

# Clifton McKee

## Disease Ecologist

Department of Epidemiology, Bloomberg School of Public Health, Johns Hopkins University

615 N Wolfe St, Room E6008 · Baltimore, MD 21205

✉ [clifton.mckee@gmail.com](mailto:clifton.mckee@gmail.com) ☎ +1 970 889 9540 🐙 [clifmckee.github.io](https://github.com/clifmckee)

## INTERESTS

disease ecology · epidemiology · data science · zoonoses · One Health · phylogenetics · evolution

## DEGREES

- 2015–2020 **PhD in Ecology** Colorado State University · Fort Collins, CO · Supervisor: Prof Colleen Webb
- 2013–2015 **MS in Ecology** Colorado State University · Fort Collins, CO · Supervisor: Prof Colleen Webb
- 2007–2011 **BS in Ecology & BA in Environmental Studies** University of Pittsburgh · Pittsburgh, PA

## RESEARCH EXPERIENCE

- 2020– **Johns Hopkins University** Research Associate & Postdoctoral Fellow · Baltimore, MD
  - Supervisor: Prof Emily Gurley
  - Co-wrote a funded NIH grant (\$3.2M, 1U01AI168287-01A1) on understanding the frequency and mechanisms of cross-species transmission of henipaviruses in Bangladesh
  - Led recruitment of teams and developed content for the Applied Modeling in Public Health workshop held in April 2022 at JHU
  - Led curation and writing of public-facing assessments of research on the ecology and spillover of SARS-related coronaviruses for the [2019 Novel Coronavirus Research Compendium](#)
  - 6 peer-reviewed articles, 3 as first or co-first author [including refs. [??](#), [??](#), [??](#)]
- 2015 & 2019 **Colorado State University** Research Assistant · Fort Collins, CO
  - Supervisor: Prof Colleen Webb
  - Assisted with data analysis and modeling of livestock movement and pathogen spread
  - Developed a [Shiny dashboard](#) to visualize county-to-county animal shipments in the US and presented the dashboard to stakeholders at USDA APHIS
  - 1 peer-reviewed article [ref. [??](#)]
- 2014–2019 **CDC Division of Vector-Borne Diseases** Regular Fellow & Guest Researcher · Fort Collins, CO
  - Supervisor: Dr Michael Kosoy
  - Independently performed DNA extraction, molecular detection, and phylogenetic analysis of bacterial pathogens in wildlife across multiple projects
  - Developed protocols and led bacterial pathogen infection experiments in rodents and fleas
  - 18 peer-reviewed articles, 7 as first or co-first author [including refs. [??](#), [??](#), [??](#), [??](#)]
- 2010 & 2013 **Emory University** Field Assistant & Field Research Specialist · Atlanta, GA
  - Supervisors: Profs Donna Maney & Brent Horton
  - Performed behavioral assays and assisted with tissue sampling of wild birds in Maine
  - 1 peer-reviewed article [ref. [??](#)]
- 2011 **University of California, Santa Cruz** Field Technician · Santa Cruz, CA
  - Supervisor: Prof Marm Kilpatrick
  - Captured wild birds and collected blood samples for West Nile virus surveillance in the Washington, DC area

## SELECTED PUBLICATIONS

A full list of publications is available on [Google Scholar](#). Repositories for projects on [GitHub](#) are indicated below.

<sup>†</sup>Equal contribution

1. **McKee CD**<sup>†</sup>, Islam A<sup>†</sup> et al. Nipah virus detection at bat roosts after spillover events, Bangladesh, 2012–2019. [Emerging Infectious Diseases](#). 2022; 28(7): 1384–1392.
2. Ruiz-Aravena M<sup>†</sup>, **McKee C**<sup>†</sup> et al. Ecology, evolution and spillover of coronaviruses from bats. [Nature Reviews Microbiology](#). 2022; 20: 299–314. [GitHub: bat\\_CoV\\_review](#)
3. **McKee CD** et al. The ecology of Nipah virus in Bangladesh: a nexus of land-use change and opportunistic feeding behavior in bats. [Viruses](#). 2021; 13(2): 169.
4. Gorsich EE et al. Model-guided suggestions for targeted surveillance based on cattle shipments in the US. [Preventive Veterinary Medicine](#). 2018; 150: 52–59.
5. **McKee C** et al. Bats are key hosts in the radiation of mammal-associated *Bartonella* bacteria. [Infection, Genetics and Evolution](#). 2021; 89: 104719.
6. **McKee CD** et al. Host phylogeny, geographic overlap, and roost sharing shape parasite communities in European bats. [Frontiers in Ecology and Evolution](#). 2019; 7: 69. [GitHub: eurobats](#)
7. Kosoy M<sup>†</sup>, **McKee C**<sup>†</sup> et al. Genotyping of *Bartonella* bacteria and their animal hosts: current status and perspectives. [Parasitology](#). 2018; 145(5): 543–562. [GitHub: genotyping-review](#)
8. **McKee CD** et al. Diversity and phylogenetic relationships among *Bartonella* strains from Thai bats. [PLOS ONE](#). 2017; 12(7): e0181696. [GitHub: thai-bats-bartonella](#)
9. Zinzow-Kramer WM et al. Genes located in a chromosomal inversion are correlated with territorial song in white-throated sparrows. [Genes, Brain and Behavior](#). 2015; 14(8): 641–654.