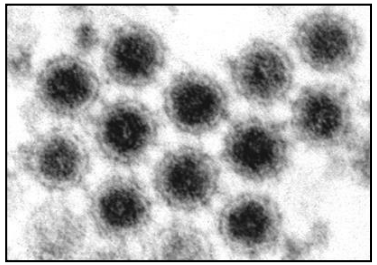
Update on EEE Virus: an Emerging Mosquito-Borne Virus of Public Heath Concern

Philip M. Armstrong

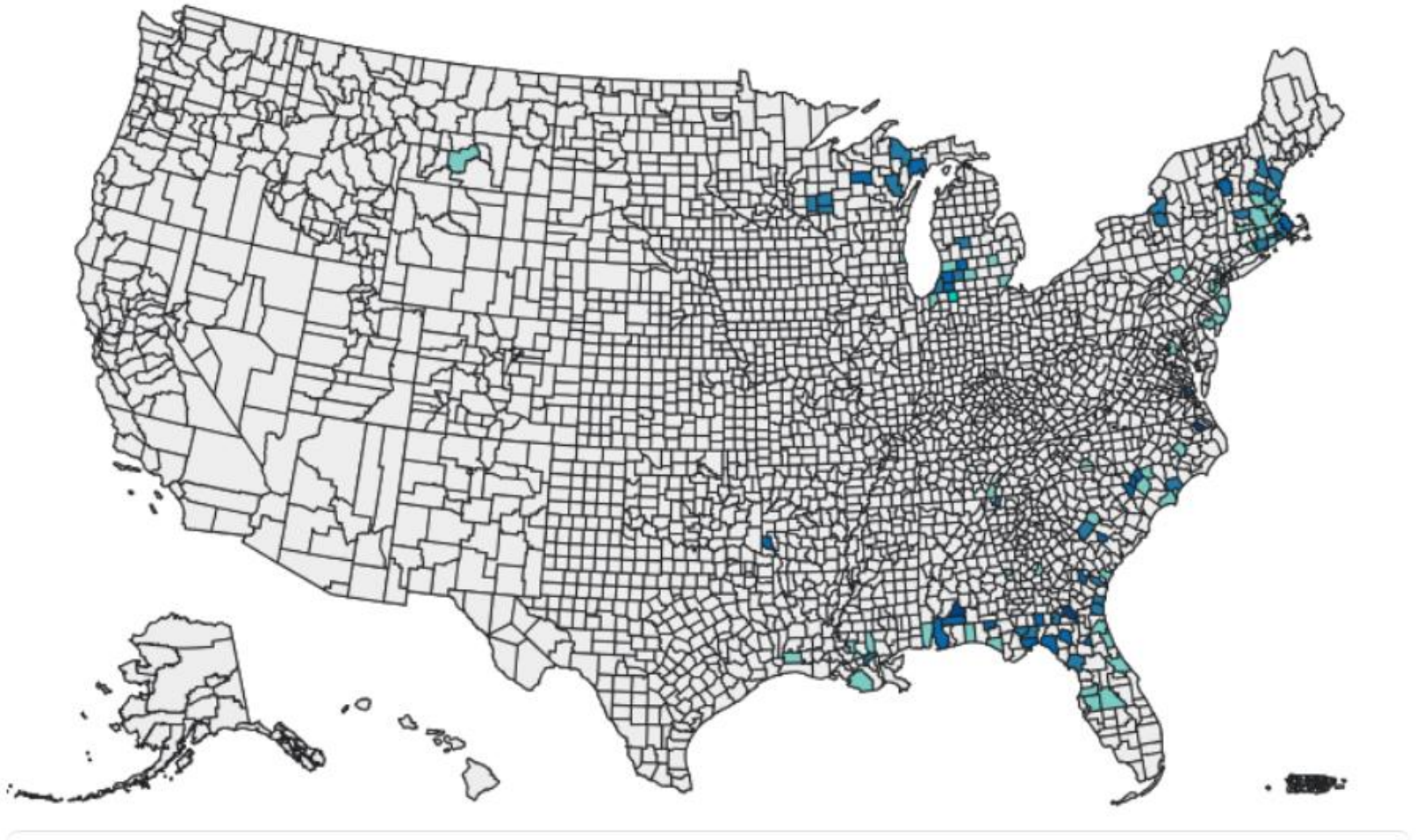
Department of Entomology
Center for Vector-Borne and Zoonotic Diseases
The Connecticut Agricultural Experiment Station
New Haven, CT

Eastern Equine Encephalitis Virus

- Most pathogenic mosquito-borne virus in North America (*Togaviridae: Alphavirus*)
  - ~10 human cases per year
  - 30% case fatality rate
  - Neurological impairment in half of survivors
  - No commercial vaccine or effective treatment
- Virus activity most common in and around freshwater swamps- highly focal
- Perpetuates in an enzootic cycle involving passerine birds and ornithophilic mosquitoes
- Principal enzootic vector in the U.S.
  - *Culiseta melanura*



Average Annual Incidence of Human EEE Cases for 2003-2023

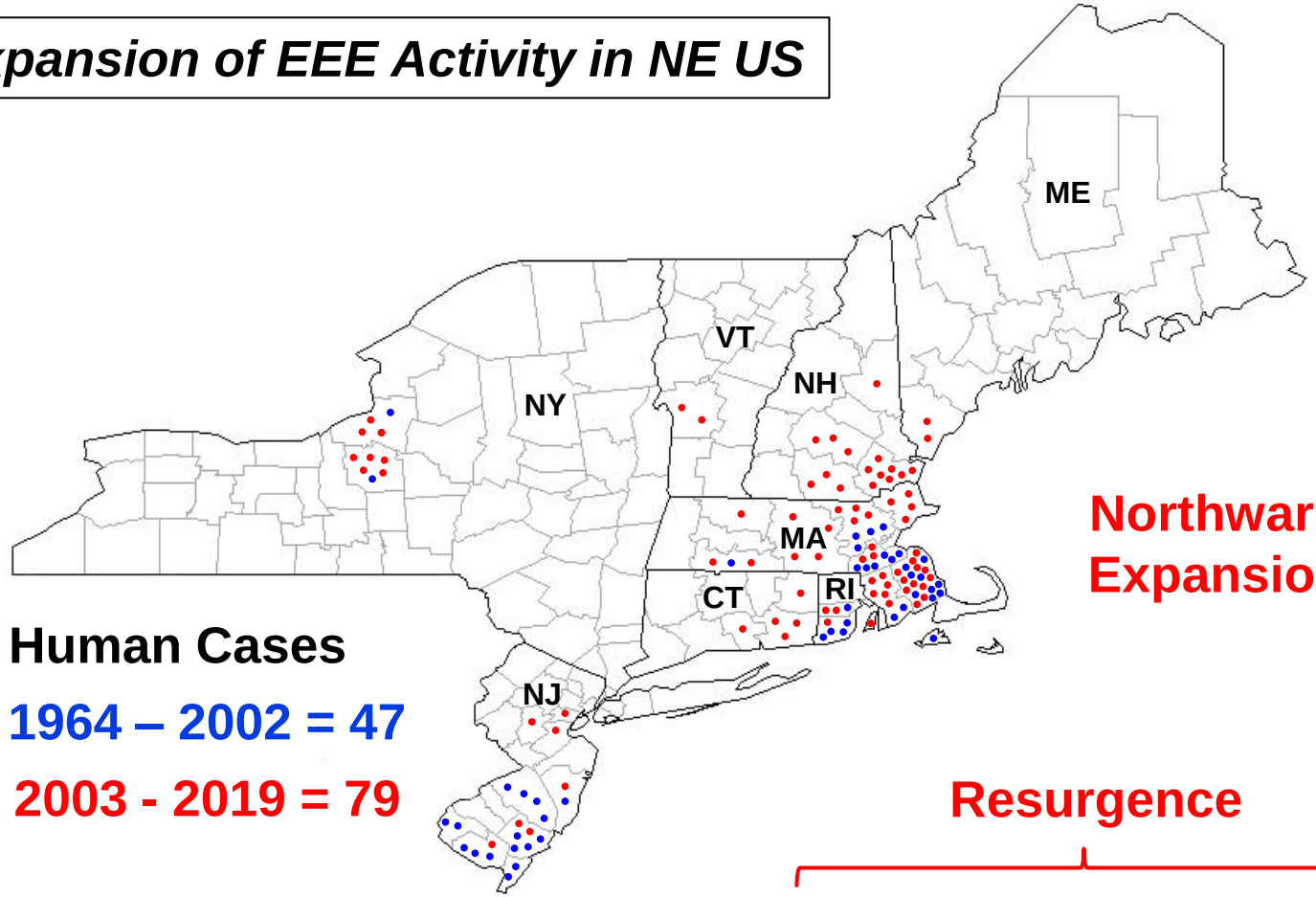


CDC

ArboNET

Resurgence and Expansion of EEE Activity in NE US

- **1964 to 2002 – sporadic outbreaks with no apparent pattern**
- **2003 – resurgence and expansion**



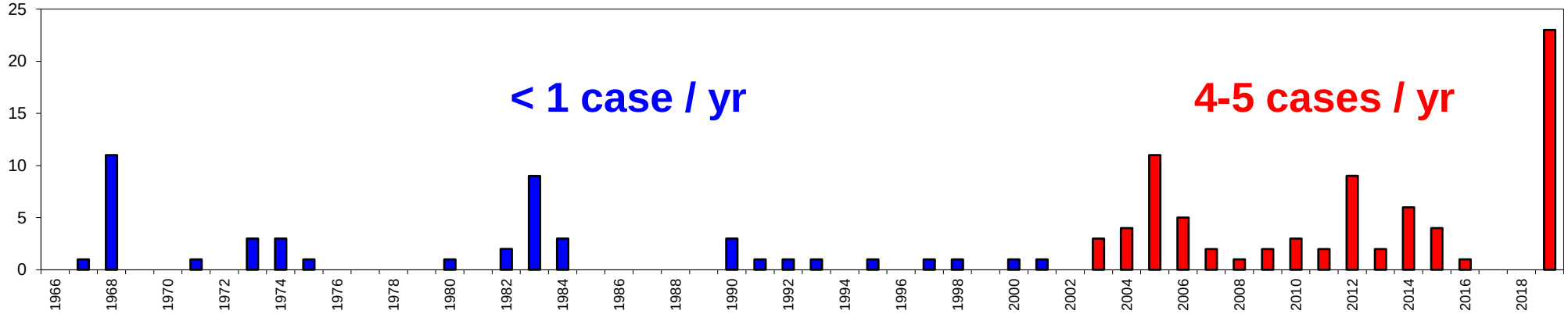
Northward Expansion

Human Cases

- 1964 – 2002 = 47

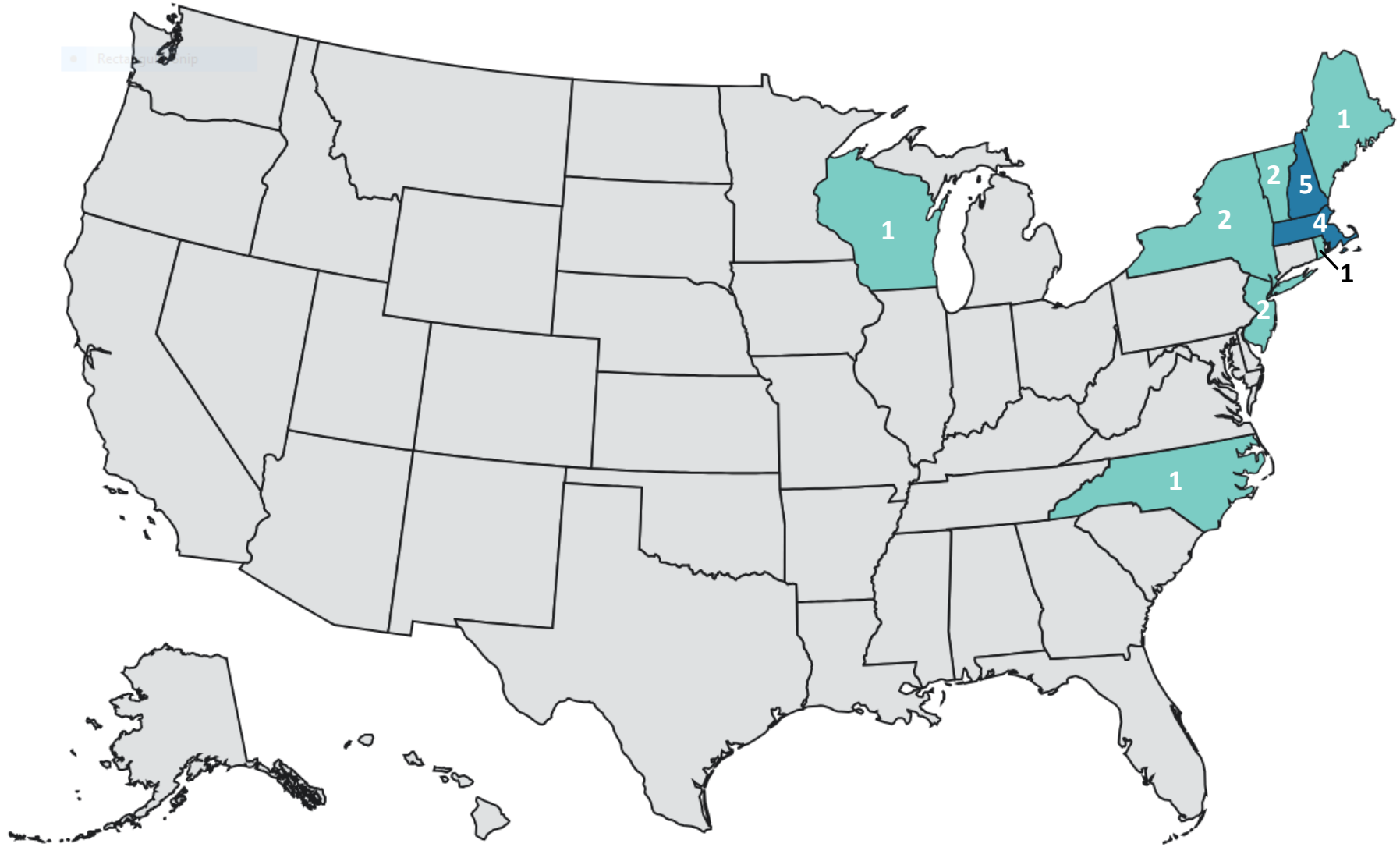
- 2003 - 2019 = 79

Resurgence



Armstrong & Andreadis J Med Entomol 2022

Human EEE Cases by State, 2024



Factors Contributing to the Resurgence of EEE in the Northeastern US

- Reforestation and wetland restoration – by mid 1800's much of the forests in the northeastern US were stripped and cedar swamps were destroyed

  - Increased habitat for *Culiseta melanura*
  - Proliferation of wetland roosting sites for birds (e.g. robins, wood thrush)

- Suburban development near critical wetland mosquito habitat

  - Increasingly expose people to the threat of EEE infection

- Changes in average temperatures and precipitation events related to climate change
  - Milder winters
  - Warmer summers
  - Extremes in both precipitation and drought

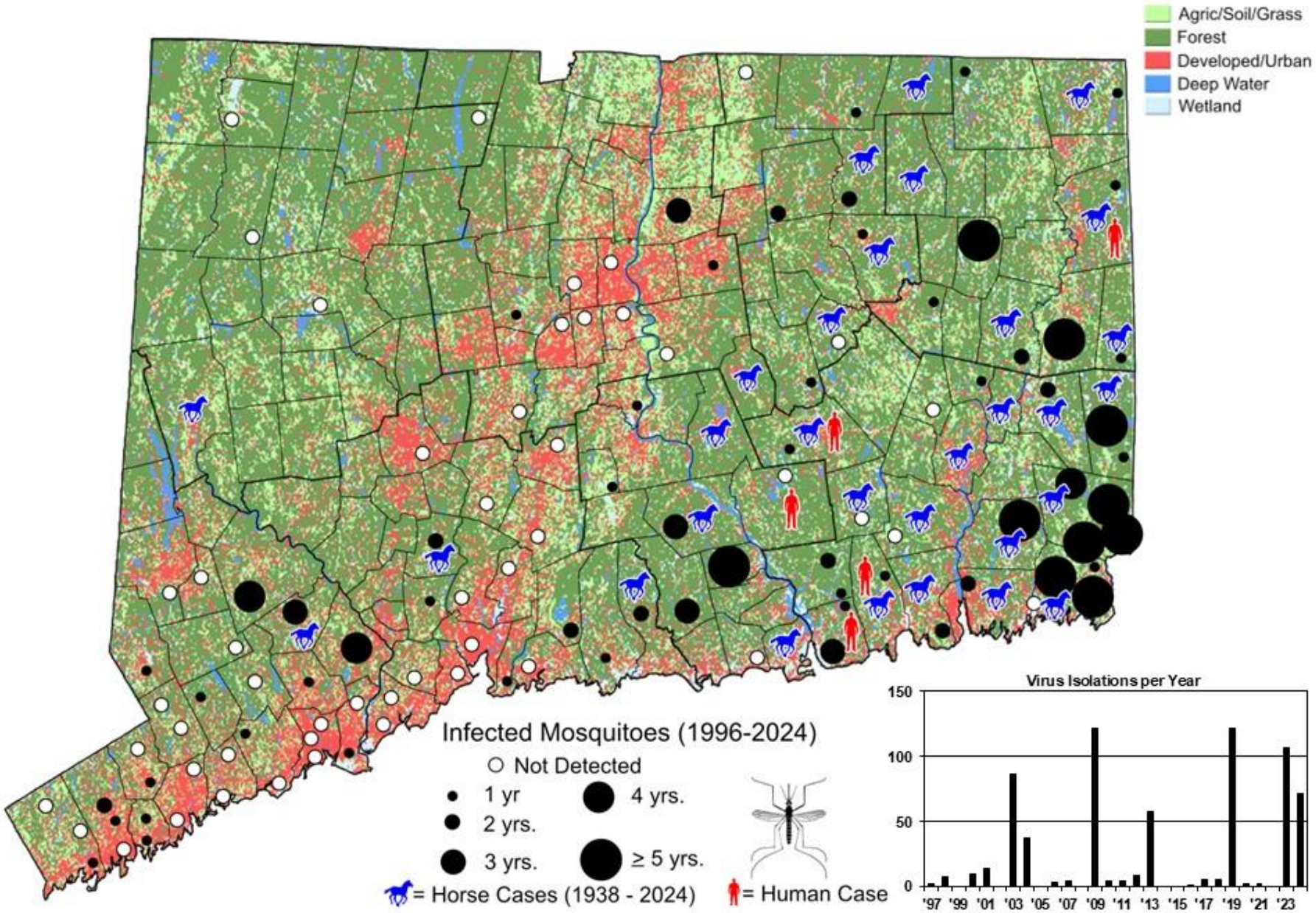
  - Enhance overwintering survival
  - Extend transmission season
  - Accelerate generation time
  - Increase frequency of blood feeding
  - Accelerate virus replication within mosquito
  - Allow mosquitoes to extend northward range

Komar & Spielman NY Acad Sci 1994
Armstrong & Andreadis J Med Entomol 2022

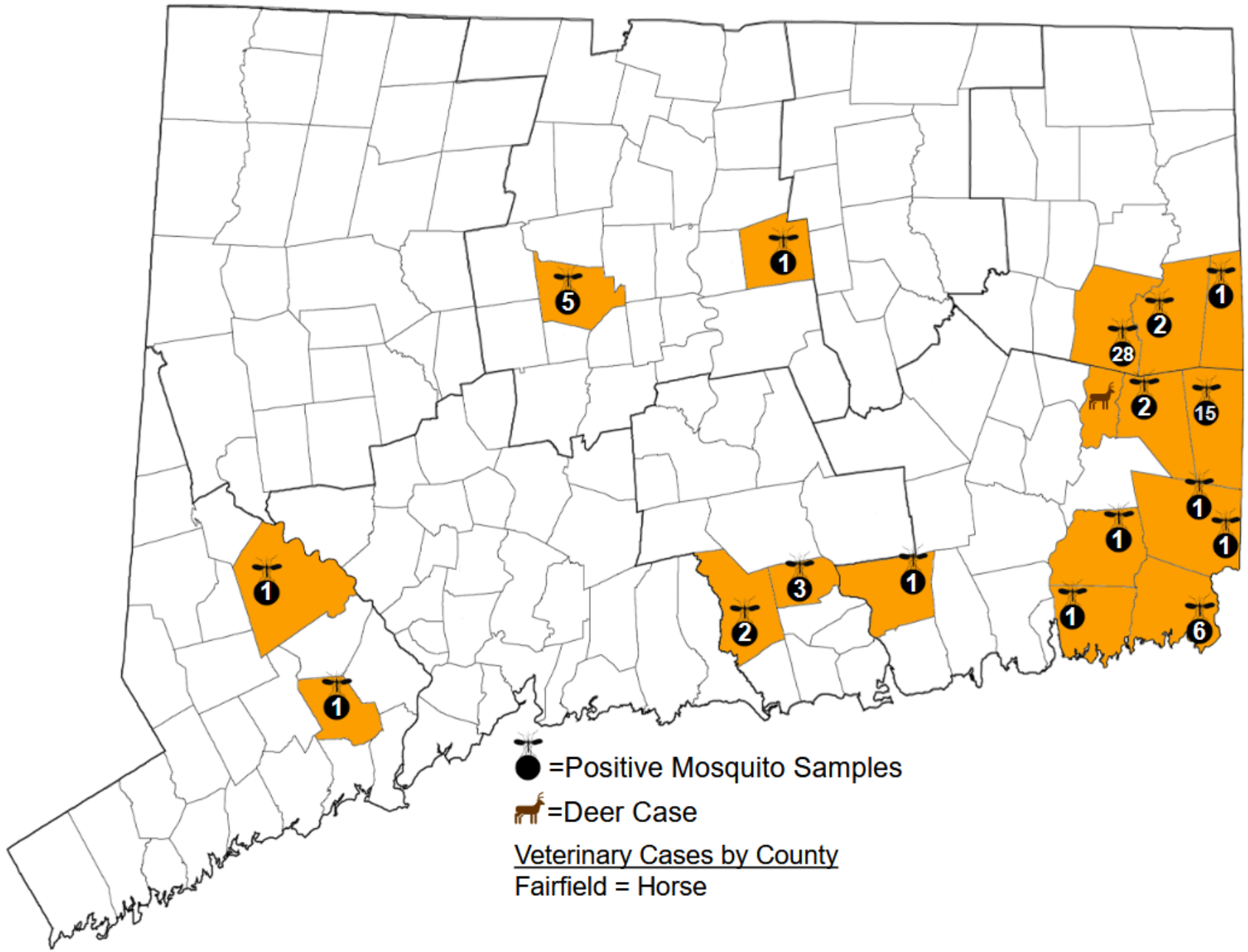
CT Mosquito Surveillance Program

- Established in response to EEE outbreak in 1996
- Mosquito trapping June-October
- 108 trapping stations
- Mosquitoes tested for virus infection in BSL-3 containment lab
- Information on virus-infected mosquitoes:
  - Early warning system
  - Assess risk of human infection
  - Guide mosquito control and disease prevention efforts

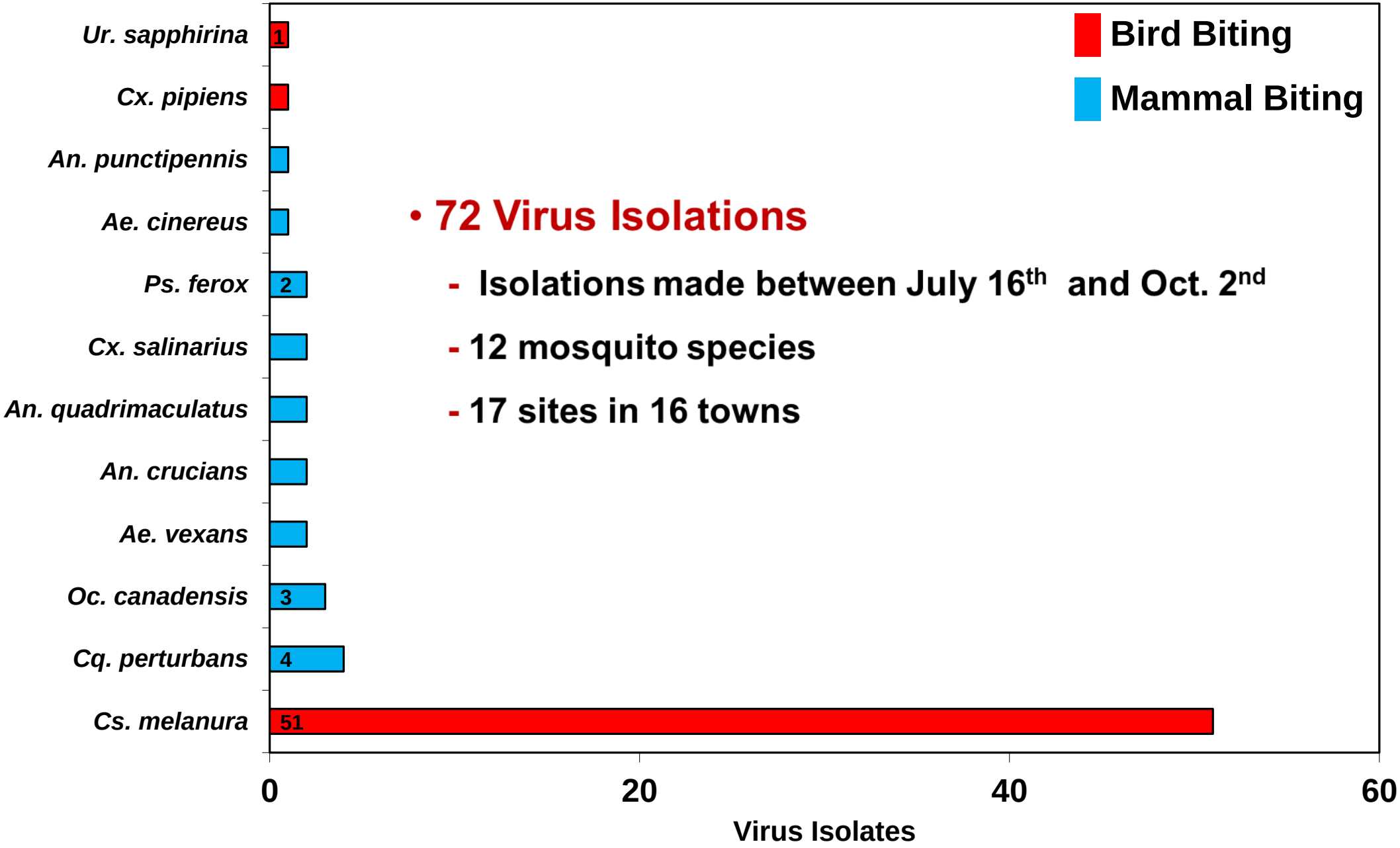
Eastern Equine Encephalitis Activity 1996-2024



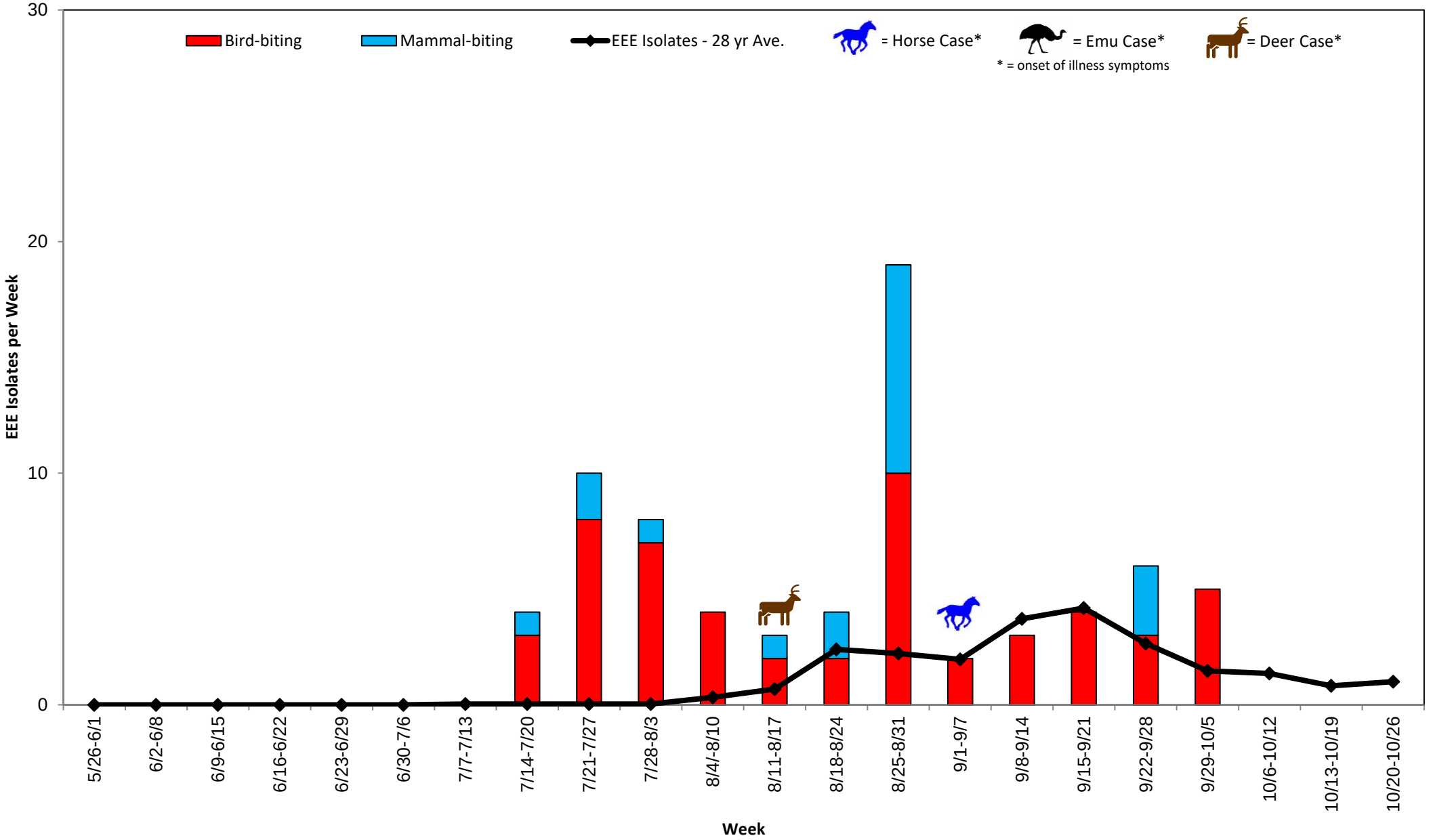
2024 Eastern Equine Encephalitis Activity



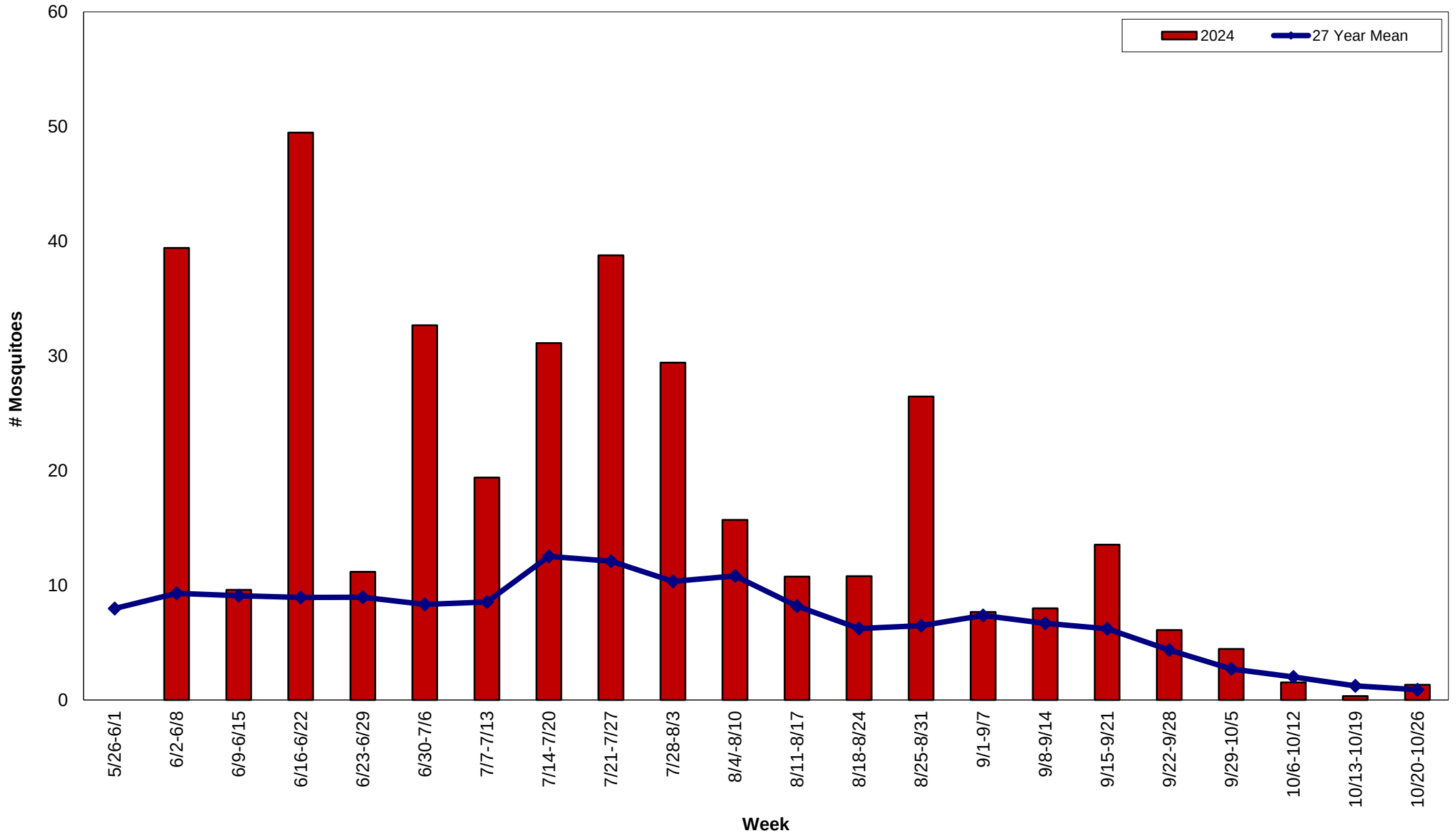
EEE Isolations from Mosquito Pools - Connecticut 2024



2024 Eastern Equine Encephalitis Isolates per Week



Culiseta melanura per Light Trap - 2024



EEE Response

1. Weekly conference calls with local health directors and elected officials
   - Provide updates on surveillance findings
   - Discuss messaging to constituents
2. Press releases issued and interviews to update and inform the public
3. Website on surveillance findings updated daily
4. Consistent messaging for personal protective measures
   - Information about EEE risk, prevention, and illness
5. Adulticide Application in Voluntown, Pachaug State Forest
   - EEE+ pools Cs. melanura, An. crucians
   - August 29: Camping Areas & State Forest Roads
   - Truck-mounted ULV application
   - NO additional EEE+ samples detected at location

Phylogenetic Analysis of EEE Virus During the 2019 Outbreak in the Northeastern US

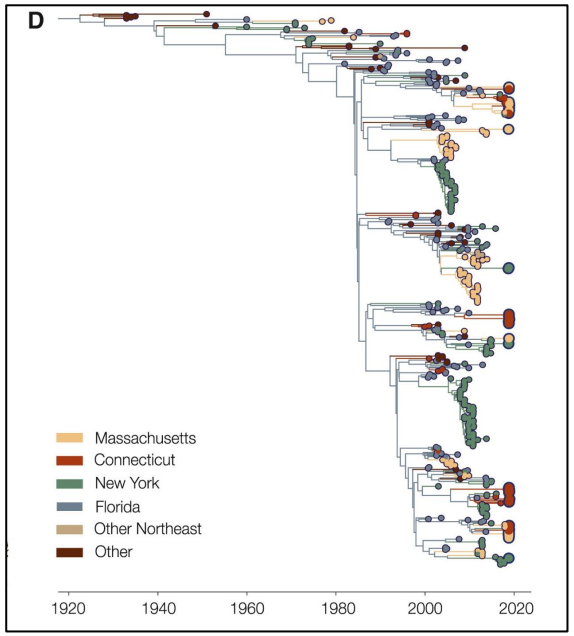
Current Biology

CellPress

Article

Dynamics of eastern equine encephalitis virus during the 2019 outbreak in the Northeast United States

Verity Hill,[1,16,*] Robert T. Koch,[1,16] Sean M. Bialosuknia,[2] Kiet Ngo,[2] Steven D. Zink,[2] Cheri A. Koetzner,[2] Joseph G. Maffei,[2] Alan P. Dupuis,[2] P. Bryon Backenson,[3] JoAnne Oliver,[4,5] Angela B. Bransfield,[6] Michael J. Misencik,[6] Tanya A. Petruff,[6] John J. Shepard,[6] Joshua L. Warren,[7,8] Mandev S. Gill,[9] Guy Baele,[10] Chantal B.F. Vogels,[1] Glen Gallagher,[11,12] Paul Burns,[11] Aaron Hentoff,[11] Sandra Smole,[11] Catherine Brown,[11] Matthew Osborne,[11] Laura D. Kramer,[2,13] Philip M. Armstrong,[1,5,15,*] Alexander T. Ciota,[2,13,15,*] and Nathan D. Grubaugh[1,7,14,15,17,*]



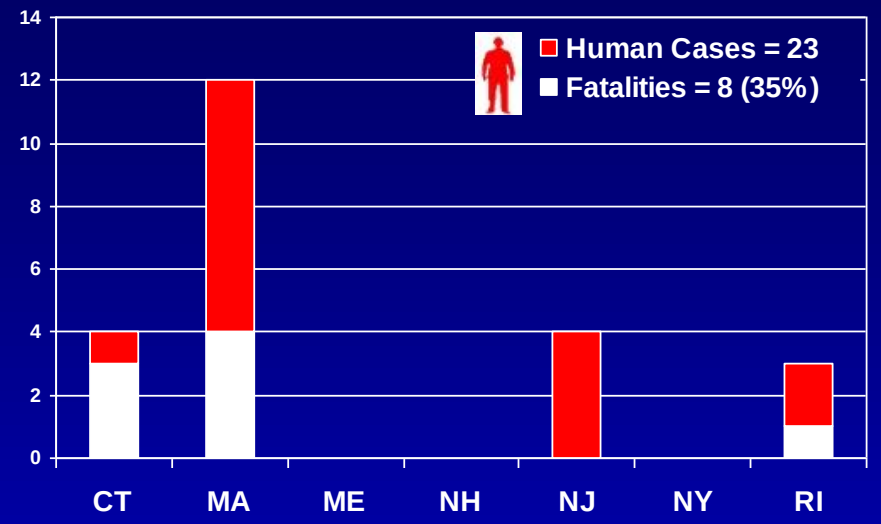
Wadsworth Center
NEW YORK STATE DEPARTMENT OF HEALTH
NEW YORK STATE

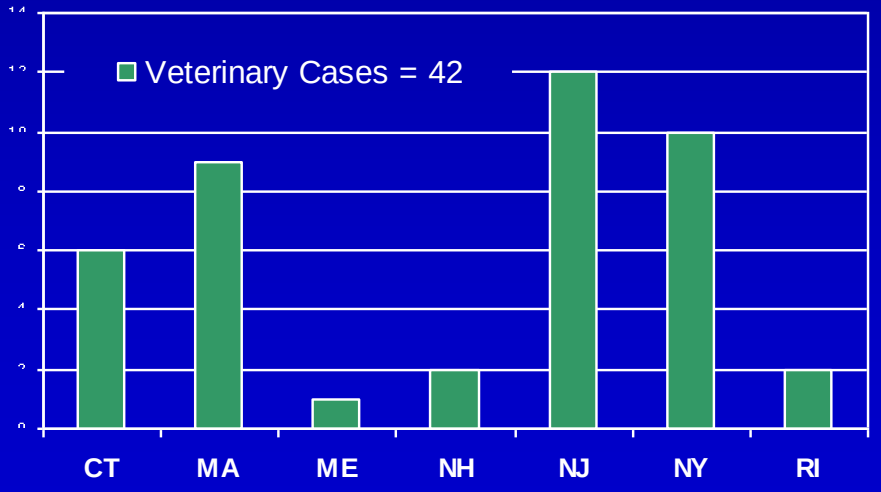
Yale
UNIVERSITY

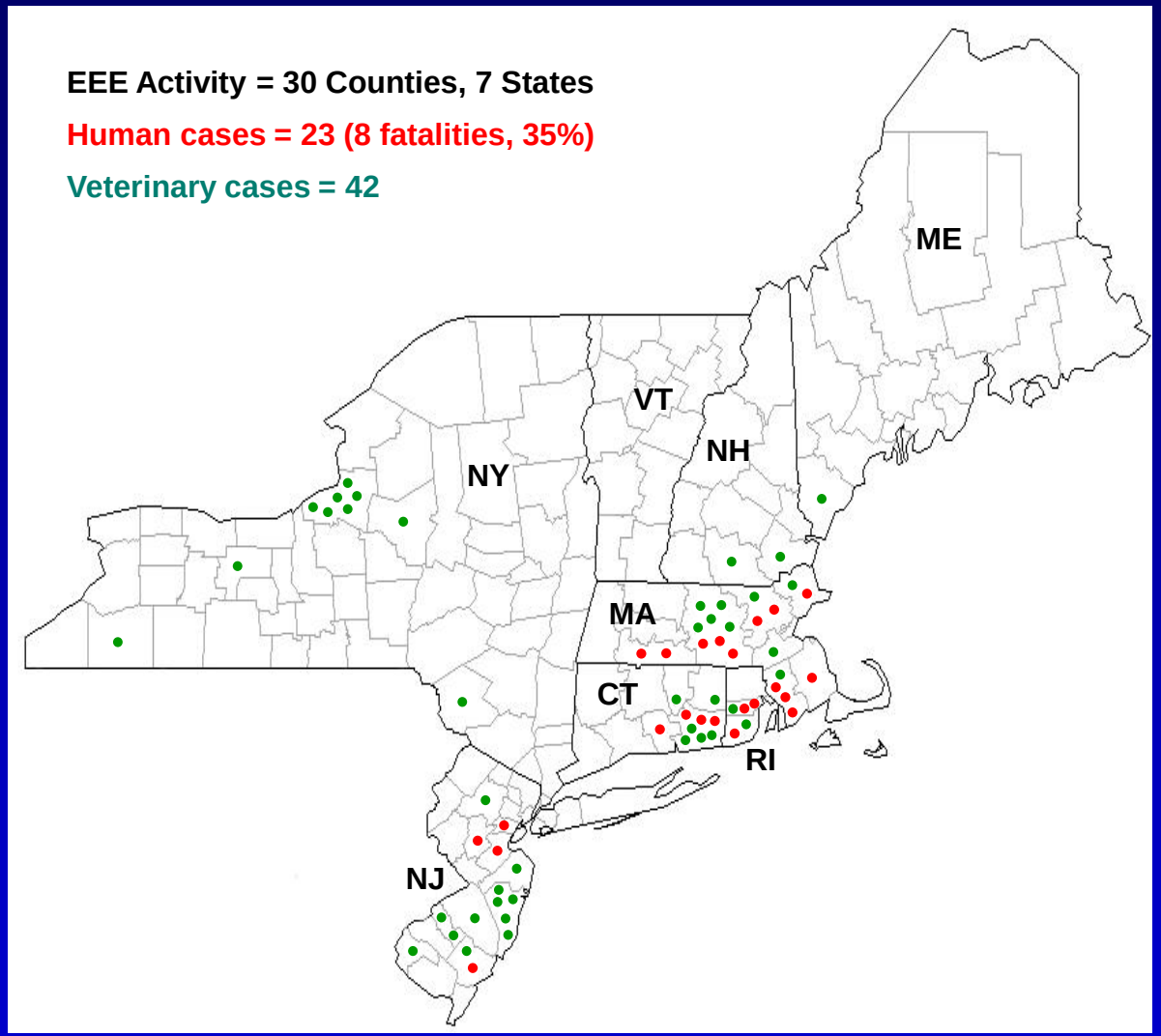
CAES
The Connecticut Agricultural Experiment Station
Putting Science to Work for Society since 1875

Massachusetts Department of Public Health

Human and Veterinary Cases of EEE in the Northeastern US - 2019

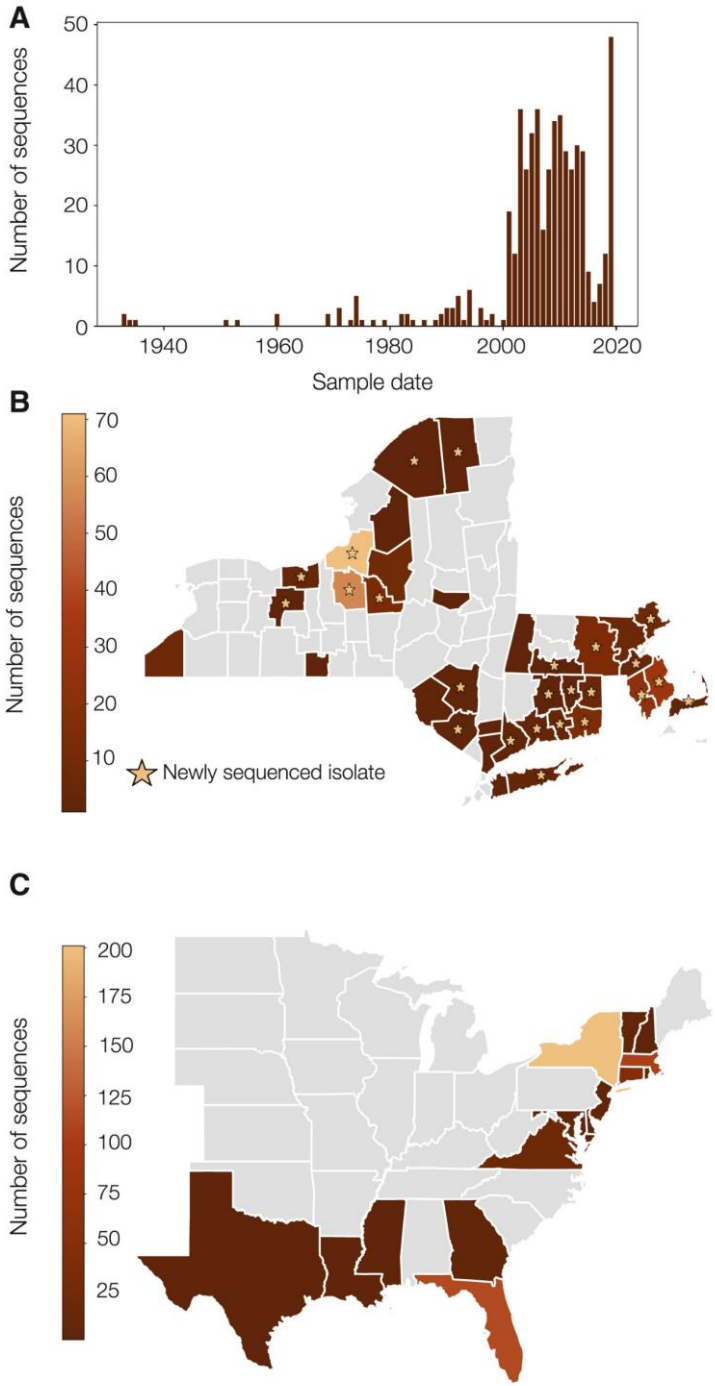






Objectives

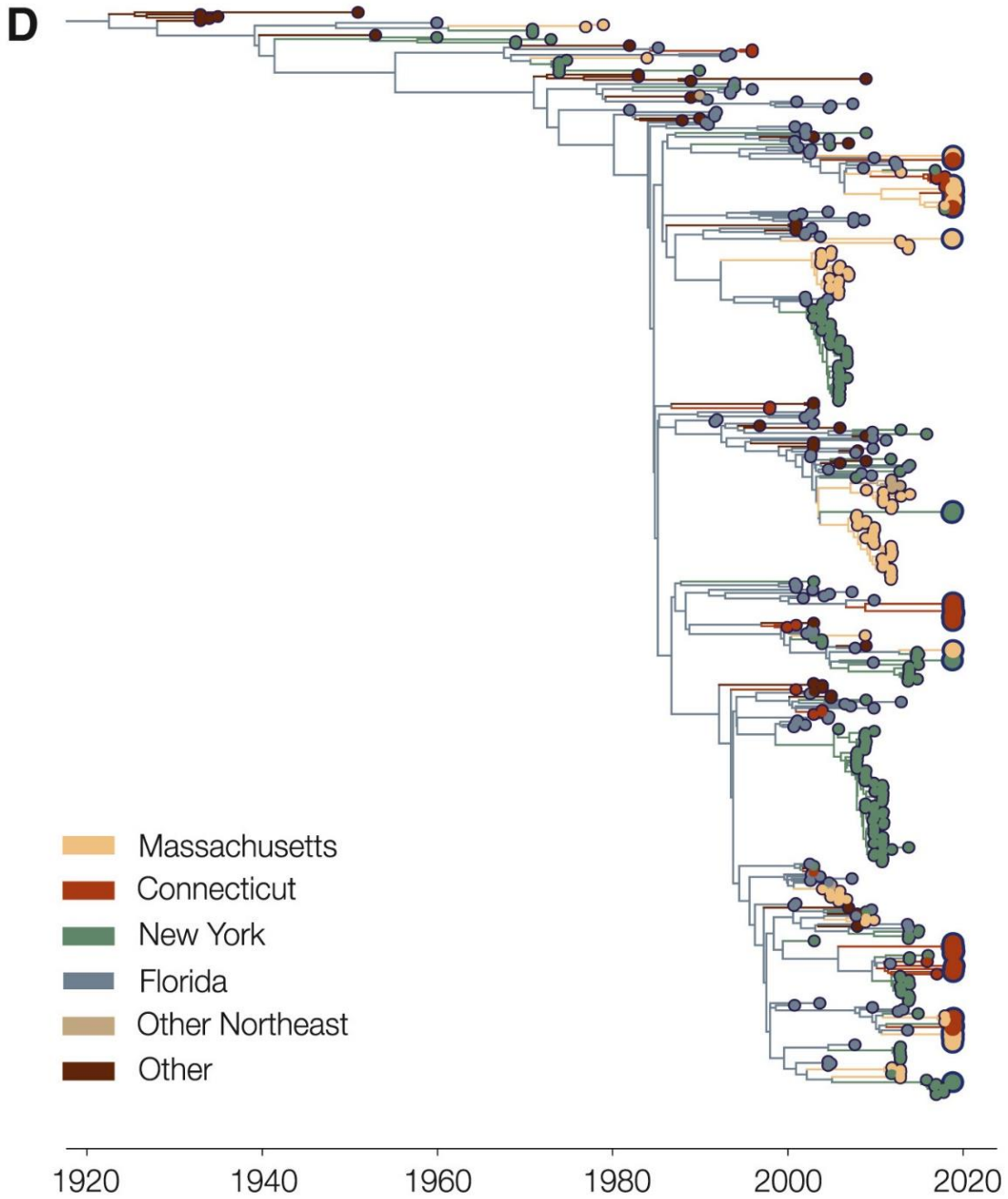
- Investigate the phylogeny of viruses during one of the largest EEE oubreaks in history
- Characterize genetic diversity of virus strains
  - Emergence of a single strain or multiple strains
- Identify viral origin(s) of the EEE oubreak
- Estimate persistence of viral lineages in northeastern foci



Sequences analyzed

- 531 strains total
  - Full genome
  - New sequences (n=80) + GenBank
- New sequences
  - Year
    - 2015-2018 (n=32)
    - 2019 (n=48)
  - location
    - Connecticut (n=38)
    - Massachusetts (n=17)
    - New York (n=25)
  - species
    - Mosquitoes (n=70)
    - Horses (n=9)
    - Turkey (n=1)

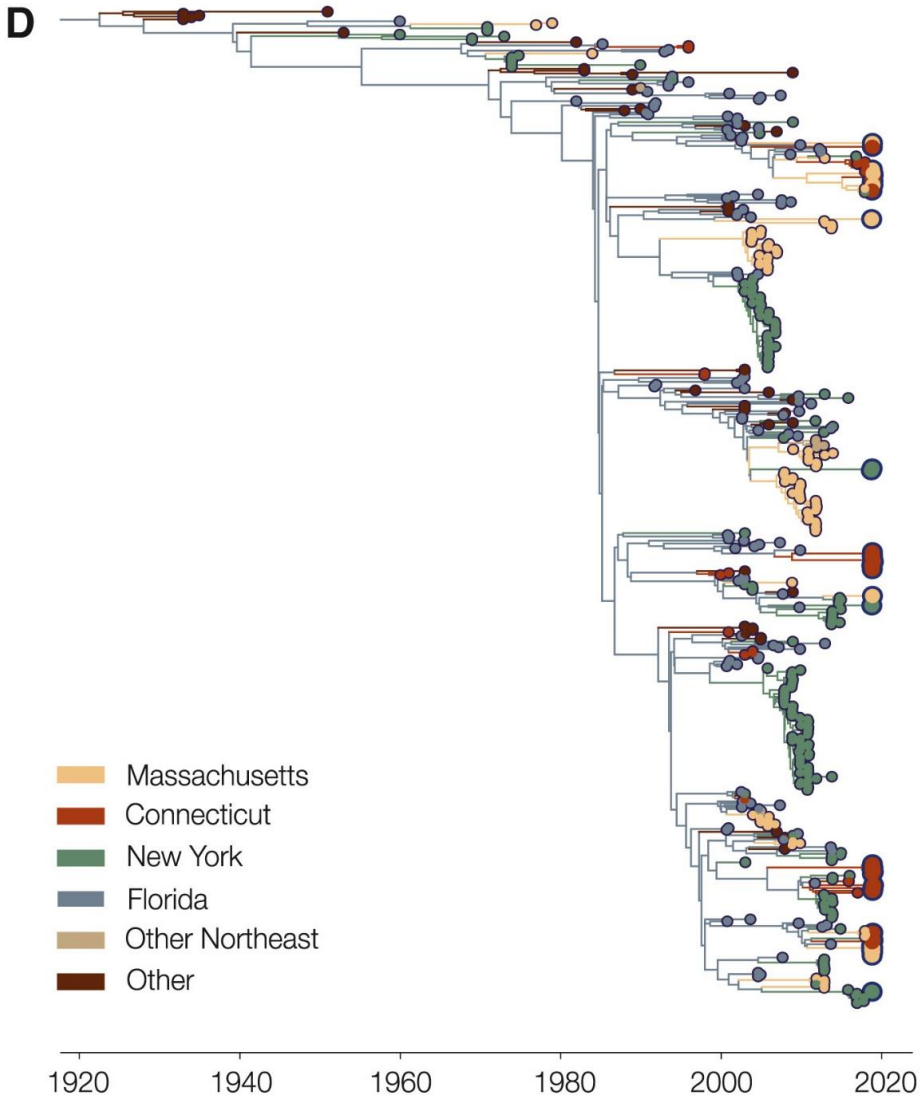
2023 Hill et al. *Current Biology*

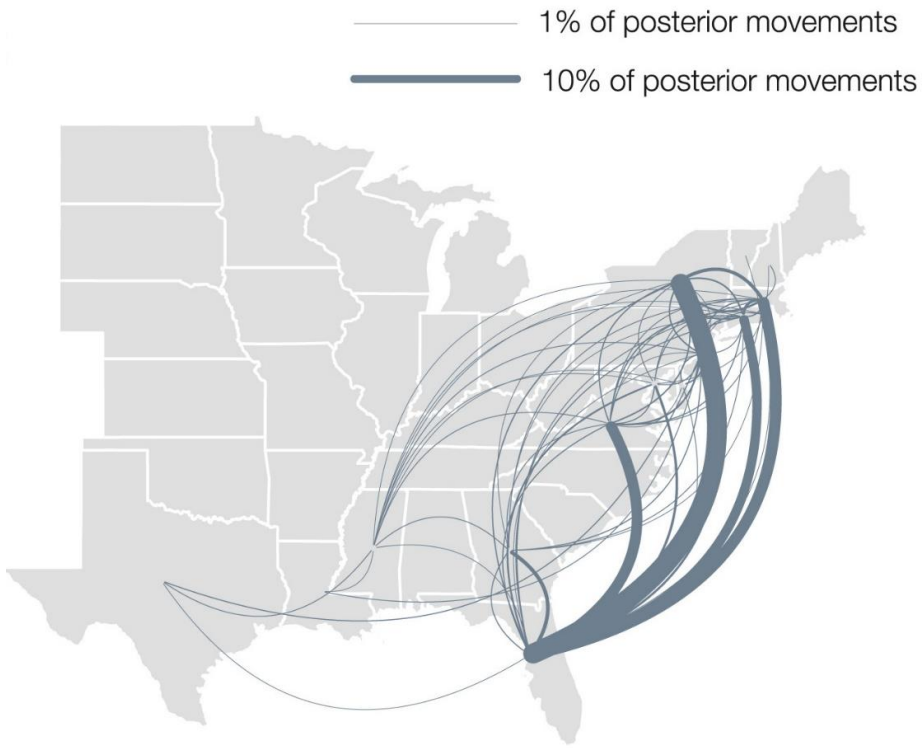


- EEE strains were highly diverse during the 2019 outbreak
- Multiple viral clades arose independently during 2019
- No shared mutations unique to 2019

2023 Hill et al. *Current Biology*

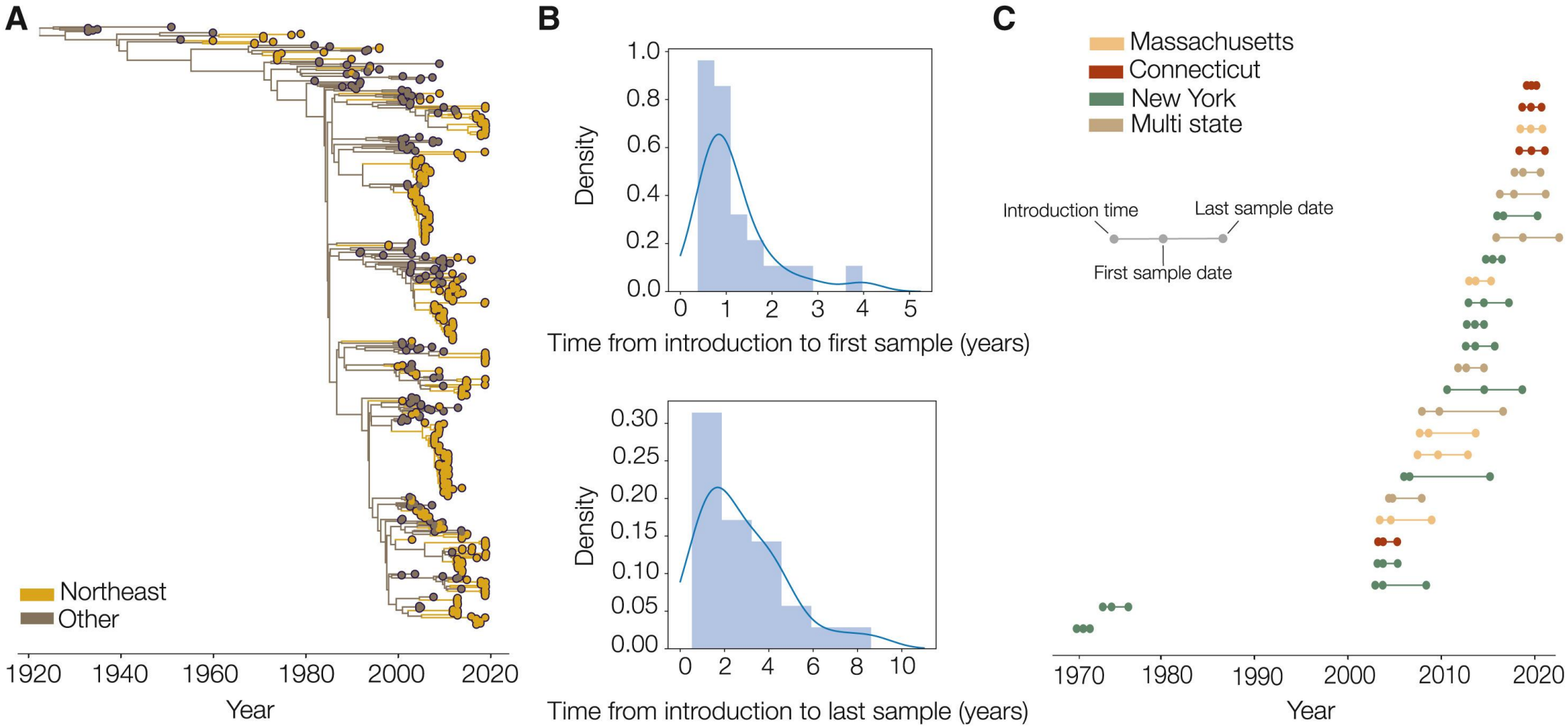
Florida serves as a major source population





2023 Hill et al. *Current Biology*

Short-term persistence of viral lineages in the Northeastern US



Conclusions

- EEE viruses were highly diverse in 2019
- Multiple viral clades arose independently during 2019
  - Multiple independent transmission chains
  - Not caused by a single introduction event
- No evidence that a more infectious variant was driving the epidemic
  - No shared mutations unique to 2019
  - No obvious superspreader strain
- Florida serves as a major source of EEE virus in northern foci
- EEE virus persist in northern foci over multiple years but without permanent establishment of local populations

Acknowledgements

The Connecticut Agricultural Experiment Station

Mosquito Collection and Identification

John Shepard
Tanya Petruff

Virus Isolation and Identification (BSL-3)

Michael Misencik
Angela Bransfield
Dr. Andrea Gloria-Soria

Seasonal Staff

Rabina Baiju
Steph Davies
Elliot Fetchin
Kendra Gluck
John McEachern
Jensen Mezzio
Mike Olson
Mike Pazareskis
Avraham Penso
Zehra Reza
Daria Rolle
Sam Rudolph
Emily Stelman
LuAnn Shaw
Liz Triana

CT Department of Public Health

Lynn Sosa
Brenda Esponda-Morrison
Karen Wolujewicz

CT Department of Agriculture

Dr. Erin Masur

UConn - CVMDL

Dr. Guillermo Risatti, Maureen Sims

CT Dept. of Energy & Environ. Protection

Roger Wolfe
Steve Rosa

U.S. Navy, Groton Sub Base

HM1 Nicholas Highers
HM2 Nate Gerry