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WISCONSIN EPI EXPRESS

IN THIS ISSUE

PROGRAM UPDATES

STAFF UPDATES: BCD welcomes the following staff to their new positions

Sarah Clifford, CDES Public Health Educator
Lynsey Kimmins, Epidemiologist for the Immunization Program
Erin Davies, HIV Surveillance Coordinator
Rachel Welsh, HIV Care Coordinator
Barry Fox, Antibiotic Stewardship Coordinator
Nancy Eberle, HAI Education and Outreach Coordinator
Daniella Fetsko, CDC PHAP Placement
Bethany Horvath, Grants Management Specialist
Jacob Dougherty, HIV Prevention Unit Supervisor
Sheila Guilfoyle, Harm Reduction Unit Supervisor
Brandon Kufalk, STI Unit Supervisor

NEW TUBERCULOSIS (TB) WEBPAGES:

The Wisconsin TB Program website has been completely updated and redesigned. Highlights of the redesign include information and resources for the general public; resources for screening, testing, diagnosis, and treatment for health professionals; information about TB Class B arrivals, and much more! Check out the new website.

ONGOING OUTBREAK INVESTIGATIONS:

Check out the Department of Health Services new Outbreaks and Investigations webpage for up-to-date information on outbreaks and investigations with wide impact in Wisconsin. For a list of past outbreaks, please see the Past Outbreaks and Investigations webpage.

Eastern Equine Encephalitis Virus Activity in Wisconsin during 2020

By: Erin Furmaga, MPH and Rebecca Osborn, MPH - Vectorborne Disease Program

Background

Eastern equine encephalitis disease (EEE), caused by the eastern equine encephalitis virus (EEEV), is transmitted by the bite of an infected mosquito. EEEV is maintained in the environment between birds and Culiseta melanura mosquitoes, a type of mosquito that breeds in swampy areas and bogs. Humans and horses can become infected incidentally when other types of mosquitoes take a blood meal from an infected bird and then go on to bite a human or a horse. The virus cannot be spread directly between horses and humans, though there has been documented EEEV transmission between two people through organ transplantation.

Some people infected with EEEV remain asymptomatic; clinical disease can range from mild febrile illness to neurological involvement such as meningitis or encephalitis. Among those who develop neurological signs, around 30% die, and those who survive often experience significant neurological sequelae. Horses are susceptible to EEE disease, with a case fatality rate close to 90% in unvaccinated animals. There is a vaccine available for horses, but not for humans. Monitoring EEE cases in horses can help alert public health officials of known EEEV activity in certain areas.

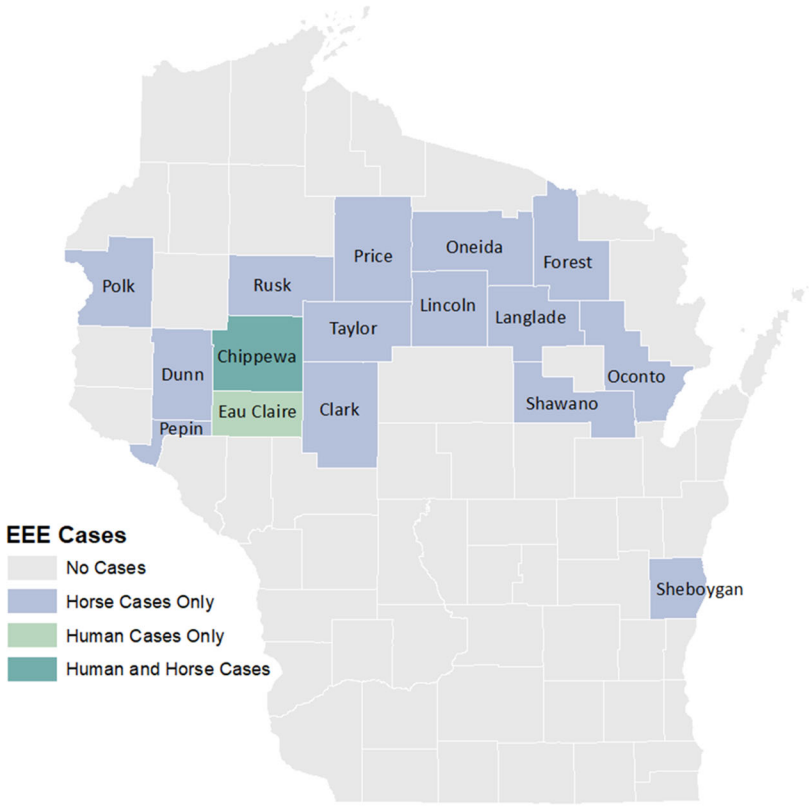
EEE in Wisconsin

EEE is rare in Wisconsin, with only three human cases reported among residents prior to 2020. During the 2020 mosquito season, however, two human cases were reported, both with histories of mosquito exposure within 10 days of illness onset in mid-summer. One case occurred in an adult female residing in Chippewa County who developed encephalitis and died 25 days post onset. The second case was reported in a female child under the age of 18 residing in Eau Claire County who also developed encephalitis, but was eventually discharged to a rehabilitation facility after a 17-day hospitalization.

During 2020, a total of 26 EEE cases in horses were reported, representing a higher than average number of equine cases. There have been three additional outbreaks of EEE in horses in Wisconsin during the last decade: in 2011, 2016, and 2017. The only two human cases documented during the same time period occurred in 2011 and in 2017, both during years with high EEEV activity in horses.

Human and equine cases of EEE in Wisconsin are more common in the northern portion of the state, where presumably more suitable habitat is available for the mosquitoes that commonly carry EEEV. Risk of EEE disease can be reduced by taking steps to prevent mosquito bites.

Horse and Human EEE Cases in WI, 2020



Data Source: Wisconsin Department of Health Services

Surveillance of Fluoroquinolone Resistance in Wisconsin

By: Dr. Erik Munson and Dr. Barry Fox—Antimicrobial Stewardship Program

Summary

Antimicrobial stewardship promotes the appropriate use of antimicrobials (including antibiotics) to improve patient outcomes, reduce microbial resistance, and decrease the spread of infections caused by multidrug-resistant organisms. In Wisconsin, this coordinated effort includes surveillance of drug-resistant organisms. In this study, it was found that fluoroquinolone resistance may have been underreported in Wisconsin, despite continued clinical use. This research identifies changes in drug use criteria and bacterial resistance, which may impact antibiotic prescribing behavior moving forward.

Background

The Surveillance of Wisconsin Organisms for Trends in Antimicrobial Resistance and Epidemiology (SWOTARE) program is a surveillance initiative operated by Marquette University in collaboration with 21 clinical microbiology laboratories. Each laboratory provides isolates of clinically-significant species annually with limited demographic information. Isolates are tested by standardized broth microdilution. Data are analyzed via minimum inhibitory concentration (MIC) frequency distribution and by categorical interpretive criteria updated yearly by Clinical and Laboratory Standards Institute (CLSI). Fluoroquinolone resistance within Gram-negative bacteria has been tracked in Wisconsin through antibiogram compilation [1] and isolate surveillance [2] approaches. Data can be further analyzed by temporal, geographic, and epidemiologic basis [3].

In 2019, CLSI published revised ciprofloxacin and levofloxacin broth microdilution breakpoints for Enterobacterales and Pseudomonas aeruginosa [4]. For both fluoroquinolone agents, P. aeruginosa-specific breakpoints were reduced by one doubling dilution, and for Enterobacterales two doubling-dilutions.

To determine impact of the CLSI revisions on Wisconsin fluoroquinolone resistance, which could effect antibiotic prescribing behavior, we applied pre-2019 [5] and current [4] CLSI breakpoints to five-year aggregate SWOTARE (2016-2020) collections of Escherichia coli, Proteus mirabilis, and P. aeruginosa.

Results

Standardized reference broth microdilution assayed each isolate using a concentration range of 0.25 mg/mL through 32 mg/mL. Fiftieth percentile (MIC50) and 90th percentile (MIC90) frequency distribution data for 1795 E. coli isolates (Table 1) revealed a broad distribution of MIC values across the testing range, particularly for ciprofloxacin. When compared to pre-2019 practice, modest decreases in percentage susceptibility were observed when updated CLSI breakpoints were applied (1.4% for levofloxacin; 3.2% for ciprofloxacin). A similar broad MIC frequency distribution was observed for 1437 isolates of P. mirabilis. However, application of revised CLSI breakpoints to this dataset resulted in up to 6.2% decreases in susceptibility (levofloxacin) when compared to pre-2019 breakpoints.

For P. aeruginosa, MIC50 and MIC90 data for ciprofloxacin (≤0.25 mg/mL; 2 mg/mL) and levofloxacin (0.5 mg/mL; 4 mg/mL) suggest a narrower MIC frequency distribution. Application of revised CLSI breakpoints to the 1384-isolate dataset resulted in 4.5—5.2% decreases in fluoroquinolone susceptibility.

By: Dr. Erik Munson and Dr. Barry Fox—Antimicrobial Stewardship Program

Conclusion

Taken together, these data suggest that in vitro fluoroquinolone resistance was underreported in Wisconsin for several years prior to the institution of revised CLSI breakpoints, and that fluoroquinolones may not have been as effective clinically before 2019 as clinicians expected.

The SWOTARE program continues to monitor this antimicrobial class for changes in these species and other Enterobacterales. Additional surveillance efforts have been undertaken for Staphylococcus aureus [6] and Streptococcus pneumoniae.

Table 1

Fluoroquinolone MIC_{50} and MIC_{90} distribution of Wisconsin surveillance isolates of *Escherichia coli*, *Proteus mirabilis*, and *Pseudomonas aeruginosa* collected from 2016-2020. Categorical interpretative data (S, susceptible; I, intermediate; R, resistant) are based on application of either previous (prior to 2019) or current (established in 2019) Clinical and Laboratory Standards Institute (CLSI) *Enterobacterales* (formerly *Enterobacteriaceae*) and *Pseudomonas aeruginosa* breakpoints.

References

Munson E, Block TK, Bowles EJ, et al. Surveillance of Wisconsin antibacterial susceptibility patterns. WMJ. 2016;115(1):29–36.

Munson E, Hueppchen E, Zeman H. Surveillance of Wisconsin Organisms for Trends in Antimicrobial Resistance and Epidemiology: introduction to the program and summary of 2016 geographic variation. WMJ. 2018;117 (3):116-121.

Munson E, Zeman H, Hueppchen E. Surveillance of Wisconsin Organisms for Trends in Antimicrobial Resistance and Epidemiology (SWOTARE): epidemiologic correlates for 2016 surveillance isolates. Gundersen Med J. 2017;10 (1):41-48.

Clinical and Laboratory Standards Institute (CLSI). Performance standards for antimicrobial susceptibility testing, M100. 29th informational supplement. Wayne, PA: CLSI; 2019.

Clinical and Laboratory Standards Institute (CLSI). Performance standards for antimicrobial susceptibility testing, M100. 28th informational supplement. Wayne, PA: CLSI; 2018.

Schulte RH, Munson E. Staphylococcus aureus resistance patterns in Wisconsin: 2018 Surveillance of Wisconsin Organisms for Trends in Antimicrobial Resistance and Epidemiology (SWOTARE) program report. Clin Med Res. 2019;17(3-4):72-81.

ORGANISM	n	CIPROFLOXACIN						LEVOFLOXACIN					
		MIC_{50}	MIC_{90}	Break-points	%S	%I	%R	MIC_{50}	MIC_{90}	Break-points	%S	%I	%R
Escherichia coli	1795	≤ 0.25	>32	Previous[a]	82.3	0.2	17.4	≤ 0.25	16	Previous[c]	82.6	0.4	17.0
				Current[b]	79.1	2.4	18.4			Current[d]	81.2	1.2	17.6
Proteus mirabilis	1437	≤ 0.25	16	Previous[a]	78.4	4.2	17.3	≤ 0.25	16	Previous[c]	83.3	2.8	13.8
				Current[b]	75.9	1.5	22.6			Current[d]	77.0	2.8	20.2
Pseudomonas aeruginosa	1384	≤ 0.25	2	Previous[e]	87.2	3.3	9.5	0.5	4	Previous[g]	86.7	4.2	9.1
				Current[f]	82.7	4.5	12.8			Current[h]	81.5	5.2	13.3

[a] CLSI *Enterobacteriaceae*/ciprofloxacin breakpoints of ≤ 1 mg/mL (susceptible), 2 mg/mL (intermediate), ≥ 4 mg/mL (resistant)
[b] CLSI *Enterobacterales*/ciprofloxacin breakpoints of ≤ 0.25 mg/mL (susceptible), 0.5 mg/mL (intermediate), ≥ 1 mg/mL (resistant)
[c] CLSI *Enterobacteriaceae*/levofloxacin breakpoints of ≤ 2 mg/mL (susceptible), 4 mg/mL (intermediate), ≥ 8 mg/mL (resistant)
[d] CLSI *Enterobacterales*/levofloxacin breakpoints of ≤ 0.5 mg/mL (susceptible), 1 mg/mL (intermediate), ≥ 2 mg/mL (resistant)
[e] CLSI *P. aeruginosa*/ciprofloxacin breakpoints of ≤ 1 mg/mL (susceptible), 2 mg/mL (intermediate), ≥ 4 mg/mL (resistant)
[f] CLSI *P. aeruginosa*/ciprofloxacin breakpoints of ≤ 0.5 mg/mL (susceptible), 1 mg/mL (intermediate), ≥ 2 mg/mL (resistant)
[g] CLSI *P. aeruginosa*/levofloxacin breakpoints of ≤ 2 mg/mL (susceptible), 4 mg/mL (intermediate), ≥ 8 mg/mL (resistant)
[h] CLSI *P. aeruginosa*/levofloxacin breakpoints of ≤ 1 mg/mL (susceptible), 2 mg/mL (intermediate), ≥ 4 mg/mL (resistant)

Communicable Disease Case Counts

This report contains a selection of reportable conditions with inclusion based on public health significance and frequency of occurrence. The case counts reflect confirmed and probable cases, for all process statuses. These numbers are not final and are subject to change as confirmatory testing and case follow-up are completed.

***Case counts should not be considered final and are subject to change.**

Disease	2020 Case Counts	2021 Case Counts				
	Total	Q1	Q2	Q3	Q4	2021 YTD
Enteric/Gastrointestinal (also includes suspect cases)						
Campylobacteriosis	1,183	172				172
Cholera[1]	0	0				0
Cryptosporidiosis	484	53				53
Cyclosporiasis	73	2				2
E. coli, Shiga toxin-producing (STEC)	290	41				41
Giardiasis	482	84				84
Hemolytic uremic syndrome	0	1				1
Listeriosis	10	3				3
Salmonellosis	694	107				107
Shigellosis	46	17				17
Typhoid fever	2	1				1
Vibriosis (non-cholera)	17	2				2
Yersiniosis	50	10				10
Invasive Bacteria						
Group A streptococcal disease	188	27				27
Group B streptococcal disease	592	156				156
Mycotic						
Blastomycosis	65	6				6
Coccidioidomycosis[1]	23	3				3
Histoplasmosis	9	4				4
Respiratory						
Coronavirus disease (COVID-19)	536,865	103,352				103,352
Please refer to the weekly respiratory virus surveillance report.						
Influenza-associated hospitalizations	3,486	5				5
Influenza, novel	0	0				0
Legionellosis	241	18				18
Tuberculosis	35	18				18
Latent TB infection	576	121				121
Sexually Transmitted						
Chlamydia trachomatis	26,439	6,933				6,933
Gonorrhea	10,282	2,521				2,521
HIV	207	57				57
Syphilis (all stages)	812	243				243
Vaccine Preventable						
Diphtheria	0	0				0
Haemophilus influenzae invasive disease	71	16				16
Hepatitis B, acute (confirmed cases only)	5	2				2
Hepatitis B, perinatal	0	0				0

Communicable Disease Case Counts (continued)

Disease	2020 Case Counts	2021 Case Counts				
	Total	Q1	Q2	Q3	Q4	2021 YTD
Vaccine Preventable (continued)						
Measles (rubeola)	4	0				0
Meningococcal disease	3	0				0
Mumps	17	6				6
Pertussis (whooping cough)	130	26				26
Poliomyelitis	0	0				0
Rubella	0	0				0
Streptococcus pneumoniae invasive disease	289	43				43
Tetanus	0	0				0
Varicella (chickenpox)	108	36				36
Vectorborne						
Babesiosis	57	2				2
Dengue virus infection[1]	8	0				0
Eastern equine encephalitis virus (EEEV)	2	0				0
Ehrlichiosis/Anaplasmosis	365	3				3
Jamestown Canyon virus infection	1	0				0
La Crosse virus infection	2	0				0
Lyme disease	1,397	37				37
Malaria[1]	5	3				3
Powassan virus infection	4	0				0
Spotted fever group rickettsioses (spotted fevers)	3	1				1
West Nile virus infection	1	0				0
Yellow fever[1]	0	0				0
Zika virus infection[1,2]	0	0				0
Zoonotic						
Brucellosis	1	0				0
Hantavirus infection	0	0				0
Leptospirosis	0	0				0
Psittacosis	0	0				0
Q Fever, acute	3	1				1
Q Fever, chronic	2	0				0
Rabies (human)	0	0				0
Toxoplasmosis	0	1				1
Tularemia	2	0				0
Other						
CP-CRE	35	11				11
Hepatitis A	12	0				0
Hepatitis C, acute	94	15				15
Hepatitis E, acute	12	3				3
Kawasaki disease	11	4				4
Lymphocytic choriomeningitis virus infection	0	0				0
Transmissible spongiform encephalopathy (human)	9	0				0

[1] Denotes diseases where all cases in Wisconsin residents are travel-associated. No local transmission occurs.
[2] Due to enhanced surveillance, asymptomatic confirmed cases are included.