TEXAS
Health and Human Services

Texas Department of State Health Services

Arbovirus Activity in Texas
2019 Surveillance Report

March 2022

Texas Department of State Health Services
Zoonosis Control Branch

Overview

Viruses transmitted by arthropods such as ticks and mosquitoes are referred to as arthropod-borne viruses or arboviruses. Most medically significant arboviruses that naturally circulate in Texas are transmitted by mosquito vectors. Arboviruses reported in Texas may include California (CAL) serogroup viruses, chikungunya virus (CHIKV), dengue virus (DENV), eastern equine encephalitis virus (EEEV), Saint Louis encephalitis virus (SLEV), western equine encephalitis virus (WEEV), West Nile virus (WNV), and Zika virus (ZIKV), many of which are endemic or enzootic in the state.

In 2019, 127 reported human arboviral disease cases were attributed to DENV (58%), WNV (25%), CHIKV (15%), and ZIKV (2%) (Table 1). In addition, there were two cases reported as arbovirus disease cases which could not be diagnostically or epidemiologically differentiated between DENV and ZIKV in one instance and between DENV and WNV in another. Local transmission of DENV, EEEV, SLEV, WEEV, and WNV was documented during 2019 (Figure 1). No reports of CAL viruses were received during 2019. Animal infections or disease caused by EEEV, SLEV, WEEV, and WNV were also reported during 2019.

Transmission cycles of each virus depend on environmental conditions, the ecology of the vectors, as well as the human and animal hosts. Since Texas is such a large state, there are many diverse habitats statewide resulting in a range of vector abundance. Some viruses are endemic state-wide while some are only sporadically endemic in specific geographic regions. CHIKV, DENV, and ZIKV are maintained in cycles between *Aedes aegypti* or *Ae. albopictus* mosquitoes and human hosts. Though the estimated geographic range of these two mosquito species includes most of Texas, the ecological and environmental conditions to facilitate local transmission to humans are typically only present in the fall and early winter in the southernmost counties in Texas. Therefore, most human cases of these viruses are imported through travel from more strongly endemic country. Contrastingly, WNV and SLEV are considered endemic in all counties in Texas, though SLEV is less often detected in human or mosquito surveillance. WNV and SLEV mostly rely on *Culex* species mosquitoes and amplifying hosts including birds to maintain their transmission cycles that expose humans to the bite of an infected mosquito. The differences in transmission cycles between arboviruses strongly impacts the patterns of human disease in Texas and this is important context for interpreting human surveillance data.

Table 1. Year-End Arbovirus Summary, Texas, 2019

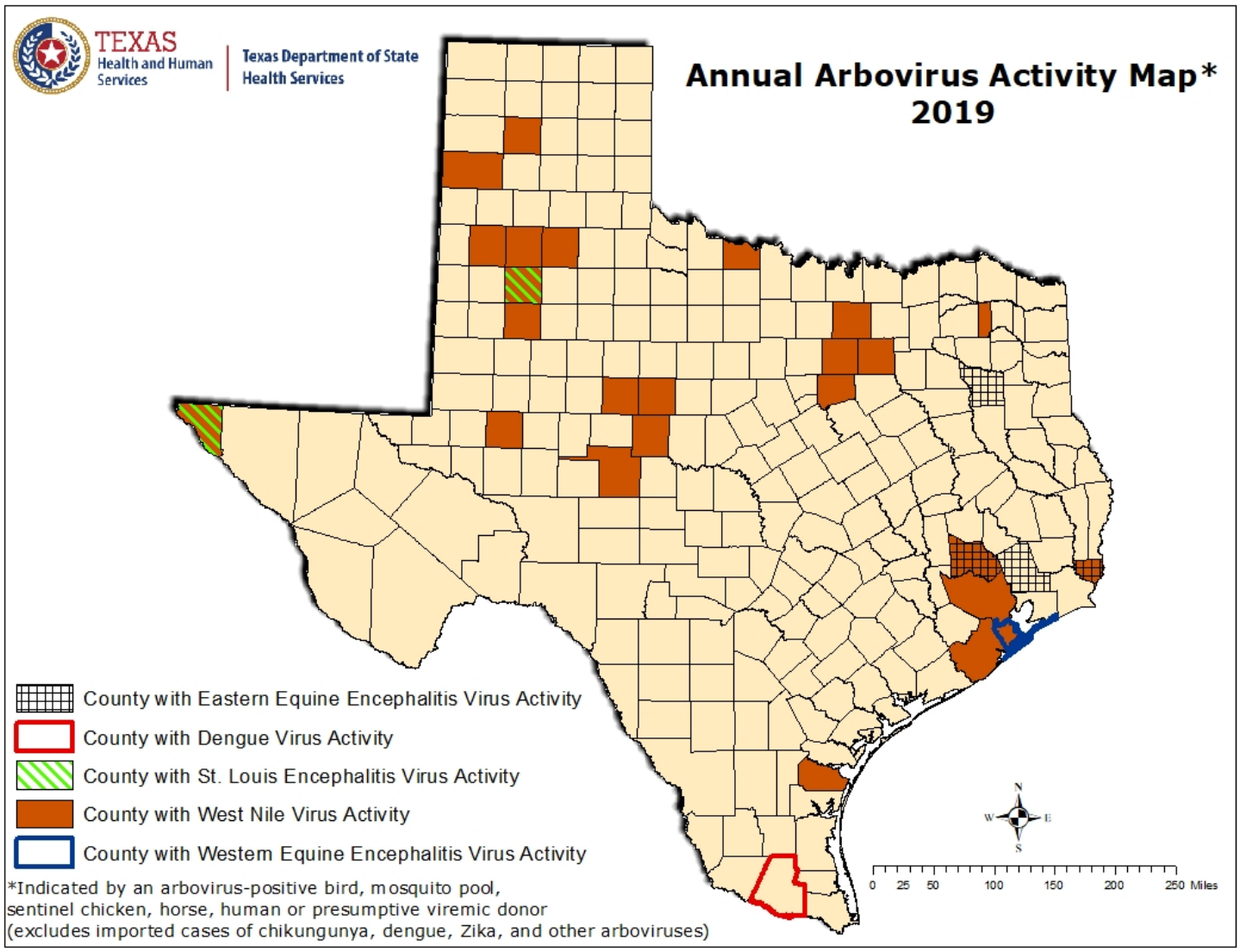
Arbovirus	Mosquito Pools	Avian	Veterinary	Sentinel Chicken	Human*					
					Fever	Neuroinvasive	Severe Dengue	TOTAL (Human)	Deaths	PVD‡
CAL	0				0	0		**0**	0	
CHIK	0				**19**	0		**19**	0	
DEN	0				**73**	0	**1**	**74**	0	
EEE	0	0	**6**	0	0	0		**0**	0	
SLE	**9**	0		0	0	0		**0**	0	
WEE	0	0		**2**	0	0		**0**	0	
WN	**133**	0	**2**	**1**	**8**	**24**		**32**	**4**	**4**
Zika**								**2**		
TOTAL	**142**	**0**	**8**	**3**	**100**	**24**	**1**	**127**	**4**	**4**

CAL - California serogroup includes California encephalitis, Jamestown Canyon, Keystone, La Crosse, Snowshoe hare and Trivittatus viruses
CHIK - Chikungunya
DEN - Dengue
EEE - Eastern equine encephalitis
SLE - Saint Louis encephalitis
WEE - Western equine encephalitis
WN - West Nile
‡PVD - Presumptive viremic blood donors are people who had no symptoms at the time of donating blood through a blood collection agency, but whose blood tested positive when screened for the presence of West Nile virus or Zika virus. Unless they meet the case reporting criteria, they are not counted as a case for official reporting purposes and are not included in the "Total" columns.
***Does not include two cases which could not be differentiated between flaviviruses (dengue and Zika; dengue and West Nile)
****Zika disease cases

Human disease case reporting relies on passive surveillance of laboratory testing results from commercial laboratories, hospitals, and public health labs as well as provider reports of suspected cases. Standardized national surveillance case definitions for arboviral diseases include multiple pathways to demonstrate evidence of infection including molecular, antibody, and other less common diagnostic assays. Molecular detection of viral genetic material is highly accurate and definitive evidence of infection but is not sensitive long after disease onset. Suspected arboviral disease is most often diagnostically assessed using serum antibody assays available at commercial laboratories. Many arboviruses are genetically closely related and can often be cross-reactive on antibody assays due to the overlap of the immune response from one related virus to another. DENV, SLEV, WNV, and ZIKV are in the genus Flavivirus and may cross-react significantly on antibody assays, while alphaviruses such as CHIKV, EEEV, and WEEV would not cross-react with flaviviruses on antibody results.

Animal surveillance is also passive and is highly dependent on resources available for specimen collection and testing. Texas does not have a state-wide mosquito control program; individual jurisdictions or mosquito control districts allocate resources to routinely collect mosquitoes using a variety of different mosquito traps. Therefore, mosquito surveillance data in Texas are not a complete representation of virus transmission in the state. Mosquito control districts, the Texas Department of State Health Services (DSHS) state arboviral laboratory, or third-party laboratories test mosquito collections (or "pools") for the presence of arboviral infection, usually by molecular methods, and report results to the Zoonosis Control Branch (ZCB). Avian reporting includes arbovirus-positive dead birds reported to DSHS, reflecting virus infection of an amplifying host. Sentinel animals are live, captive populations (usually chickens) which are serially tested for presence of antibodies to arboviruses over time, reflecting exposure to infected mosquitoes. In Texas, the only sentinel population that routinely reports results is a sentinel chicken program located in Galveston county. Unlike human cases which have varied travel and exposure history, mosquito, sentinel, and avian data demonstrate definitive evidence of local transmission of the detected virus. Finally, veterinary reports include clinically ill animals, mostly equine species, which were shown to have molecular or antibody evidence of infection with an arbovirus. Veterinary cases typically acquire their infection in the county of residence but may also have complex travel history prior to onset of illness, similar to a human case.

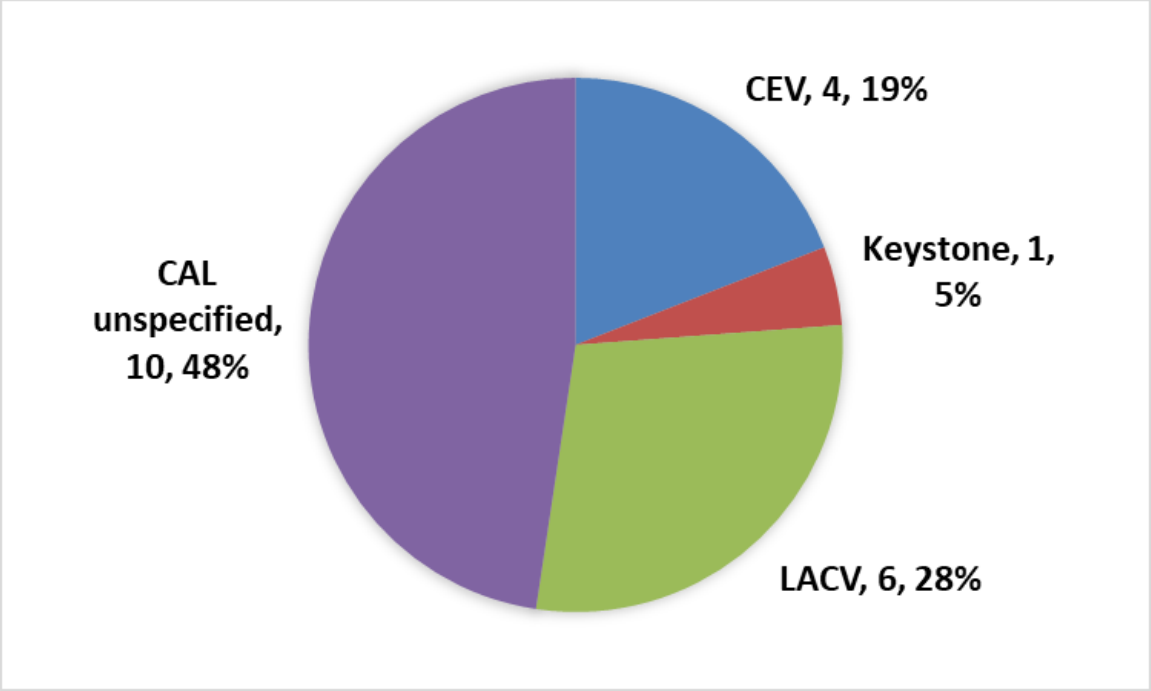
Figure 1. Texas Counties Reporting Arbovirus Activity* in Any Species, 2019



California Serogroup Viruses

California serogroup viruses are bunyaviruses and include California encephalitis virus (CEV), Jamestown Canyon virus, Keystone virus, La Crosse virus (LACV), snowshoe hare virus, and Trivittatus virus. These viruses are maintained in a cycle between mosquito vectors and vertebrate hosts in forest habitats. Most CAL serogroup virus disease cases are caused specifically by LACV but differentiating between related CAL serogroup viruses by antibody-based testing can be challenging. In the United States (U.S.), approximately 50-150 reported cases of human neuroinvasive disease are caused by LACV each year, mostly in mid-Atlantic and southeastern states; a variety of CAL serogroup viruses are native to Texas but rarely reported (Centers for Disease Control and Prevention [CDC], 2022). From 2002-2018, CEV, Keystone virus, LACV, and unspecified CAL serogroup virus were detected by human and animal surveillance (Figure 2). In this period, Texas reported a total of six cases of human CAL serogroup virus disease (annual median: 0 cases, range: 0-3 cases/year): one case of CEV neuroinvasive disease with unknown travel history and five cases of LACV neuroinvasive disease, two of which were imported from other U.S. states. No imported or locally acquired CAL serogroup virus disease human cases or animal infections were reported in 2019 in Texas.

Figure 2. Reports of Human and Animal CAL Serogroup Viruses by Specific Virus, 2002-2019 (N=21)



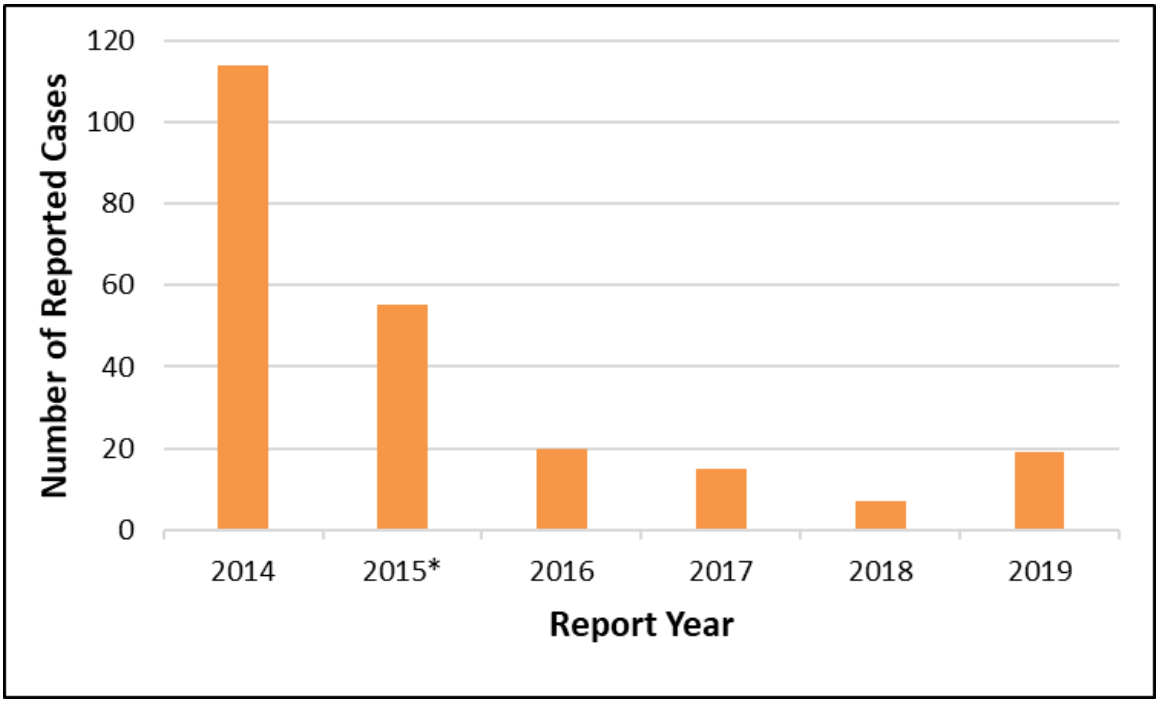
Note: Imported human cases are excluded from figure 2.

Chikungunya Virus

Chikungunya virus is an alphavirus that is maintained in a cycle between *Aedes aegypti* or *Ae. albopictus* mosquitoes and human hosts. Since 2004, several extensive outbreaks have been reported from countries in Africa, Asia, Europe, and the Indian and Pacific Oceans. In the Americas, the first local transmission of CHIKV was reported in the Caribbean in late 2013 (CDC, 2020b). Since then, locally acquired cases of chikungunya disease (CHIK) have been reported throughout the region, including the U.S.

Prior to the emergence of CHIKV in the Americas in 2013, Texas had reported fewer than five travel associated CHIK cases. In contrast, from 2014-2018, Texas reported a total of 211 travel associated CHIK cases (annual median: 20 cases, range: 7-114 cases/year) and one locally acquired case in Cameron County (2015) (Figure 3). In 2019, Texas reported 19 travel-associated cases of CHIK and no locally acquired cases. Reported cases traveled to Asia (primarily India) (12, 63%), the Caribbean (3, 16%), Mexico (2, 11%), Africa (1, 5%), and South America (1, 5%). Though 2019 showed a slight increase in CHIK cases in Texas, the risk of infection to travelers has decreased steadily since the emergence of the virus due to lower CHIKV circulation in endemic regions.

Figure 3. Human Chikungunya Cases Reported in Texas, 2014-2019 (N=230)

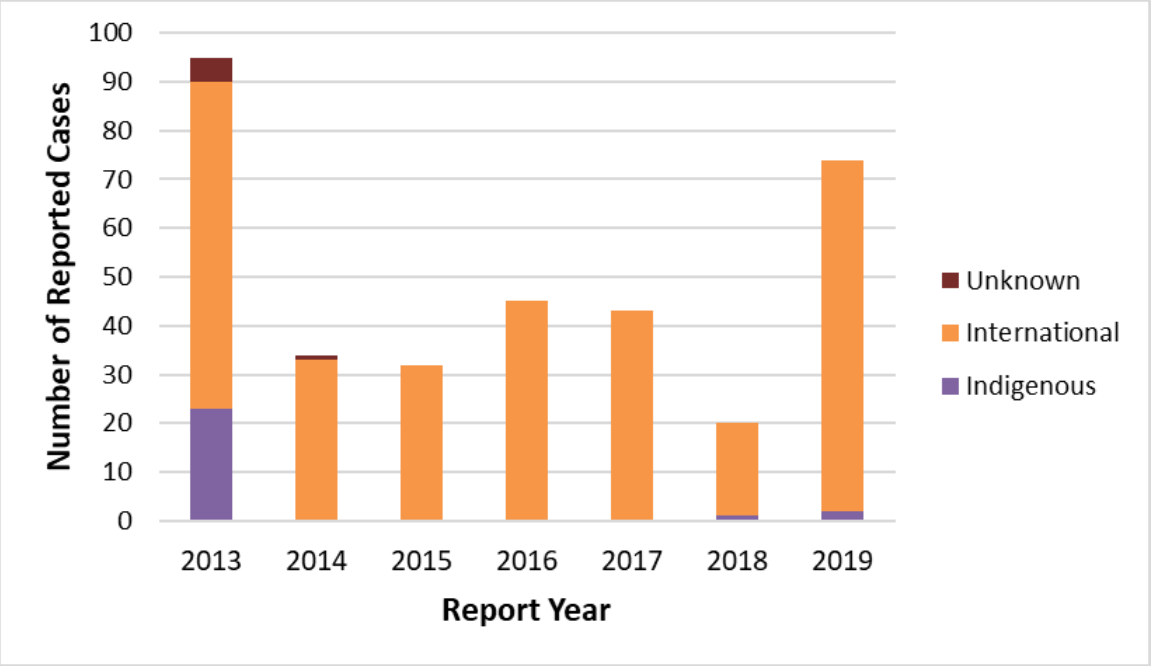


*Includes one locally acquired case.

Dengue Virus

Dengue virus is a flavivirus that is maintained in a cycle between *Ae. aegypti* or *Ae. albopictus* mosquitoes and human hosts. It is established throughout the tropical and subtropical Americas, including northern Mexico. Human cases are most often imported into the U.S. as a result of travel to a dengue-endemic country, but locally-acquired cases have been reported in Florida, Hawaii, and Texas (CDC, 2020a). From 2002-2018, Texas reported a total of 432 cases of dengue (annual median: 20.5 cases, range: 1-95 cases/year). During this time period, 28 cases of locally acquired dengue were reported from the Lower Rio Grande Valley region of Texas: 24 in Cameron County, 2 in Hidalgo County, 1 in Starr County, and 1 in Willacy County. Dengue transmission in south Texas is usually between September and November and often associated with simultaneous high dengue transmission levels in adjacent cities in northern Mexico. In recent years, a moderate sized outbreak in south Texas occurred in 2013, but no additional local human cases were detected until 2018 (Figure 4).

Figure 4. Reported Cases of Dengue in Texas by Acquisition, 2013-2019 (N=343)

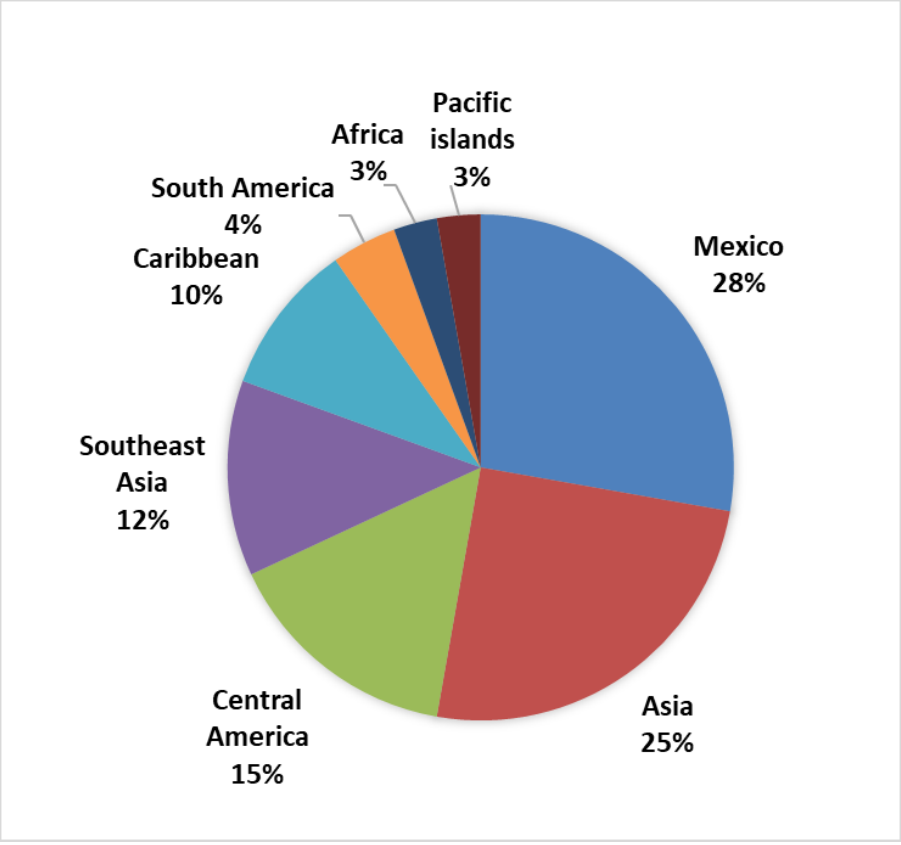


Locally acquired Texas cases are likely an underestimate of the true level of transmission in this region for many reasons, but socioeconomic and infrastructure differences between Texas and Mexico does make Texas lower risk for sustained dengue transmission. Many south Texans may choose to seek medical care for dengue symptoms in Mexico, where clinical diagnosis is common and laboratory test results are

not easily transmitted back to the U.S. Additionally, for those previously infected with dengue in their lifetime, a secondary or tertiary dengue infection usually causes a shortened period of detectable antibodies often used to diagnose dengue, making it more difficult to diagnose dengue in a population with a long history of possible exposure in Texas or Mexico.

In 2019, Texas reported 72 travel-associated cases of dengue and two locally acquired cases of dengue in Hidalgo County (Figure 1, 4). Most imported cases reported travel to Mexico (28%), Asia (25%), central America (15%), southeast Asia (12%), and the Caribbean (10%) (Figure 5). Globally, dengue activity in 2019 was much higher than recent years, and this trend was especially strong in Central America, South America, and Mexico. The increased risk of dengue exposure was demonstrated by the strong increase in cases for 2019 compared to prior years (Figure 4). Additionally, there was an impact from the increased use of public health testing to identify cases by molecular methods when only antibody testing was used early in the course of infection.

Figure 5. Reported Cases of Imported Dengue by Region of Acquisition, Texas, 2019 (N=72)

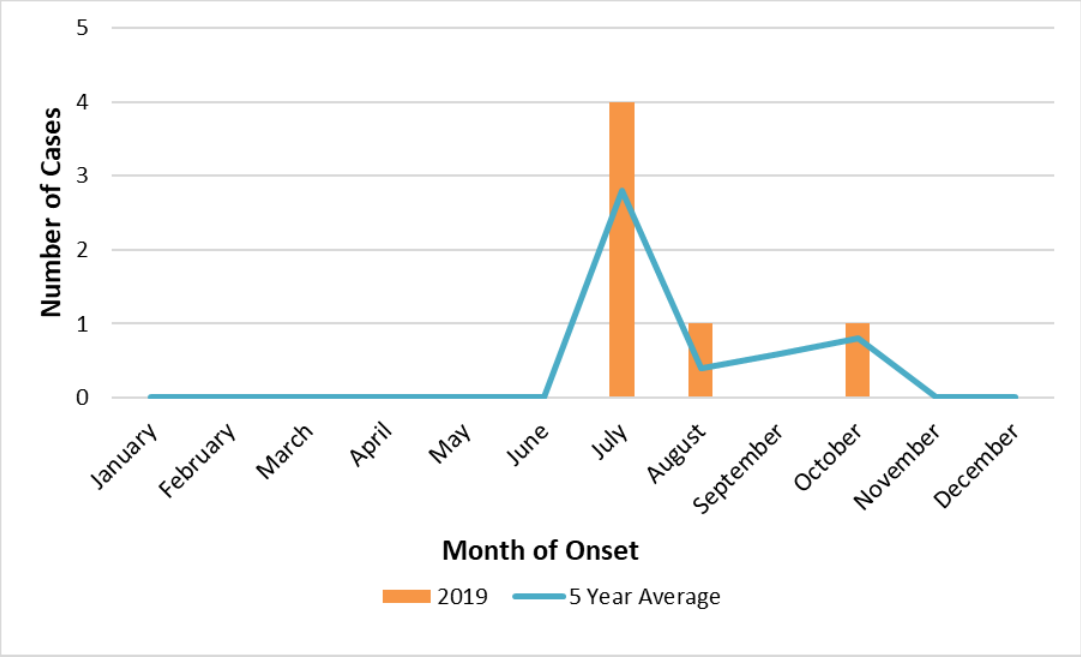


Eastern Equine Encephalitis Virus

Eastern equine encephalitis virus is an alphavirus that is maintained in a cycle primarily between *Culiseta melanura* mosquitoes and avian hosts in freshwater hardwood swamps. Since *C. melanura* feeds almost entirely on birds, a different mosquito "bridge" vector poses infection risk to humans and equines and can include *Aedes*, *Coquillettidia*, and *Culex* genera. EEEV is endemic only to North America and the Caribbean, though closely related viruses are endemic further south in the Americas. An average of 11 cases of Eastern Equine Encephalitis (EEE) are reported primarily in the eastern U.S. each year, though a significant outbreak in the northeastern U.S. occurred in 2019 (CDC, 2021a). Portions of northeast Texas bordering Louisiana contain habitat suitable for EEEV transmission and EEEV-infected horses have been reported from this part of the state.

From 2002-2018, Texas reported 90 equine cases of EEE (annual median: 3 cases, range: 0-29 cases/year) from many counties in east Texas and 79 antibody-positive sentinel chickens in Galveston county (reported in sporadic years with a range of 0-28 cases/year). No human disease or mosquito infections were detected in this period. In 2019, six equine cases of EEE were reported in Texas, with three from Orange county and one case each in Liberty, Montgomery, and Smith counties. The equine cases reported in 2019 followed the typical seasonality of EEE in Texas, with onset of illness in the summer and fall (Figure 6). No sentinel, human, or mosquito reports were received in 2019.

Figure 6. Eastern Equine Encephalitis Cases in Equines by Month of Disease Onset, 2019 (N=6)



Saint Louis Encephalitis Virus

SLEV virus is a member of the Japanese encephalitis serocomplex in the family Flaviviridae along with WNV. SLEV is maintained in a cycle between *Culex* species mosquitoes and wild birds, with occasional transmission to humans and other mammalian species. Wild birds (e.g. sparrows and blue jays) are amplifying hosts and do not develop disease. Humans are dead end hosts and do not transmit the virus to other people. The geographic range of SLEV extends from North to South America, but the majority of human cases have occurred in the eastern and central U.S., where periodic epidemics have occurred since the 1930s (CDC, 2021b). In Texas and states with milder climates, SLEV can circulate year-round. Historically in Texas, SLEV has been reported in mosquito pools, sentinel chickens, horses, and humans. Most infected humans are clinically asymptomatic. Since SLEV is genetically related to other endemic flaviviruses, especially WNV, cross-reactivity is an important consideration for providers diagnosing patients using antibody-based methods. Transmission of SLEV via blood transfusion is rare but can occur. According to the Association for the Advancement of Blood & Biotherapies (AABB), there are no Food and Drug Administration (FDA) licensed blood donor screening tests for SLEV (AABB, 2009). From 2003-2018, Texas reported 38 cases of SLE in humans (annual median = 1 case, range: 0-18 cases/year). In 2019, nine SLEV positive mosquito pools were reported. Eight were from El Paso county and one pool was from Lubbock county (Figure 1); historically, SLEV is frequently detected in mosquitoes in El Paso county. No human cases were reported in 2019.

West Nile Virus

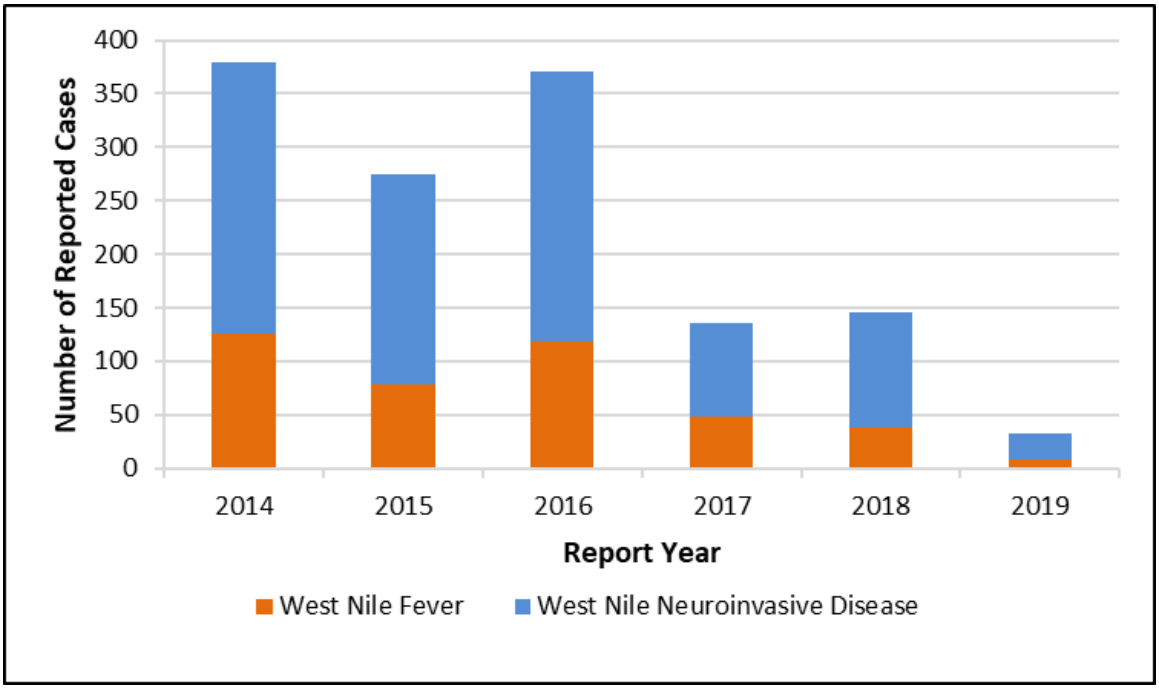
WNV is a flavivirus maintained in a cycle between mosquitoes (primarily *Culex* species) and birds. Prior to the introduction of WNV to New York City in 1999, WNV was only documented in humans, birds, and other mammalian species in countries located within the Eastern Hemisphere. After 1999, WNV was detected in new geographical areas outside of New York state and spread west throughout the U.S. By 2002, WNV established its presence in the U.S. and in that same year, a multi-state outbreak occurred. Both West Nile neuroinvasive and non-neuroinvasive disease were reported, with the majority of the human cases reported as West Nile neuroinvasive disease (WNND). As with similar neurotropic flaviviruses like SLEV, WNV is most frequently detected in human surveillance in its severe clinical form of neuroinvasive disease. Milder febrile illness is more commonly caused by infection with WNV but less reported.

West Nile virus was first reported in Texas in 2002 and initially only human WNND was reportable. Subsequently, West Nile fever (WNF) became a reportable condition in 2003. In 2002, 202 WNND cases were reported. In 2003, 720 WNV disease cases (WNF and

WNND) were reported. In 2011, Texas reported its lowest number of human WNV disease cases at 27, but then a record high number of 1,868 cases were reported in 2012. From 2002-2018, a total of 5,558 human WNV disease cases were reported in Texas (annual median = 189 cases, range: 27-1,868 cases/year). Within the past five years, steady reports of human West Nile cases have been reported (Figure 7). In 2019, 32 human WNV disease cases were reported: 24 (75%) WNND and 8 (25%) WNF.

Additionally, there were four presumptive viremic blood donors (PVDs) reported by blood collection agencies; these individuals are asymptomatic blood donors who test positive for WNV on donor screening tests and represent likely infections with WNV. Since most of the population infected by WNV are asymptomatic, screening the blood supply for WNV helps assess the potential burden of disease in the population. Note that PVDs are not considered West Nile cases unless symptoms consistent with WNV disease develop within two weeks of their positive blood screening test and follow-up West Nile antibody testing verifies the infection.

Figure 7. Human West Nile Disease Cases Reported in Texas, 2014-2019



Since its establishment in Texas, WNV is the most commonly reported arboviral infection in humans, birds, equines, other animals, and mosquitoes. As with other arboviral diseases, human WNV disease cases are reported by county of residence, but this may not reflect the location of infection with WNV in each case due to

widespread disease transmission risk and possible patient travel outside of the residence county during the disease incubation period. However, since its emergence in Texas in 2002, the vector species, virus, and appropriate conditions for transmission are present in most parts of the state from late spring to late fall. Risk of WNV infection is present throughout Texas during the appropriate season, even in the absence of the detection of WNV in non-human surveillance samples such as mosquitoes.

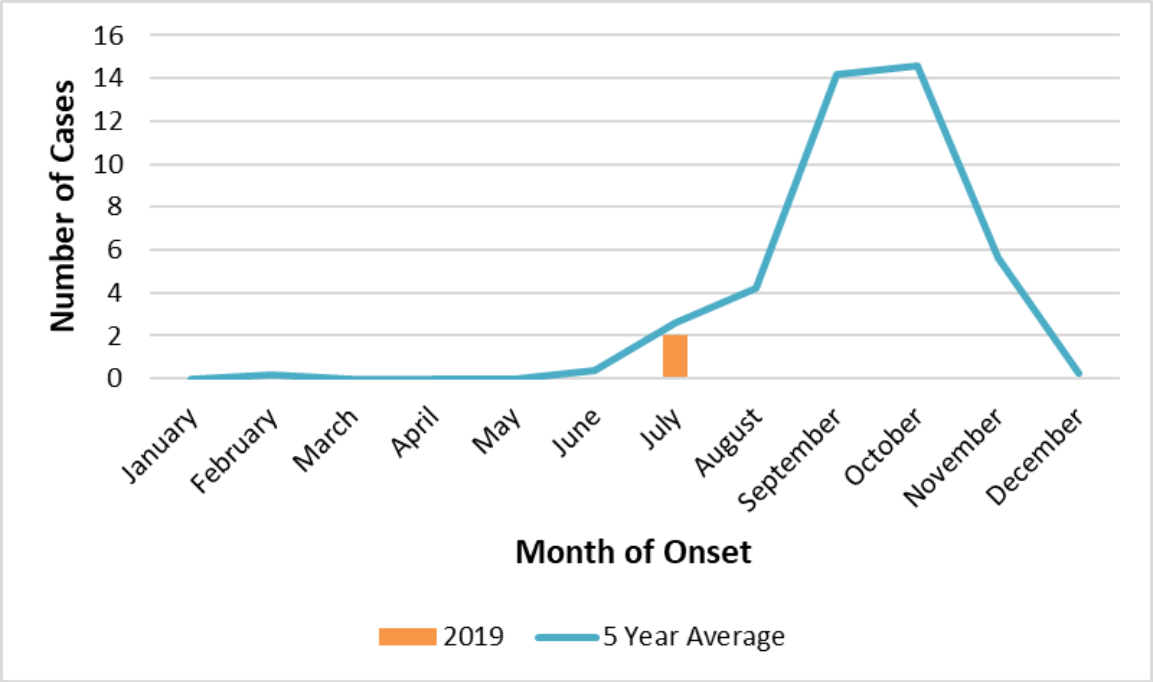
During 2019, evidence of WNV activity (human, horse, mosquito, or sentinel chickens) was reported from 24 (9%) of the 254 counties in Texas (Figure 1, Table 2). Eight (3%) counties reported WNV-positive mosquito pools, 16 (6%) reported human WNV disease cases, one (0.4%) reported PVDs, two (0.9%) reported veterinary WNV disease cases, one (0.4%) reported a WNV-positive sentinel chicken, and no county reported WNV-positive dead birds. WNV infection was reported in 133 mosquito pools, one sentinel chicken, and two veterinary cases, including one horse and one eagle (Table 2). Veterinary WNV cases typically peak in late summer to fall, usually with up to 15 cases per month (Figure 8). In 2019, with few reported veterinary cases, this trend was not as clearly observed.

Table 2. WNV Activity Reported by Species and County, Texas, 2019

County	WNV							
	M	A	V	SC	H			
					WNF	WNND	PVD‡	TOTAL
Brazoria	0					1		1
Dallas	35					1		1
Deaf Smith	0							0
Denton	4							0
El Paso	26		1		3	13	4	16
Franklin	0					1		1
Floyd	0				1			1
Galveston	0			1				0
Hale	0					1		1
Harris	25					2		2
Lamb	0				1			1
Liberty	0							0
Lubbock	28					1		1
Lynn	0				1			1
Midland	0					1		1
Nolan	0					1		1
Montgomery	2							0
Orange	0		1					0
Potter	0					1		1
Runnels	0				1			1
Smith	0							0
Tarrant	12				1			1
Taylor	1							0
Tom Green	0					1		1
Total Number of Reports	133	0	2	1	8	24	4	32

M-Mosquito A-Avian E-Equine SC-Sentinel Chicken H-Human
WNV-West Nile Virus WNF-West Nile Fever WNND-West Nile Neuroinvasive Disease
PVD-Presumptive Viremic Blood Donor
‡PVDs are not included in the "Total" column.

Figure 8. Equine West Nile Virus Disease Cases in Texas by Month of Disease Onset, 2019 (N=2)



Due to the importance of WNV in Texas, additional analysis of human disease data was performed. The median age at onset of illness was 47 years (range: 24-92 years) for all cases. The majority (41%) of all WNV disease cases were in Hispanic, white persons (Table 4). Of the 24 reported cases of WNND, 14 (58%) presented with encephalitis, including meningoencephalitis, and seven (29%) presented with meningitis only (Table 3). The top three clinical signs and symptoms reported for WNND cases were fever (92%), CSF pleocytosis (88%), and altered mental state (67%). The top three clinical signs and symptoms reported for WNF cases were fever (100%), headache (100%), chills (79%), and nausea or vomiting (75%); note that fever or chills must be present to report as WNF. All WNND cases were hospitalized (100%), while only one WNF case (13%) reported hospitalization. There were four deaths attributed to WNV (17%) among reported cases of WNND in 2019. No WNV-related deaths were reported among WNF cases.

Table 3. Clinical Characteristics of Reported Human WNV Disease Cases, Texas, 2019

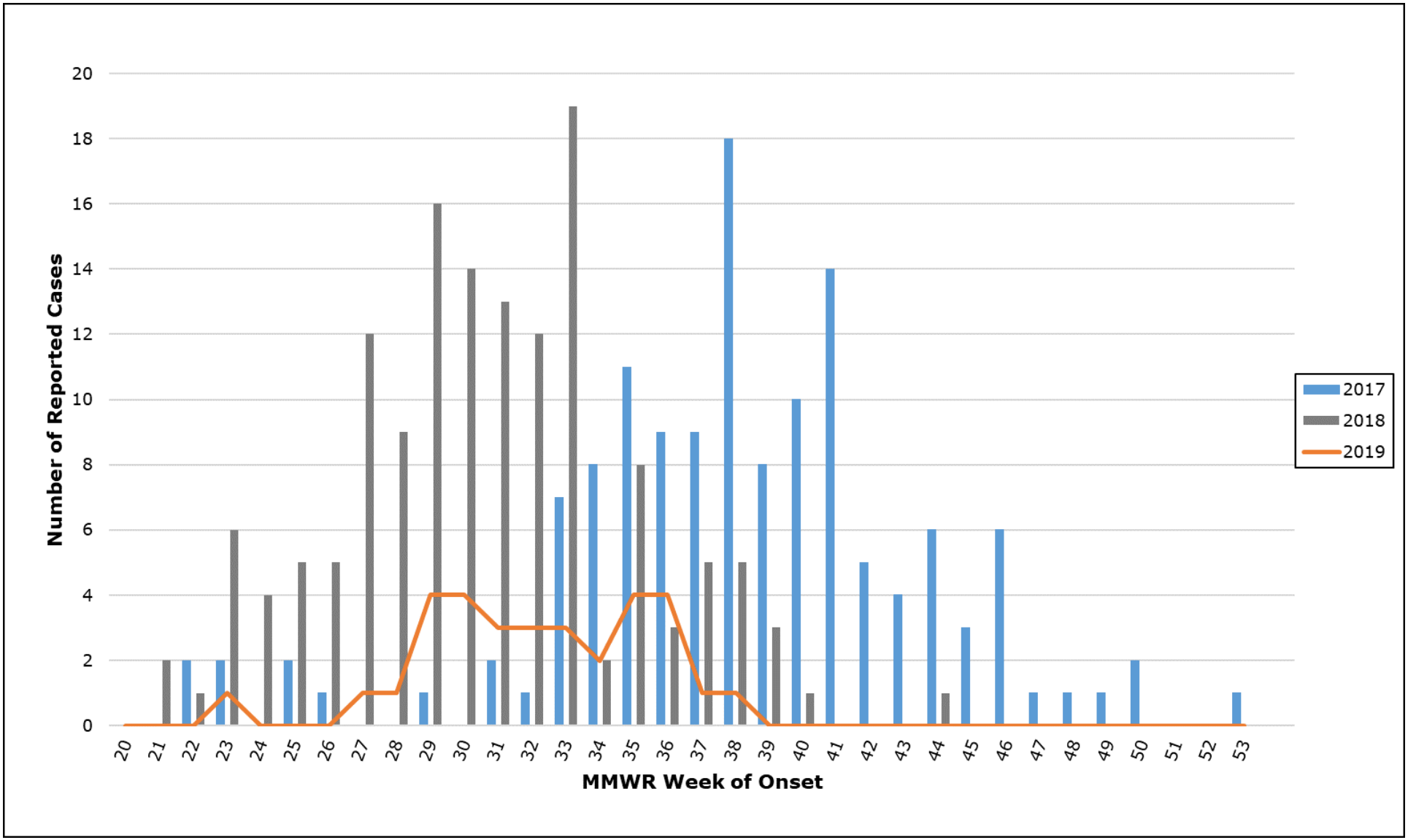
Characteristic	WNND (N=24)		WNF (N=8)	
	Number	%	Number	%
Acute Flaccid Paralysis	-	-	-	-
Encephalitis/meningoencephalitis	14	58	-	-
Febrile Illness	3	13	8	100
Guillain-Barré Syndrome	-	-	-	-
Other Neuroinvasive Presentation	-	-	-	-
Meningitis	7	29	-	-
Clinical Signs/Symptoms				
Altered Mental Status	16	67	-	-
Arthralgia	6	25	2	25
Chills	14	58	6	75
CSF Pleocytosis	21	88	-	-
Fever	22	92	8	100
Headache	14	58	8	100
Myalgia	12	50	5	63
Nausea or Vomiting	12	50	6	75
Rash	2	8	5	63
Severe Malaise	14	58	-	-
Stiff Neck	9	38	-	-
Clinical Course				
Hospitalized	24	100	1	13
Median Length of Stay (Days)	9		2	
Death	4	17	-	-

Table 4. Demographic Characteristics of Reported Human WNV Disease Cases, Texas, 2019

Characteristic	WNND (N=24)		WNF (N=8)	
	Number	%	Number	%
Gender				
Male	15	63	6	75
Female	9	38	2	25
Age Group at Onset (years)				
<1-9	-	-	-	-
10-19	-	-	-	-
20-29	1	4	-	-
30-39	2	8	3	38
40-49	1	4	1	13
50-59	4	17	1	13
60-69	3	13	2	25
70-79	7	29	1	13
80+	6	25	-	-
Race/Ethnicity				
American Indian/Alaska Native/White, Non-Hispanic	1	4	-	-
Black, non-Hispanic	1	4	-	-
Unknown, Hispanic	1	4	-	-
Unknown, Non-Hispanic	1	4	-	-
White, Hispanic	12	50	1	13
White, Non-Hispanic	7	30	5	63
White, Unknown	1	4	2	25

In 2019, the statewide incidence of all human WNV disease cases was 0.1 cases per 100,000 population (Table 5). DSHS Public Health Region (PHR) 9/10 reported the highest incidence of WNV disease (1.2 cases per 100,000 population) (Table 6). PHR 1 had the second highest incidence of WNV disease (0.7 cases per 100,000 population) while the remaining PHRs had too few human cases to calculate accurate incidence rates (Table 6). Onsets of illness for all human WNV disease cases ranged from MMWR week 20 (mid-May) to MMWR week 38 (Mid-September) (Figure 9). The median week of illness onset in 2018 was MMWR week 30 (late August), which is slightly later than the median illness onset in 2017 (MMWR week 32, mid-August).

Figure 9. Human Cases of WNV Disease Reported in Texas, by MMWR Week of Onset, 2017-2019



See https://wwwn.cdc.gov/nndss/downloads.html for more information about MMWR week calendars

Table 5. Reported Human WNV Disease Incidence Rates in Counties with Five or More* Cases, 2019

County	Population**	WNF and WNND Cases	Incidence Rate (per 100,000)	Only WNND Cases	Incidence Rate (per 100,000)
El Paso	852,224	16	1.9	13	1.5
All Texas Counties	**29,001,602**	**32**	**0.1**	**24**	**0.1**

* Calculation of rates is not recommended when there are fewer than five events in the numerator because the calculated rate can be unstable and exhibit wide confidence intervals.

** 2019 population projections accessed 01/28/2022 Texas Demographic Center https://demographics.texas.gov

Table 6. Reported Human WNV Disease Cases and Incidence Rates by DSHS Public Health Region (PHR), 2019

PHR	Population**	WNF and WNND Cases	Incidence Rate (per 100,000)
1	870,876	6	0.7
2/3	8,499,439	4	*
4/5N	1,556,174	1	*
6/5S	7,620,466	3	*
7	3,587,909	0	*
8	3,034,252	0	*
9/10	1,560,920	18	1.2
11	2,271,566	0	*
TOTAL	**29,001,602**	**32**	**0.1**

See https://www.dshs.texas.gov/regions/state.shtm for map depicting DSHS PHRs

* Calculation of rates is not recommended when there are fewer than five events in the numerator because the calculated rate can be unstable and exhibit wide confidence intervals.

** 2019 population projections accessed 1/28/2022, Texas Demographic Center https://demographics.texas.gov

Western Equine Encephalitis Virus

Western equine encephalitis virus is an alphavirus maintained in a cycle between *Culex tarsalis* mosquitoes and avian hosts (Equine Disease Communication Center (EDCC), 2020). Western equine encephalitis (WEE) is a rare illness in humans and is most often reported from the western U.S. and Canada.

From 2002-2011, evidence of WEEV activity in any species was reported from only five (2%) of the 254 counties in Texas: four counties reported WEE-positive mosquito pools, and one county reported an equine WEE disease case. No WEEV-infected humans or birds were reported during this time frame. From 2012-2018, no WEEV activity was detected by human or animal surveillance in Texas. In 2019, two sentinel chickens in Galveston county were antibody positive against WEEV. No other animal or human reports were received during the year.

Zika Virus

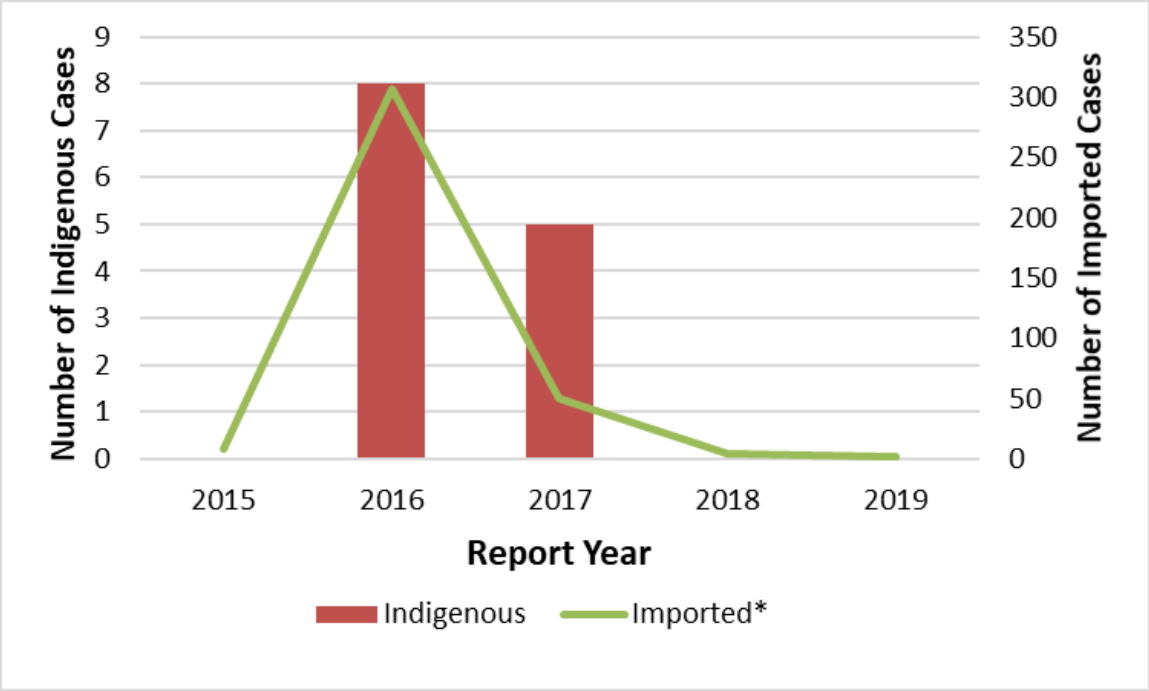
Zika virus is a flavivirus that is maintained in a cycle between *Ae. aegypti* or *Ae. albopictus* mosquitoes and human hosts. Zika virus was first discovered in 1947 and is named after the Zika forest in Uganda. The first human cases of disease caused by Zika virus were detected in the 1950s and, since then, sporadic outbreaks of Zika virus disease (ZIKVD) have been reported in tropical Africa, Southeast Asia, and the Pacific Islands. In late 2015, the first local transmission of ZIKV in the Americas was reported in Brazil. Beginning in 2016, locally acquired cases of ZIKVD were widely reported throughout Latin America, the Caribbean, and the southernmost parts of Florida and Texas (CDC, 2021c). In subsequent years, ZIKV became established in many other global regions including central Africa, south and southeast Asia; isolated transmission even occurred in the south of France, where typically only one possible vector is present, *Ae. albopictus.*

Similar to WNV and many other arboviral infections, the majority of infections with ZIKV are asymptomatic. Cases of ZIKV *disease* (individuals with compatible symptoms) and ZIKV *infection* (individuals who report no symptoms) became nationally notifiable in 2016, though sporadic cases were reported previously. Unique among arboviruses, ZIKV can be transmitted sexually and can cause neurological and structural birth defects (primarily microcephaly) and fetal loss if a pregnant woman is infected during gestation. ZIKV congenital disease cases are reported in newborns with medical issues consistent with Congenital Zika Syndrome (CZS) and a maternal exposure to a Zika exposure area during pregnancy. ZIKV asymptomatic infections are not included in public data reports and congenital ZIKVD cases are not specified within the overall disease case total given the minimal impact on distribution of cases across the state

and to maintain patient confidentiality.

During 2016, Texas reported 315 ZIKVD cases, including eight locally acquired cases: six transmitted by mosquitoes in Cameron county and two sexually transmitted cases (Figure 10). Additionally, three ZIKVD cases in 2016 were imported from southern Florida, where ZIKV mosquito transmission also occurred. During 2017, Texas reported 55 ZIKVD cases, five of which were locally transmitted by mosquitoes in Cameron and Hidalgo counties. In 2018, Texas reported four imported ZIKVD cases, and in 2019, only two imported cases were reported. This declining trend reflects the decrease in ZIKV activity throughout the Americas and globally, as the vast majority of Texas cases are acquired during travel, most often to Mexico, the Caribbean, and Central America. However, the continued presence of the mosquito vectors and possible environmental conditions conducive to ZIKV transmission in south Texas will remain a public health consideration even with minimal ZIKV activity globally.

Figure 10. Human Cases of ZIKV Disease Reported in Texas by Acquisition, 2015-2019



*Imported total includes congenital cases whose mothers were infected outside the U.S. and three non-congenital cases infected in south Florida 2016

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Resources

DSHS Arboviral Diseases webpage:
https://www.dshs.texas.gov/idcu/disease/arboviral/

CDC La Crosse Encephalitis Virus webpage: https://www.cdc.gov/lac/ CDC

Chikungunya Virus webpage: https://www.cdc.gov/chikungunya/ CDC

Dengue Virus webpage: https://www.cdc.gov/dengue/

CDC Eastern Equine Encephalitis webpage:
https://www.cdc.gov/EasternEquineEncephalitis/

CDC Saint Louis Encephalitis Virus webpage: https://www.cdc.gov/sle/

CDC West Nile Virus webpage: https://www.cdc.gov/westnile/

CDC Zika webpage: https://www.cdc.gov/zika/

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