; PCR for *B. anthracis* was equivocal; *B. anthracis* gamma phage susceptibility was negative (resistant). CDC ruled out *B. anthracis*, diagnosis of cutaneous anthrax from a non-anthraxis *Bacillus* species made. No secondary cases were detected. This case underscores the interconnectedness of human, animal and environment, diagnostic complexity, and public health relevance of toxin-producing, non-anthraxis *Bacillus* infections. Disrupted skin integrity with environmental exposure was the most plausible transmission pathway. Rapid interagency coordination across clinical, laboratory and public health partners enabled definitive diagnosis and appropriate management.



Friday, July 10, 2026

10:30-12:00 Session X: Tickborne Disease

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



Ornithodoros turicata ticks. Photo provided by Job Lopez,
Baylor College of Medicine



Did the Prairie Dogs Volunteer as Tribute?

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Black-tailed Prairie dogs (*Cynomys ludovicianus*) are native to short-grass prairie habitats of the western North American plains. In Texas, prairie dogs are found in the Panhandle, and in western portions of the state.

Sporadic epizootics of plague (*Yersinia pestis*) have decimated prairie dog colonies throughout the plains of Texas. Prairie dogs lack natural immunity to plague, and a colony may experience over 95% mortality within 78 hours of infection with plague. Tularemia (*Francisella tularensis*) has also been implicated in prairie dog colony die-offs.

The CDC identifies *Y. pestis* and *F. tularensis* as high priority biological agents as they pose significant threats to public health and safety. The sudden loss of a colony is therefore a call for concern due to the public health implications.

A prairie dog die off was reported to the Texas Department of State Health Services on 8/17/2025. Active surveillance of burrows detected numerous soft ticks of several life stages. The soft ticks were submitted to Baylor College of Medicine where the tick species was confirmed as *Ornithodoros turicata* (*O. turicata*). Polymerase chain reaction was used to determine the presence of *Y. pestis* and *F. tularensis* in tick samples, but results were negative. Molecular testing of these samples was expanded to metatranscriptomics, which detected a high prevalence of a novel *Babesia* species related to *Babesia duncani* and *Babesia conradae*.

Babesia, an intraerythrocytic protozoan parasite, affects a wide range of domestic and wild mammals, birds, and humans. The host-vector relationship dynamic may involve several species of hard ticks, and the pathogenesis is similar despite the host and hard tick species. This is the first reported observation of *O. turicata* harboring a novel *Babesia* species, related to *B. duncani* and *B. conradae*.



Addressing Challenges in Molecular Surveillance: Examining the Influence of Tick and Spirochete Biology on Relapsing Fever Spirochete Detection

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Borrelia turicatae is a relapsing fever (RF) spirochete spread by *Ornithodoros turicata* ticks. This pathogen is often neglected and can go unnoticed by health care providers, partly because of the unique biology of both the tick and the bacteria. The ticks feed quickly (2 to 60 minutes), are rarely found on the host, and can endure years of starvation. Consequently, endemic areas for *O. turicata* are poorly defined and people do not realize that they have been parasitized. Further confounding health care provider awareness is a poor understanding of the prevalence of *B. turicatae* in naturally infected tick populations. Both published and unpublished studies seldom detect RF spirochetes in ticks when using molecular methods such as metagenomics, metatranscriptomics, or qPCR. However, our research led us to reason that current techniques for detecting *B. turicatae* in ticks might be limited. They often overlook the life cycle of the pathogen and vector, which includes the infectious dose imbibed by ticks, spirochete depletion from extended tick starvation, and bacterial replication after blood feeding. To address these factors, we infected cohorts of *O. turicata* with a high (10,000 spirochetes per μ l) and low (100 spirochetes per μ l) dose of *B. turicatae*. Over the following year, we are assessing *B. turicatae* loads throughout the vector's life cycle (e.g., prolonged starvation and blood feeding). Our findings will likely underscore the need to better align molecular surveillance with the biological dynamics of RF spirochetes in the vector.



The Dynamics and Epidemiological Implications of Vertical Transmission of *Borrelia turicatae* from the Argasid Vector, *Ornithodoros turicata*

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Ornithodoros ticks are long lived (>20 years) vectors of several pathogens of medical and veterinary importance, including tick-borne relapsing fever (RF). *Ornithodoros turicata* is found throughout the Southern United States and Mexico and transmits *Borrelia turicatae*, which is responsible for RF in the Americas. Spirochetes colonize *O. turicatae* when the tick ingests blood from an infected vertebrate host. The pathogens are maintained through the molt (transstadial transmission) and subsequently transmitted during its next bloodmeal. Furthermore, *B. turicatae* is capable of being transmitted from adult female ticks to their progeny; however, we do not know if there are phenotypic differences in transovarial transmission (ToT) between strains of *B. turicatae*. Understanding the maintenance cycle of RF *Borrelia* within tick populations is critical, particularly given the growing ecological interaction between these ticks and humans. To address ToT, we took two approaches. First, we used a laboratory tick-mouse model to infect female *O. turicata* with isolates of *B. turicatae*. Second, we evaluated field collected female *O. turicata* that were naturally infected with *B. turicatae*. From both groups, female ticks were allowed to reproduce, and their offspring were reared to 2nd instar nymphs. These nymphs were fed on naïve mice, and we assessed spirochete infection in murine blood. To date, we confirmed ToT of two *B. turicatae* laboratory isolates and from three populations of naturally infected field collected ticks. As efforts persist in clarifying ToT, a more comprehensive understanding of the maintenance cycle of *B. turicatae* will be achieved.



POSTER

Modeling and Evaluating the Impact of Integrated Public Health Interventions on West Nile Virus Incidence in Harris County, Texas (2024–2025)

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West Nile virus (WNV), a mosquito-borne arbovirus, was a significant public health concern in Harris County, Texas, in 2024. The county experienced a high case count due to an unusually wet summer that enhanced mosquito breeding conditions. This study evaluated the impact of Harris County's integrated WNV prevention initiative, including ultra-low volume (ULV) spraying, larviciding, home inspections, community outreach, and enhanced epidemiologic response, on reducing WNV incidence in 2024 and 2025.

This retrospective study used laboratory-confirmed human WNV cases, mosquito pool testing (qPCR), records of vector control interventions, and environmental data. Difference-in-Differences (DiD) and Interrupted Time Series (ITS) models assessed case trends before and after ULV spray events, adjusting for confounders. Integrated response activities included rapid epidemiologic case interviews to identify exposure locations, followed by collaboration with the Mosquito Vector Control Division (MVCD) for notification, targeted property inspections, pesticide application when appropriate, and dissemination of community-level prevention guidance. This early intervention strategy was implemented to contain WNV transmission.

In 2024, Harris County Public Health (excluding the City of Houston) reported 56 human WNV cases, and 680 mosquito samples tested positive. ULV spray events began on August 9, 2024, covering approximately 81,640 acres in high-risk areas. Before spraying, 41 cases were reported in June and July; after spraying, cases declined to 15 from August through December. In 2025, 216 positive mosquito pools and 10 human cases were reported, underscoring the continued importance of surveillance and rapid response. DiD analysis demonstrated a 63% reduction in WNV incidence in sprayed areas, from 11.83 to 4.74 cases per 100,000 population. Although unsprayed areas showed seasonal declines, the additional reduction suggests an independent intervention effect. ITS analysis revealed a significant downward trend following intervention. These findings highlight the importance of sustained surveillance, integrated vector control, and early public health intervention to prevent future outbreaks.



POSTER

***Culicoides* Surveillance at Urban Green Spaces in Houston, Texas**

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Culicoides, commonly called biting midges, are tiny blood feeding flies with painful bites. In addition to being a nuisance, *Culicoides* transmit pathogens of human and animal concern worldwide. In the United States, ruminants (cattle, sheep, horses, and white-tailed deer) can become infected with bluetongue virus, epizootic hemorrhagic disease virus, or vesicular stomatitis virus following an infected *Culicoides* bite. These diseases can cause indirect and direct economic losses for producers through reductions in animal product yield, fetal abortions, or death. Oropouche virus (OROV), which affects humans, is endemic to the Amazon Basin. During an outbreak from late 2023-2024, non-travel related cases were reported as far north as Cuba while travel-related cases were diagnosed in the United States. Oropouche virus can be spread through the bite of infected *Culicoides paraensis* and some mosquito species. Infections typically present as flu-like symptoms with an extended recovery period, but severe complications such as meningoencephalitis or adverse fetal outcomes can occur in rare cases.

Despite the impacts of midge-borne diseases, *Culicoides* remain an understudied vector in the United States. Few studies have been performed looking at *Culicoides* species presence in Texas, especially in the Gulf Coast region. Therefore, we began *Culicoides* surveillance at urban green spaces in Houston with potential risk for the introduction of *Culicoides*, their associated pathogens, or high levels of human and animal interactions. Surveillance will be conducted from September 2025 to September 2026 at five sites. To date, over 170 specimens representing at least 17 species have been morphologically identified. Possible vector species, *Culicoides paraensis* and *Culicoides stellifer*, have been collected at multiple sites. Genetic confirmations of the morphological identifications will be performed. Once complete, we aim to create resources to help public health officials understand risks for midge-borne diseases and assist with morphological identification of regional species.



POSTER

Investigation of Transplant-Associated West Nile Virus Cluster in Texas, 2024

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Many zoonotic diseases pose a risk of transmission via donated blood products, tissues, and organs, despite donor screening efforts. West Nile Virus (WNV) is of particular concern because organ donor WNV screening tests are not nationally required, WNV cases are on the rise thereby exposing more potential organ donors, and research demonstrates possible sequestration of live WNV in the kidneys.

In 2024, the Texas Department of State Health Services (DSHS) Zoonosis Control Branch (ZCB) collaborated with CDC, the DSHS Healthcare Safety Unit, and regional and local partners to investigate possible organ-based exposure in two Texas kidney recipients who developed fatal neuroinvasive WNV disease. Traditional vectorborne and rare organ-transmitted exposure routes were fully investigated through additional public health testing, RNA sequencing, and organ recipient tracebacks.

In 2024, DSHS identified WNV infection by PCR testing in a recent kidney recipient via transplantation (subsequently referred to as “Kidney 2” recipient). Upon investigation, the kidneys and the liver from the deceased donor were transplanted to three recipients in Texas. The donor was negative by nucleic acid amplification screening in blood for WNV, which demonstrated a lack of systemic viremia but which may not detect virus sequestered within organs. The liver recipient remained uninfected and well throughout this investigation. Kidney 2 recipient’s and the donor’s WNV infection were confirmed by public health laboratory testing over the next few months while Kidney 1 recipient remained initially asymptomatic. However, 5 months post-transplant, Kidney 1 recipient became symptomatic and subsequently died. Kidney 2 recipient died from their illness and shortly afterward, Kidney 1 recipient’s WNV infection was confirmed by public health testing. Sequence data from laboratory testing were available for each recipient but not the donor. Sequence analysis revealed that the WNV strains in each recipient were highly related (98.8%).

The small changes between the recipient strains are better explained by replication of the virus in each patient than by two separate natural infection events. Genetic evidence demonstrated that both kidney recipients acquired their WNV disease through organ transplantation rather than natural exposure. Kidney 2 recipient’s incubation period was the longest known for a kidney-derived WNV transmission event.



POSTER

Disseminated Cutaneous Sporotrichosis with Progressive Fungal Osteomyelitis in an Immunocompromised Host

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Disseminated sporotrichosis is an uncommon but severe manifestation of infection with *Sporothrix* species, typically occurring in immunocompromised hosts. We present a fatal case of disseminated fungal osteomyelitis complicated by septic shock in a 57-year-old man with type 2 diabetes mellitus, cirrhosis, and presumed rheumatoid arthritis on immunosuppressive therapy.

The patient developed a progressive ulcerative and eschar-forming rash involving the hands, arms, face, and lower extremities several months after immunosuppression. He denied significant soil or gardening exposure but reported being scratched by a stray cat, our suspected source of inoculation. Imaging demonstrated destructive changes concerning for osteomyelitis of the distal femur, proximal tibia, fibular head, and patella of the left leg, as well as involvement of the left third phalanx. CT revealed innumerable hypoattenuating hepatic lesions. Skin biopsy at an outside facility showed granulomatous dermatitis with mold growth on culture (not initially speciated).

Fungal evaluation showed persistently elevated serum 1,3- β -D-glucan with negative testing for histoplasmosis, coccidioidomycosis, cryptococcosis, and aspergillosis. Plasma microbial cell-free DNA testing (Karius) detected *Sporothrix* species, prompting initiation of liposomal amphotericin B. Definitive diagnosis was confirmed when *Sporothrix* grew from left knee, from both cyst fluid and bone specimens. Step-down therapy was limited by antifungal intolerance. Itraconazole was reduced to once daily due to severe gastrointestinal side effects. Subsequent posaconazole therapy was notable for altered mental status and visual hallucinations. He ultimately developed progressive osteomyelitis requiring left above-knee amputation. Despite amputation, the patient was found to have a positive culture of *Pseudomonas aeruginosa* from both left leg and hand, resulting in septic shock and ultimately death.

This case underscores the aggressive nature of zoonotic sporotrichosis in immunosuppressed patients, the diagnostic value of microbial cell-free DNA testing, antifungal tolerability, and superimposed bacterial infection resulting in death.



POSTER

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

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The Defense Food Analysis and Diagnostic Laboratory (FADL) has a rich 80-year history of providing trusted expertise and technical knowledge to support critical missions within the Department of War. The FADL is comprised of 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). 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. The Rabies Fluorescent Antibody Virus Neutralization (FAVN) test is our most requested test. FAVN results are used to validate vaccine efficacy against rabies for Military Working Dogs (MWDs) and Privately Owned Animals (POAs). The Diagnostic Section also performs Direct Fluorescent Antibody Testing (DFA) on postmortem animal brain tissue for rabies confirmation. The Diagnostic operations team provides continuous training offered to Veterinary Corps Officers and staff globally, decreasing error rate and increasing productivity in operational workflow. For the Year 2025, the Diagnostic laboratory analyzed over 9,000 FAVN serological samples and over 150 DFA brain tissue samples. These results described are achieved through exceptional quality control and meticulous efforts from all team members from “sample processing to resulting.” The FADL Diagnostic Section provides high-quality technical support, analyzing thousands of samples and supporting the Department of War. With professional personnel expertise and capabilities, the FADL Diagnostic Section is a vital asset, contributing to the safety and well-being of animals and personnel.



POSTER

Strongyloidiasis Epidemiology and Diagnostic Gaps in a Southern U.S. Safety-Net Health System

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Strongyloidiasis, with an estimated global burden of 300–600 million cases, is a common, potentially life-threatening neglected tropical disease caused by *Strongyloides* species, endemic in tropical and subtropical regions, including the southern US. It is underdiagnosed due to low provider awareness and imperfect diagnostics. The clinical standard diagnostic—multiple stool ova-and-parasite (O&P) tests—has poor sensitivity and is difficult for patients and laboratories to complete correctly; consequently, serologic testing is widely used despite subpar performance, particularly in immunocompromised hosts. This study aims to characterize *Strongyloides* prevalence and diagnostic use in a US health system serving a large at-risk population. We conducted a retrospective analysis of all patients tested via *Strongyloides* IgG between January 2022 and December 2024 across a safety-net health system serving the residents of Harris County, TX (Harris Health). We used Epic SlicerDicer to extract deidentified electronic health data, including serology and stool O&P results, demographics, and immunosuppressive medication use within 3 months of testing. We analyzed these data using descriptive statistics. 2,244 unique patients underwent *Strongyloides* IgG testing; 48.6% (1,091/2,244) of the cohort were women, the average age was 42.1 years, and 77.6% (1,741/2,244) of patients identified as Hispanic. 18.2% (408/2,244) had a positive *Strongyloides* IgG result; of these, only 26.5% (108/408) had concomitant stool O&P testing performed, of which only 2.8% (3/108) revealed *Strongyloides* larvae. Only 83.6% (341/408) of seropositive patients received standard-of-care treatment with ivermectin. 19.3% (79/408) of seropositive patients were prescribed an immunosuppressant within 3 months of the *Strongyloides* IgG testing encounter. Though strongyloidiasis is a common infection among Harris Health patients, stool O&P, the clinical diagnostic standard, is infrequently ordered. As new generation tests become available, comparisons of old and new diagnostics will help identify a high-performing screening strategy for US patients.



POSTER

Arbovirus Surveillance in Equines Using Diagnostic Testing from a Medical Diagnostic Laboratory

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West Nile Virus (WNV); Eastern Equine Encephalitis Virus (EEE); and Western Equine Encephalitis Virus (WEE) have severe morbidity and mortality in humans and horses due to their role as dead-end hosts. Equine surveillance is informative for epidemiological insight into human infections due to the shared mosquito vectors and transmission cycle. Records from clinical blood specimens were submitted for PCR and ELISA testing of WNV, EEE, and WEE at the Texas A&M Veterinary Medical Diagnostic Laboratory from 2013 to 2025 for the detection of these agents from 2013 to 2025. Descriptive statistics and spatial analysis were performed on the data for all organisms, with a particular focus on horses.

Of 6,538 WNV tests performed, test positivity was highest in horses (10.2%) and mules (9.8%). Of 2,828 EEE tests performed, test positivity was highest in horses (3.1 %) and mules (5.6%). No positives were detected for WEE from the 863 tests processed. For EEE, miniature horses/ponies (5.3%) and gaited walking horses (3.9%) had the highest positivity. For WNV, the highest positivity occurred in Quarter Horses (12%), unknown breed (9.1%), gaited walking horses (8.4%), draft horses (8.0%), miniature horses/ponies (7.9%), and Warmblood English performance horses (7.5%). Horses aged 1 to <5 years had the highest positivity for both WNV (20.3%) and EEE (4.8%). For horses, Public Health Region 3 had the highest WNV, and Public Health Region 5 had the highest EEE test positivity.

Horses in certain occupational roles and age groups demonstrate increased risk of arboviral infection, providing epidemiological signals relevant to veterinary practice and public health surveillance. Implementing a collaborative One Health approach and including equine surveillance in public health monitoring strengthens vector control planning, clinical awareness, and prevention strategies for both veterinary and human populations.



POSTER

Enteroid-Based Assessment of SARS-Cov-2 Host Range

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Although the COVID-19 pandemic has ended, SARS-CoV-2 remains a significant public health concern. The continued emergence of novel variants, particularly those arising from animal reservoirs with a potential spill back into human populations, poses ongoing risks. Understanding the host range of SARS-CoV-2 is therefore critical; however, knowledge of susceptible animal species, especially wildlife, remains limited.

Traditional approaches, such as experimental infections in live animals under BSL-3 conditions, are costly, time-consuming, and logistically challenging. Computational methods rely on known ACE2 sequences and still require biological validation, while pseudovirus assays assess viral entry but cannot distinguish between abortive and productive infections.

Although SARS-CoV-2 is primarily a respiratory pathogen, gastrointestinal infection and enteric complications are frequently reported. The viral entry factors ACE2 and TMPRSS2/4 are highly expressed in the intestinal epithelium, making the gut a relevant site for studying viral susceptibility. We employed species-specific intestinal stem cell derived enteroids (“mini-guts”) that recapitulate functional intestinal tissue to evaluate susceptibility and permissiveness to SARS-CoV-2 infection.

Enteroids derived from species previously reported as susceptible or resistant demonstrated robust viral replication in human and rhesus macaque cultures. In contrast, horse and pig enteroids were resistant to infection, while modest but productive replication was observed in goat, sheep, and cow enteroids. The feline enteroid tested did not support viral replication; however, this was the only cat enteroid in our collection that could be passaged following loss of mesenchymal cells, suggesting potential individual genetic differences in susceptibility that warrant further investigation.

Our findings validate enteroid cultures as a powerful platform for assessing the host range of SARS-CoV-2. Ongoing efforts focus on expanding this approach to wildlife species to support the development of strategic surveillance networks aimed at identifying high-risk hosts, monitoring viral evolution, and guiding interventions to prevent future spillback of novel variants.



POSTER

Descriptive Analysis of *Coxiella burnetii* Data at TVMDL, 2019-2026

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Coxiella burnetii is the obligate, intracellular causative agent responsible for worldwide Q fever cases. Few sources provide a current descriptive look at *C. burnetii* in human or animal populations. We present an analysis of animal-origin *C. burnetii* data generated at TVMDL from 2019-2026.

Analysis was conducted using data stored in TVMDL's laboratory information management system (LIMS). Based on laboratory protocol, submitter goals, and regulatory requirements, samples were run on one of three test types: rtPCR, ELISA, or IFA. A total of 16,849 test results were retrieved from 14,614 distinct specimens. Of the total results, 1,223 (7.26%) were "positive/detected," 96(0.57%) were "suspect" and 15,530 (92.17%) were "negative/not detected." Calendar year 2021 had the greatest number of test results at 2,823 (16.75%) and 2025 contained the greatest number of positive results at 334 (14.52%).

Most specimens were derived from livestock species commonly associated with Q fever such as sheep (7,418 [50.76%]), goats (5,343 [36.56%]) and cattle (1,148 [7.86%]). Analysis on sheep data shows that the most frequently submitted diagnostic test was ELISA (5,743[77.42%]). The test which most frequently yielded a positive result was IFA (502[17.23%]).

Exact animal location data is not always provided for specimens submitted to TVMDL. Thus, the geographic distribution was evaluated using an "as close as possible" approach based on available information for either the animal or submitting veterinarian, with most specimens originating from Texas.

Our review provides insight into the distribution of *C. burnetii* in the US by utilizing the passive surveillance data of samples submitted to TVMDL. Although diagnostic laboratory data is subject to referral bias, it remains a valuable tool in monitoring risk for zoonotic diseases such as Q fever.



POSTER

Process of Determining Whether WNV Infection is Linked to Recent Blood Transfusion

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Transmission of West Nile virus (WNV) through blood transfusion was first reported in the United States in 2021. Since then, the FDA and the Centers for Disease Control and Prevention (CDC) advised blood collection agencies and public health departments to investigate individuals suspected of having West Nile Virus infection linked to receiving a blood transfusion in the 4 weeks prior to their positive WNV test. Nonreactive minipools are released for transfusion, whereas reactive minipools prompt reflex testing of each individual donation and are excluded from donation. Although implementation of WNV donor screening has substantially improved blood safety, a residual risk of transfusion-associated WNV transmission persists.

In September 2025, a 60-year-old Asian male with a history of cancer was reported to Harris County Public Health (HCPH) after testing positive for WNV IgM within 30 days of receiving a blood transfusion. The patient had received four blood transfusions from four different blood donors over a three-day period. This temporal association prompted initiation of a traceback investigation to determine whether any implicated donor units had evidence of WNV infection.

The traceback investigation involved coordination among Texas state health officials, the CDC, HCPH, the hospital blood bank, and the regional blood center. Of the four transfused segments, two underwent WNV NAT minipool testing and the other additional two blood segments were screened individually for WNV. All four transfused blood segments tested negative for WNV by NAT.

Transfusion-associated WNV infection was ultimately excluded, as further diagnostic testing identified other causes for the patient's illness. This case highlights the continued importance of timely traceback investigations to ensure blood safety, even in the setting of comprehensive donor screening programs.



POSTER

State-Wide 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. In recent years, the geographic range of established tick species has expanded, and invasive tick species have emerged, reshaping the epidemiology of tick-borne disease. 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 integrates community-based collection with advanced molecular epidemiology techniques to characterize tick distribution and pathogen prevalence across diverse ecological regions of the state. Additionally, this study functions as a community resource, offering free tick identification and pathogen testing for individuals and empowers residents to contribute valuable data. We have solicited ticks from the public using a website and targeted social media advertisements. We also collaborated with 18 of the Texas Wildlife Management Areas run by Texas Parks and Wildlife to obtain ticks collected from hunter-harvested animals. A total of 1,068 ticks has been submitted for analysis from November 2023 to February 2025. These samples are comprised of 10 species submitted from 254 counties. Pathogen testing has identified 34% (363/1068) of ticks as *Rickettsia* positive, 7% (75/1068) as *Ehrlichia* positive, and no samples have tested positive for *Borrelia*. By leveraging community engagement and modern molecular tools, this citizen-driven surveillance model strengthens early detection capacity, enhances situational awareness, and supports more targeted public health responses to mitigate the growing impact of tick-borne diseases in Texas.



POSTER

Investigating the Prevalence of *Rickettsia* in Houston Animal Shelters

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Spotted Fever Group *Rickettsia* (SFGR) are of growing public health concern due to an increase in cases over the last two decades. SFGR includes *Rickettsia rickettsii*, the causative agent of Rocky Mountain Spotted Fever, which can be deadly if left untreated, as well as other pathogenic and endosymbiont rickettsial strains. We believe Texans are at increasing risk due to factors such as rising temperatures, increased urbanization, and changing land use patterns allowing for increased tick exposure. To better understand the risk of SFGR in Texas, ticks were collected from two Houston area animal shelters for identification and testing for *Rickettsia* spp. pathogens. A total of 697 ticks were collected over a two-year period. We identified five species of hard ticks and one species of soft tick parasitizing shelter dogs. Approximately 40% of ticks tested were positive for *Rickettsia*. Samples positive for *Rickettsia* were then sequenced to identify the specific species present. We identified both *Rickettsia parkeri* and *Candidatus Rickettsia andeanae* in *Amblyomma maculatum* ticks and *Rickettsia buchneri* in *Ixodes scapularis* ticks. We believe this data can help improve disease surveillance and public health preparedness for emerging rickettsial infections in Texas and across the US Gulf Coast.



POSTER

Comparing Mosquito Abundance and Species Diversity in BG-Sentinel and BG-Counter 2 Mosquito Traps in Houston, TX

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Houston's subtropical climate supports an abundant mosquito population and creates favorable conditions for arbovirus transmission. As climate change alters temperature, rainfall, and extreme weather patterns, Houston may become increasingly vulnerable to arbovirus outbreaks. Proactive vector surveillance is therefore essential for early detection, risk assessment, and outbreak preparedness. The objective of this study was to compare a standard BG-Sentinel trap with the BG-Counter 2 trap to evaluate differences in mosquito abundance, species diversity, and non-mosquito captures collected by both traps placed in parallel across Houston. Trapping was conducted between January 3, 2023, and January 22, 2026, with 218 paired trap-nights completed across 3 unique trap locations. We found that the BG-Counter 2 traps captured overall more mosquitoes and had slightly richer species diversity compared with the BG-Sentinel traps. While BG-Counter 2 traps are more expensive than BG-Sentinel traps, they more efficiently collected mosquitoes in urban environments.



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 on the conference website (www.diseasesinnature.com) and must be completed and submitted by midnight Friday, July 17, 2026, 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.

Commercial Support

This event received no commercial support.

Disclosure of Financial Conflict of Interest

- Sarah Hamer was a consultant for Pfizer.
- Michael Allen was a consultant for Memsel Corp.
- Sara Lawhon works with NG Biotech Laboratories in her development of lateral flow devices.

All financial relationships listed have been mitigated. No other speakers or planning committee members for this educational activity have financial relationships to disclose.

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Accreditation and Designation Statements (continued)

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A maximum of 17.5 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 17.5 CE hours in the clinical category for full attendance for veterinarians and for LVTs.