

CURRICULUM VITAE
CLIFTON D. MCKEE, Ph.D.

PROFESSIONAL DATA

Contact Information

Johns Hopkins University
Bloomberg School of Public Health
Department of Epidemiology
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Website & Social Media

Website: clifmckee.github.io
GitHub: [clifmckee](https://github.com/clifmckee)
Bluesky: [clifmckee.bluesky.social](https://bluesky.social/@clifmckee)

EDUCATION AND TRAINING

Degrees

Ph.D. / 2020 · Ecology · Colorado State University · Fort Collins, CO
Thesis: Evolutionary and ecological processes in microparasite communities of bats
Supervisor: Prof. Colleen Webb

M.S. / 2015 · Ecology · Colorado State University · Fort Collins, CO
Thesis: Spatial, demographic, and phylogenetic patterns of *Bartonella* diversity in bats
Supervisor: Prof. Colleen Webb

B.S. / 2011 · Ecology and Evolution · University of Pittsburgh · Pittsburgh, PA
B.A. / 2011 · Environmental Studies · University of Pittsburgh · Pittsburgh, PA
magna cum laude

Postdoctoral Training

2020–2022 · Johns Hopkins Bloomberg School of Public Health · Baltimore, MD
Member: [Infectious Disease Dynamics](#) · [Bat One Health](#)
Supervisor: Prof. Emily Gurley

PROFESSIONAL EXPERIENCE

Johns Hopkins University

Faculty Research Associate · Department of Epidemiology, Bloomberg School of Public Health (2023–present)

Postdoctoral Fellow · Department of Epidemiology, Bloomberg School of Public Health (2020–2022)

Centers for Disease Control and Prevention

Research Fellow · Bacterial Diseases Branch, Division of Vector-Borne Diseases (2015–2017)

PUBLICATIONS

Journal Articles (Peer Reviewed)

*Corresponding author, †Equal contribution, ‡Student advisee

[42] Loo SL, Jung SM, Contamin L, Howerton E, Bents SJ, Hochheiser H, Runge MC, Smith CP, Carcelén EC, Yan K, Lemaitre JC, ..., **McKee C**, ..., Shea K, Viboud C, Lessler J, Truelove S. Scenario projections of COVID-19 burden in the US, 2024–2025. *JAMA Network Open*. 2025; 8(9): e2532469. DOI: [10.1001/jamanetworkopen.2025.32469](https://doi.org/10.1001/jamanetworkopen.2025.32469)

[41] Bradburne C, Islam A, Bird I, Abbott E, Harrison S, Chunn M, Radune D, Hasan MR, Janes B, Lovett S, Lagergren J, ..., **McKee C**, ..., Gurley ES. Genomic surveillance detection of SARS-CoV-1-like viruses in Rhinolophidae bats, Bandarban Region, Bangladesh. *Emerging Infectious Diseases*. 2025; 31(8): 1652–1656. DOI: [10.3201/eid3108.250071](https://doi.org/10.3201/eid3108.250071)

[40] Schwantes CJ, Sánchez CA, Stevens T, Zimmerman R, Albery G, Becker DJ, Brookson CB, Kading RC, Keiser CN, Khandelwal S, Kramer-Schadt S, ..., **McKee C**, ..., Carlson CJ. A minimum data standard for wildlife disease research and surveillance. *Scientific Data*. 2025; 12: 1054. DOI: [10.1038/s41597-025-05332-x](https://doi.org/10.1038/s41597-025-05332-x)

[39] Verrett TB, Falvo CA, Benson E, Jones-Slobodian DN, Crowley DE, Dale AS, Lunn TJ, Ruiz-Aravena M, Rynda-Apple A, **McKee CD**, Clark KL, Gofton AW, Peel AJ, Plowright RK, Becker DJ. Bat One Health. *Borrelia* lineages adjacent to zoonotic clades in black flying foxes (*Pteropus alecto*), Australia, 2018–2020. *Emerging Infectious Diseases*. 2025; 37(7): 1415–1420. DOI: [10.3201/eid3107.241864](https://doi.org/10.3201/eid3107.241864)

[38] Niu Y‡, **McKee CD***. Bat viral shedding: a review of seasonal patterns and risk factors. *Vector-Borne and Zoonotic Diseases*. 2025; 25(4): 229–239. DOI: [10.1089/vbz.2024.0091](https://doi.org/10.1089/vbz.2024.0091)

[37] Jackson J‡, Shanta IS, **McKee C**, Luby SP, Haider N, Sharker Y, Plowright R, Hudson P, Gurley E. Identifying weather patterns affecting household date palm sap consumption in Bangladesh, 2013–2016. *PLOS ONE*. 2024; 19(11): e0313904. DOI: [10.1371/journal.pone.0313904](https://doi.org/10.1371/journal.pone.0313904)

[36] **McKee CD**, Yu EX, Garcia A‡, Jackson J‡, Koyuncu A, Rose S, Azman AS, Lobner K, Sacks E, Van Kerkhove MD, Gurley ES. Superspreading of SARS-CoV-2: a systematic review and

meta-analysis of event attack rates and individual transmission patterns. *Epidemiology & Infection*. 2024; 152: e121. DOI: [10.1017/S0950268824000955](https://doi.org/10.1017/S0950268824000955)

[35] McKee CD*, Peel AJ, Hayman DTS, Suu-Ire R, Ntiamoa-Baidu Y, Cunningham AA, Wood JLN, Webb CT, Kosoy MY. Ectoparasite and bacterial population genetics and community structure indicate extent of bat movement across an island chain. *Parasitology*. 2024; 151(7): 708–721. DOI: [10.1017/S0031182024000660](https://doi.org/10.1017/S0031182024000660)

[34] Mathis SM, Webber AE, León T, Murray EL, Sun M, White LA, Brooks LC, Green A, Hu AJ, Rosenfeld R, Shemetov D, ..., McKee CD, ..., Borcherding RK. Evaluation of FluSight influenza forecasting in the 2021–22 and 2022–23 seasons with a new target laboratory-confirmed influenza hospitalizations. *Nature Communications*. 2024; 15:6289. DOI: [10.1038/s41467-024-50601-9](https://doi.org/10.1038/s41467-024-50601-9)

[33] Cortes-Azuero O, Lefrancq N, Nikolay B, McKee C, Cappelle J, Hul V, Ou TP, Hoem T, Lemey P, Rahman MZ, Islam A, Gurley ES, Duong V, Salje H. The genetic diversity of Nipah virus across spatial scales. *The Journal of Infectious Diseases*. 2024; 230(6): e1235–e1244. DOI: [10.1093/infdis/jiae221](https://doi.org/10.1093/infdis/jiae221)

[32] Jung S-m, Loo SL, Howerton E, Contamin L, Smith CP, Carcelén EC, Yan K, Bents SJ, Levander J, Espino J, Lemaitre JC, ..., McKee CD, ..., Viboud C, Lessler J. Potential impact of annual vaccination with reformulated COVID-19 vaccines: lessons from the US COVID-19 scenario modeling hub. *PLOS Medicine*. 2024; 21(4): e1004387. DOI: [10.1371/journal.pmed.1004387](https://doi.org/10.1371/journal.pmed.1004387)

[31] Lemaitre JC, Loo SL, Kaminsky J, Lee EC, McKee C, Smith C, Jung S-m, Sato K, Carceles E, Hill A, Lessler J, Truelove S. *flepiMoP*: the evolution of a flexible infectious disease modeling pipeline during the COVID-19 pandemic. *Epidemics*. 2024; 47: 100753. DOI: [10.1016/j.epidem.2024.100753](https://doi.org/10.1016/j.epidem.2024.100753)

[30] Howerton E, Contamin L, Mullany LC, Qin MM, Reich NG, Bents SJ, Borcherding RK, Jung SM, Loo SL, Smith CP, Levander J, ..., McKee C, ..., Viboud C, Lessler J. Evaluation of the US COVID-19 Scenario Modeling Hub for informing pandemic response under uncertainty. *Nature Communications*. 2023; 14: 7260. DOI: [10.1038/s41467-023-42680-x](https://doi.org/10.1038/s41467-023-42680-x)

[29] Fagre AC, Islam A, Reeves WK, Kading RC, Plowright RK, Gurley ES, McKee CD*. *Bartonella* infection in fruit bats and bat flies, Bangladesh. *Microbial Ecology*. 2023; 86: 2910–2922. DOI: [10.1007/s00248-023-02293-9](https://doi.org/10.1007/s00248-023-02293-9)

[28] Szentiványi T, McKee C, Jones G, Foster JT. Trends in bacterial pathogens of bats: global distribution and knowledge gaps. *Transboundary and Emerging Diseases*. 2023; 9285855. DOI: [10.1155/2023/9285855](https://doi.org/10.1155/2023/9285855)

[27] Seidlova V, Straková P, Kejíková R, Nemcova M, Bartoňíčka T, Salát J, Dufková L, Šikutová S, Mendel J, McKee C, Zukal J, Pikula J, Rudolf I. Detection of *Leptospira* species in bat cadavers, Czech and Slovak Republics. *Emerging Microbes & Infections*. 2022; 11(1): 2211–2213. DOI: [10.1080/22221751.2022.2117095](https://doi.org/10.1080/22221751.2022.2117095)

[26] Kejíková R, McKee C, Straková P, Šikutová S, Mendel J, Rudolf I. First detection of *Bartonella* spp. in bat bugs *Cimex pipistrelli* (Hemiptera: Cimicidae), Central Europe. *Parasitology Research*. 2022; 121(11): 3341–3345. DOI: [10.1007/s00436-022-07668-4](https://doi.org/10.1007/s00436-022-07668-4)

- [25] Goodrich I, **McKee C**, Margos G, Kosoy M. Molecular characterization of a novel relapsing fever *Borrelia* species from the desert cottontail (*Sylvilagus audubonii*) in New Mexico, USA. *Journal of Wildlife Diseases*. 2022; 58(3): 646–651. DOI: [10.7589/JWD-D-21-00148](https://doi.org/10.7589/JWD-D-21-00148)
- [24] **McKee CD^{*†}**, Islam A[†], Rahman MZ, Khan SU, Rahman M, Satter SM, Islam A, Yinda CK, Epstein JH, Daszak P, Munster VJ. Nipah virus detection at bat roosts after spillover events, Bangladesh, 2012–2019. *Emerging Infectious Diseases*. 2022; 28(7): 1384–1392. DOI: [10.3201/eid-2807.212614](https://doi.org/10.3201/eid-2807.212614)
- [23] Rice BL[†], Lessler J[†], **McKee C[†]**, Metcalf CJ^{E†}. Why do some coronaviruses become pandemic threats when others do not? *PLOS Biology*. 2022; 20(5): e3001652. DOI: [10.1371/journal.pbio.3001652](https://doi.org/10.1371/journal.pbio.3001652)
- [22] Ruiz-Aravena M[†], **McKee C[†]**, Gamble A, Lunn T, Morris A, Snedden CE, Yinda CK, Port JR, Buchholz DW, Yeo YY, Faust C, ..., Munster VJ, Plowright RK. Ecology, evolution and spillover of coronaviruses from bats. *Nature Reviews Microbiology*. 2022; 20: 299–314. DOI: [10.1038/s41579-021-00652-2](https://doi.org/10.1038/s41579-021-00652-2)
- [21] Redd AD, Peetluk LS, Jarrett BA, Hanrahan C, Schwartz S, Rao A, Jaffe AE, Peer AD, Jones CB, Lutz CS, **McKee CD**, ..., Grabowski MK, Gurley ES, the Novel Coronavirus Research Compendium Team. Curating the evidence about COVID-19 for frontline public health and clinical care: the Novel Coronavirus Research Compendium. *Public Health Reports*. 2022; 137(2): 197–202. DOI: [10.1177/00333549211058732](https://doi.org/10.1177/00333549211058732)
- [20] Islam A, **McKee C**, Ghosh PK, Abedin J, Epstein JH, Daszak P, Luby SP, Khan SU, Gurley ES. Seasonality of date palm sap feeding behavior by bats in Bangladesh. *EcoHealth*. 2021; 18: 359–371. DOI: [10.1007/s10393-021-01561-9](https://doi.org/10.1007/s10393-021-01561-9)
- [19] Zorrilla VO, Lozano ME, Espada LJ, Kosoy M, **McKee C**, Valdivia HO, Arevalo H, Troyes M, Stoops CA, Fisher ML, Vásquez GM. Comparison of sand fly trapping approaches for vector surveillance of *Leishmania* and *Bartonella* species in ecologically distinct, endemic regions of Peru. *PLOS Neglected Tropical Diseases*. 2021; 15(7): e0009517. DOI: [10.1371/journal.pntd.0009517](https://doi.org/10.1371/journal.pntd.0009517)
- [18] **McKee CD^{*}**, Islam A, Luby SP, Salje H, Hudson PJ, Plowright RK, Gurley ES. The ecology of Nipah virus in Bangladesh: a nexus of land-use change and opportunistic feeding behavior in bats. *Viruses*. 2021; 13(2): 169. DOI: [10.3390/v13020169](https://doi.org/10.3390/v13020169)
- [17] **McKee C^{*}**, Bai Y, Webb C, Kosoy M. Bats are key hosts in the radiation of mammal-associated *Bartonella* bacteria. *Infection, Genetics and Evolution*. 2021; 89: 104719. DOI: [10.1016/j.meegid.2021.104719](https://doi.org/10.1016/j.meegid.2021.104719)
- [16] Goodrich I, **McKee C**, Kosoy M. *Trypanosoma* (*Herpetosoma*) diversity in rodents and lagomorphs of New Mexico with a focus on epizootological aspects of infection in Southern Plains woodrats (*Neotoma micropus*). *PLOS ONE*. 2020; 15(12): e0244803. DOI: [10.1371/journal.pone.0244803](https://doi.org/10.1371/journal.pone.0244803)
- [15] Rudolf I, Blažejová H, Mendel J, Straková P, Šebesta O, Rettich F, Čabanová V, Miterpáková M, Betášová L, Peško J, Barbušinová E, **McKee C**, Osikowicz L, Šikutová S, Hubálek Z, Kosoy M. *Bartonella* species in medically important mosquitoes, Central Europe. *Parasitology Research*.

2020; 119(8): 2713–2717. DOI: [10.1007/s00436-020-06732-1](https://doi.org/10.1007/s00436-020-06732-1)

[14] Goodrich I, **McKee C**, Kosoy M. Longitudinal study of bacterial infectious agents in a community of small mammals in New Mexico. *Vector-Borne and Zoonotic Diseases*. 2020; 20(7): 496–508. DOI: [10.1089/vbz.2019.2550](https://doi.org/10.1089/vbz.2019.2550)

[13] **McKee CD***, Krawczyk AI, Sándor AD, Görföl T, Földvári M, Földvári G, Dekeukeleire D, Haarsma A-J, Kosoy MY, Webb CT, Sprong H. Host phylogeny, geographic overlap, and roost sharing shape parasite communities in European bats. *Frontiers in Ecology and Evolution*. 2019; 7: 69. DOI: [10.3389/fevo.2019.00069](https://doi.org/10.3389/fevo.2019.00069)

[12] Bai Y, Osinubi MOV, Osikowicz L, **McKee C**, Vora NM, Rizzo MR, Recuenco S, Davis L, Niezgoda M, Ehimiyein AM, Kia GSN, Oyemakinde A, Adeniyi OS, Gbadegesin YH, Saliman OA, Ogunniyi A, Ogunkoya AB, Kosoy MY, Idanre Bat Festival Investigation Team. Human exposure to novel *Bartonella* species from contact with fruit bats. *Emerging Infectious Diseases*. 2018; 24(12): 2317–2323. DOI: [10.3201/eid2412.181204](https://doi.org/10.3201/eid2412.181204)

[11] Kellner A, Carver S, Scorza V, **McKee CD**, Lappin M, Crooks KR, VandeWoude S, Antolin MF. Transmission pathways and spillover of an erythrocytic bacterial pathogen from domestic cats to wild felids. *Ecology and Evolution*. 2018; 8(19): 9779–9792. DOI: [10.1002/ece3.4451](https://doi.org/10.1002/ece3.4451)

[10] **McKee CD***, Osikowicz LM, Schwedhelm TR, Maes SE, Enscore RE, Gage KL, Kosoy MY. Acquisition of *Bartonella elizabethae* by experimentally exposed oriental rat fleas (*Xenopsylla cheopis*; Siphonaptera, Pulicidae) and excretion of *Bartonella* DNA in flea feces. *Journal of Medical Entomology* 2018; 55(5): 1292–1298. DOI: [10.1093/jme/tjy085](https://doi.org/10.1093/jme/tjy085)

[9] Kosoy M[†], **McKee C[†]**, Albayrak L, Fofanov Y. Genotyping of *Bartonella* bacteria and their animal hosts: current status and perspectives. *Parasitology*. 2018; 145(5): 543–562. DOI: [10.1017/S0031182017001263](https://doi.org/10.1017/S0031182017001263)

[8] Gorsich EE, **McKee CD**, Gear DA, Miller RS, Portacci K, Lindström T, Webb CT. Model-guided suggestions for targeted surveillance based on cattle shipments in the U.S. *Preventive Veterinary Medicine*. 2018; 150: 52–59. DOI: [10.1016/j.prevetmed.2017.12.004](https://doi.org/10.1016/j.prevetmed.2017.12.004)

[7] **McKee CD***, Osikowicz LM, Schwedhelm TR, Bai Y, Castle KT, Kosoy MY. Survey of parasitic bacteria in bat bugs, Colorado. *Journal of Medical Entomology*. 2018; 55(1): 237–241. DOI: [10.1093/jme/tjx155](https://doi.org/10.1093/jme/tjx155)

[6] **McKee CD***, Kosoy MY, Bai Y, Osikowicz LM, Franka R, Gilbert AT, Boonmar S, Rupprecht CE, Peruski LF. Diversity and phylogenetic relationships among *Bartonella* strains from Thai bats. *PLOS ONE*. 2017; 12(7): e0181696. DOI: [10.1371/journal.pone.0181696](https://doi.org/10.1371/journal.pone.0181696)

[5] Urushadze L, Bai Y, Osikowicz L, **McKee C**, Sidamonidze K, Putkaradze D, Imnadze P, Kandaurov A, Kuzmin I, Kosoy M. Prevalence, diversity, and host associations of *Bartonella* strains in bats from Georgia (Caucasus). *PLOS Neglected Tropical Diseases*. 2017; 11(4): e0005428. DOI: [10.1371/journal.pntd.0005428](https://doi.org/10.1371/journal.pntd.0005428)

[4] Bai Y, Urushadze L, Osikowicz L, **McKee C**, Kuzmin I, Kandaurov A, Babuadze G, Natradze I, Imnadze P, Kosoy M. Molecular survey of bacterial zoonotic agents in bats from the country of Georgia (Caucasus). *PLOS ONE*. 2017; 12(1): e0171175. DOI: [10.1371/journal.pone.0171175](https://doi.org/10.1371/journal.pone.0171175)

[3] **McKee CD***, Hayman DTS, Kosoy MY, Webb CT. Phylogenetic and geographic patterns of bartonella host shifts among bat species. *Infection, Genetics and Evolution*. 2016; 44: 382–394. DOI: [10.1016/j.meegid.2016.07.033](https://doi.org/10.1016/j.meegid.2016.07.033)

[2] Zinzow-Kramer WM, Horton BM, **McKee CD**, Michaud JM, Tharp GK, Thomas JW, Tuttle EM, Yi S, Maney DL. Genes located in a chromosomal inversion are correlated with territorial song in white-throated sparrows. *Genes, Brain and Behavior*. 2015; 14(8): 641–654. DOI: [10.1111/gbb.12252](https://doi.org/10.1111/gbb.12252)

[1] Bai Y, Hayman DTS, **McKee CD**, Kosoy MY. Classification of *Bartonella* strains associated with straw-colored fruit bats (*Eidolon helvum*) across Africa using a multi-locus sequence typing platform. *PLOS Neglected Tropical Diseases*. 2015; 9(1): e0003478. DOI: [10.1371/journal.pntd.0003478](https://doi.org/10.1371/journal.pntd.0003478)

Articles, Editorials, and Other Publications (Not Peer Reviewed)

Deposited in a Pre-Print Server

[2] Ingala M, Oliveira H, Frank LE, Hussain M, Kazam A, Becker DJ, Cummings C, Dalannast M, Kingston T, Krauel J, Mavian C, **McKee CD**, ..., Lauterbur ME. Bats in Habitats, Bats as Habitats: an integrative ecological framework for understanding synergistic interactions across levels of community organization. *EcoEvoRxiv*. 2025. DOI: [10.32942/X2RW59](https://doi.org/10.32942/X2RW59)

[1] **McKee CD***, Webb CT, Kosoy MY, Bai Y, Osikowicz LM, Suu-Ire R, Ntiamoa-Baidu Y, Cunningham AA, Wood JL, Hayman DT. Manipulating vector transmission reveals local processes in bacterial communities of bats. *bioRxiv*. 2021. DOI: [10.1101/2021.03.03.433743](https://doi.org/10.1101/2021.03.03.433743)

HONORS AND AWARDS

Vice President for Research Fellowship · Colorado State University (2018)
Department of Biology Travel Award · Colorado State University (2014 & 2017)
Sharon E. and David E. Kabes Scholarship · Colorado State University (2015)
GDPE Research Grant · Colorado State University (2014)
Department of Biology Graduate Fellowship · Colorado State University (2013)
Phi Beta Kappa · University of Pittsburgh (2011)

EDITORIAL AND OTHER INVITED PEER REVIEW ACTIVITIES

Journal Peer Review Activities

Acta Chiropterologica · Acta Tropica · Annals of the New York Academy of Sciences · BMC Microbiology · BMJ · Current Zoology · Ecology and Evolution · Frontiers in Microbiology · Frontiers in Veterinary Science · Infection, Genetics and Evolution · Journal of Animal Ecology · Journal of Medical Entomology · Journal of Zoological Systematics and Evolutionary Research · Microbial Ecology · Microbial Pathogenesis · Molecular Ecology · mSphere · Nature Microbiology · Parasitology Research · Pathogens and Global Health · PLOS Neglected Tropical Diseases · PLOS ONE · PNAS Nexus · The European Zoological Journal · The Lancet Planetary Health · The Science of

Nature · Scientific Reports · Systematic Biology · Tropical Biomedicine · Veterinary Microbiology · Viruses · Zoonoses and Public Health

Proposal Peer Reviews

Netherlands Organization for Health Research and Development (ZonMw), Infectious Disease Control Program (2023)

PROFESSIONAL ACTIVITIES

Society Membership

North American Society for Bat Research (2021–present) · American Society of Tropical Medicine and Hygiene (2021–present) · Society for the Study of Evolution (2019 & 2021) · American Society of Naturalists (2019) · Ecological Society of America (2014–2019)

PRACTICE ACTIVITIES

Software and Other Product Development

The Flexible Epidemic Modeling Pipeline ([flepiMoP](#)) · A software suite for simulating a wide range of compartmental models of infectious disease transmission [[Available on GitHub](#)]

[USAMM R Shiny Visualization](#) · Developed tool for visualizing estimated county-to-county animal shipments in the US · Presented to stakeholders at USDA APHIS (2015)

Other Practice Activities

Bat Virus Spillover Virus Compendium (Bat-Com) · Led team of researchers to curate and write public-facing summaries and assessments of research articles on the spillover of SARS-CoV, SARS-CoV-2, and related coronaviruses

[2019 Novel Coronavirus Research Compendium \(NCRC\)](#) · Curated and wrote public-facing summaries and assessments of research articles on the Ecology & Spillover of SARS-CoV-2 and related coronaviruses (2020–2021)

Media Dissemination

[Climate Change Likely to Expand the Range of an Asian Bat and the Deadly Disease it Carries](#) · Interview with *Inside Climate News* (2025)

[Nipah virus: Of Fruit and Bats](#) · [Interview with This Podcast Will Kill You](#) (2024)

[Lurking in the Shadows](#) · Feature article in *The Scientist Magazine* (2014)

[Disease on the Wing](#) · YouTube video produced by *The Scientist Magazine* (2014)

CURRICULUM VITAE
CLIFTON D. MCKEE, Ph.D.
PART II

TEACHING

Academic Advisees

Elias Chan · Master of Science, Epidemiology · Johns Hopkins Bloomberg School of Public Health (2024–2025) · Thesis: Exploratory analysis of collected bat and tree data from date palm sap harvesting in Bangladesh from December 2023 to March 2024

Yannan Niu · Master of Health Science, Epidemiology · Johns Hopkins Bloomberg School of Public Health (2023–2024) · Thesis: Bat viral shedding: a review of seasonal patterns and risk factors

Capstone Advisees

Juanita Losier · Master of Public Health · Johns Hopkins Bloomberg School of Public Health (2024–present)

Master's Thesis Reader

Andrés Garcia · Master of Health Science, Epidemiology · Johns Hopkins Bloomberg School of Public Health (2023–2024) · Thesis: Literature review on risk factors for transmission of *Orientia tsutsugamushi* in Thailand, Vietnam, and Malaysia

Jules Jackson · Master of Science, Epidemiology · Johns Hopkins Bloomberg School of Public Health (2022–2023) · Thesis: Identifying weather patterns affecting household date palm sap consumption in Bangladesh, 2013–2016

Doctoral Thesis Committee

Darshan Sreenivas · National Centre for Biological Sciences · Bengaluru, India (2024–present)

Final Oral Exam Participation

Laura MacKenzie · External Examiner for PhD viva · School of Biological Sciences, University of Aberdeen · Aberdeen, Scotland (2023)

Classroom Instruction: Instructor of Record

Johns Hopkins University

[Introduction to R for Public Health Researchers](#) (140.604.73/79) · Co-Instructors: Ava Hoffman, Carrie Wright · Winter/Summer Institutes (2023–present, enrollment: 16–35)

The One Health Approach to Epidemiology and Global Public Health (340.610.81) · Co-Instructor: Emily Gurley · Spring Fourth Term (2023–present, enrollment: 35–45)

Classroom Instruction: Teaching Assistant

Johns Hopkins University

Topics in Infectious Disease Epidemiology (340.668.89) · Teaching Assistant (2022)

The One Health Approach to Epidemiology and Global Public Health (340.610.81) · Teaching Assistant (2021 & 2022)

Epidemiology of Infectious Diseases (340.627.01) · Teaching Assistant (2020 & 2021)

Colorado State University

Molecular and General Genetics (BZ 350) · Teaching Assistant & Recitation Instructor (2014, 2018 & 2019)

Introduction to Evolution (BZ 220) · Teaching Assistant (2018)

Ecology (LIFE 320) · Teaching Assistant (2017)

Ornithology (BZ 335) · Teaching Assistant & Laboratory Instructor (2014 & 2015)

Attributes of Living Systems (LIFE 102) · Teaching Assistant & Laboratory Instructor (2013)

Other Teaching

Lecturer · Ecology and Environment module for the Coursera course [One Health Investigations of Outbreaks and Spillovers](#) (2024–2025)

Coordinator & Content Developer · Applied Modeling in Public Health Workshops · Johns Hopkins Bloomberg School of Public Health (2022–present)

Content Developer & Co-Instructor · Zombiecology: Workshop on Disease Ecology · National Science Olympiad · Colorado State University (2018)

Teaching Excellence Recognition

Introduction to R for Public Health Researchers (140.604.79) · Summer Institute 2025

The One Health Approach to Epidemiology and Global Public Health (340.610.81) · Spring Fourth Term 2024–2025

Introduction to R for Public Health Researchers (140.604.73) · Winter Institute 2025

Introduction to R for Public Health Researchers (140.604.79) · Summer Institute 2024

Introduction to R for Public Health Researchers (140.604.73) · Winter Institute 2024

Introduction to R for Public Health Researchers (140.604.79) · Summer Institute 2023

RESEARCH AND PRACTICE FUNDING

External Sponsored Grants and Contracts

Current Support

Project Title: Atlantic Coast Center for Infectious Disease Dynamics and Analytics

Dates: 09/12/2023 – 09/11/2028

Sponsoring Agency: CDC Center for Forecasting and Outbreak Analytics

Principal Investigator: Shaun Truelove

Main Grant Objective: Lead recruitment and logistics for Applied Modeling in Public Health workshop series; assist with workshop content; participate in model development for forecasts and scenario projections of COVID-19, influenza, and RSV cases and hospitalizations

Role: Research Associate

Project Title: Ecology of Nipah Virus in Bangladesh (58-3022-3-029)

Dates: 09/01/2023 – 08/31/2026

Sponsoring Agency: USDA/ARS

Principal Investigator: Emily Gurley

Main Grant Objective: Provide support for field work, data analysis, and writing manuscripts; draft protocols for approval, collate and analyze data coming from the field and the laboratory, and lead development of manuscripts for publication

Role: Research Associate

Project Title: Solving Opportunities for Spillover (SOS): Frequency and Mechanisms of Cross-species Transmission of Henipaviruses in Bangladesh (1U01AI168287-01A1)

Dates: 01/03/2023 – 01/02/2028

Sponsoring Agency: NIH/NIAID

Principal Investigator: Emily Gurley

Main Grant Objective: Provide support for field work, data analysis, and writing manuscripts; draft protocols for approval, collate and analyze data coming from the field and the laboratory, and lead development of manuscripts for publication

Role: Research Associate

Past Support

Project Title: Safety and Healthcare Epidemiology Prevention Research Development (SHEP-heRD) (75D30121F00005)

Dates: 09/03/2021 – 09/02/2024

Sponsoring Agency: Centers for Disease Control

Principal Investigator: Shaun Truelove

Main Grant Objective: Lead recruitment and logistics for Applied Modeling in Public Health workshop series; assist with workshop content; participate in model development for forecasts and scenario projections of COVID-19, influenza, and RSV cases and hospitalizations

Role: Research Associate

Project Title: Preventing emergence and spillover of bat pathogens in high risk global hotspots (G166-19-W7329)

Dates: 10/01/2018 – 09/30/2022

Sponsoring Agency: DARPA/Montana State University

Principal Investigator: Raina Plowright (Project Director), Emily Gurley (Site PI)

Main Grant Objective: Work with the team in Bangladesh to develop and implement protocols to sample bats, including identifying roosts best suited for sampling, ensuring protocols are aligned with broad aims of this grant, and that work is delivered on time; real-time analysis of virus detection data

Role: Postdoctoral Fellow

Project Title: COVID-19 Technical Lead in the Implementation of the Strategic Preparedness (202548990)

Dates: 08/03/2022 – 11/03/2022

Sponsoring Agency: World Health Organization

Principal Investigator: Emily Gurley

Main Grant Objective: Support COVID-19 technical lead to improve evidence-based guidance by completing a systematic review of COVID-19 superspreading

Role: Postdoctoral Fellow

PRESENTATIONS

Invited Seminars

Invited Talks

Developing One Health surveillance systems for emerging zoonotic pathogens: moving towards pandemic prevention · University of Oklahoma School of Biological Sciences · Norman, OK (2025)

Developing One Health surveillance systems for emerging zoonotic pathogens: moving towards pandemic prevention · University of Michigan School of Public Health · Ann Arbor, MI (2024)

Shadows on the wall: interpreting multiplex viral sero-surveillance in bats and domesticated animals in Bangladesh · Global Virus Network Annual Meeting · Durban, South Africa (2024)

[Environmental and behavioral drivers of cross-species Nipah virus transmission in Bangladesh](#) · Emerging Infectious Diseases: Ecology and Evolution Workshop · International Centre for Theoretical Sciences · Bengaluru, India (2024)

[Ecological stressors and pathogen shedding](#) · Emerging Infectious Diseases: Ecology and Evolution Workshop · International Centre for Theoretical Sciences · Bengaluru, India (2024)

Investigating the ecology of Nipah and other bat-borne viruses at the human-animal interface in Bangladesh · Uniformed Services University of the Health Sciences · Bethesda, MD (2024)

Investigating Nipah virus spillover at the human-animal interface in Bangladesh · Cornell University College of Veterinary Medicine · Ithaca, NY (2023)

Global change, infectious disease, and public health: the need for ecological interventions · WHO GOARN/RCCE Collective Service · Virtual (2022)

Campus or Departmental Talks

Investigating the ecology of Nipah and other bat-borne viruses at the human-animal interface in Bangladesh · Johns Hopkins Bloomberg School of Public Health · Baltimore, MD (2023)

[Bad roommates? Inferring bacterial interactions in coinfected individuals](#) · Colorado State University Vice President Office of Research Symposium · Fort Collins, CO (2018)

Scientific Meetings

Oral Presentations

Shared food resources between bats, humans, and domestic animals in Bangladesh with implications for viral spillover · North American Symposium on Bat Research · Edmonton, Canada (2025)

The Bat Virus Spillover Evidence Compendium (Bat-Com): What we know, and don't know, about the most important bat zoonoses · American Society of Tropical Medicine and Hygiene · New Orleans, LA (2024)

Empowering researchers through Publish-Review-Curate workflows · Society for Scholarly Publishing · Boston, MA (2024)

Superspreading of SARS-CoV-2: a systematic review and meta-analysis · American Society of Tropical Medicine and Hygiene · Chicago, IL (2023)

Comprehensive time tree analysis identifies bats as key to the radiation of mammal-associated *Bartonella* bacteria · Evolution · Providence, RI (2019)

Timing the diversification of a mammal parasite, *Bartonella* · Ecological Society of America · New Orleans, LA (2018)

Timing the diversification of a mammal parasite, *Bartonella* · Front Range Student Ecology Symposium · Fort Collins, CO (2018)

Long-term monitoring of *Bartonella* spp. bacteria in a captive colony of fruit bats and experimental evidence of bat flies as vectors of bartonella · Ecological Society of America · Portland, OR (2017)

Long-term monitoring of *Bartonella* spp. bacteria in a captive colony of fruit bats and experimental evidence of bat flies as vectors of bartonella · International Symposium on Infectious Diseases of Bats · Fort Collins, CO (2017)

Host phylogenetic distance and ectoparasite overlap predict *Bartonella* sharing in European bats · Front Range Student Ecology Symposium · Fort Collins, CO (2017)

Phylogeography of *Bartonella* bacteria in *Eidolon* spp. fruit bats across Africa · Ecological Society of America · Baltimore, MD (2015)

Phylogeography of *Bartonella* in *Eidolon* fruit bats across Africa · Front Range Student Ecology Symposium · Fort Collins, CO (2015)

Poster Presentations

The Bat Virus Spillover Evidence Compendium (Bat-Com): what do we know about viral spillover from bats after approximately 60 years of reported outbreaks? · World One Health Congress · Cape Town, South Africa (2024)

Nipah virus detection at bat roosts following spillover events in Bangladesh, 2012–2019 · International Conference on Emerging Infectious Diseases · Atlanta, GA (2022)

Manipulating vector transmission reveals local processes in bacterial communities of bats · Ecology

and Evolution of Infectious Disease · Princeton, NJ (2019) · **Poster award**

Dispersal of hosts and vectors predicts bacterial community structure across an island chain · Front Range Student Ecology Symposium · Fort Collins, CO (2019) · **Poster award**

Timing the diversification of a mammal parasite, *Bartonella* · Colorado State University Graduate Student Showcase · Fort Collins, CO (2017)

Linking patterns of bacterial parasite diversity across host and vector communities · Ecology and Evolution of Infectious Disease · Santa Barbara, CA (2017)

Phylogeography of *Bartonella* bacteria in *Eidolon* spp. fruit bats across Africa · Ecology and Evolution of Infectious Disease · Athens, GA (2015)

Large-scale patterns of *Bartonella* prevalence and diversity in African fruit bats · Ecological Society of America · Sacramento, CA (2014)

Large-scale patterns of *Bartonella* prevalence and diversity in African fruit bats · Ecology and Evolution of Infectious Disease · Fort Collins, CO (2014)

A novel method of isolating multi-locus sequence data for characterizing *Bartonella* diversity in bats · Front Range Student Ecology Symposium · Fort Collins, CO (2014)

ADDITIONAL INFORMATION

Personal Statement

I am an infectious disease ecologist interested in zoonotic pathogens and their dynamics within host populations and at the human-animal interface. Overall, my research sits firmly within One Health, seeking to understand disease emergence at the intersection between public health, animal ecology, and environmental change. I use a combination of fieldwork, statistical modeling, molecular genetics, and phylogenetics to investigate pathogen persistence in animal reservoirs, evolution of host specificity, and ecological drivers of pathogen spillover.

Keywords

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

Bioinformatics and Phylogenetics: Multiple sequence alignment (CLUSTAL, MAFFT), maximum likelihood (MEGA, IQ-Tree, RAxML) and Bayesian (MrBayes) phylogenetic inference, inference of population genetic structure (STRUCTURE) and recombination (ClonalFrame, SplitsTree), cophylogeny (ParaFit, PACo), ancestral state reconstruction and phylodynamics (BEAST)

Computing and Data Visualization: High proficiency in R for data manipulation, statistical analysis, and visualization (base and tidyverse, ggplot2, igraph), generating reports with R Markdown, and interactive web pages with Shiny; experience with git, L^AT_EX, and Python (NumPy, Pandas, seaborn)

Modeling: Proficient in deterministic and stochastic models for infectious disease dynamics and hierarchical Bayesian modeling (JAGS)