Louise Hillier Moncla

Curriculum vitae

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University of Pennsylvania
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I. Education and employment

2022- **Assistant Professor (tenure-track)**
Department of Pathobiology, School of Veterinary Medicine
University of Pennsylvania, Philadelphia, PA

2017-2022 **Post-doctoral Research Fellow**
Mentor: Dr. Trevor Bedford
Fred Hutchinson Cancer Research Center, Seattle, WA

2012-2017 **Ph.D. in Microbiology**
Mentor: Dr. Thomas Friedrich
Thesis title: “Disentangling the relative contributions of selection and stochastic processes in RNA virus evolution”
University of Wisconsin-Madison, Madison, WI

2008-2012 **Bachelor of Science in Biology**, Genetics and Development (Distinction and Honors)
Bachelor of Musical Arts (High Distinction)
Mentor: Dr. Beth Shapiro (2010-2012)
Honors thesis title: “An Examination of Polar Bear and Brown Bear Phylogeny Using Nuclear Genes as Molecular Markers”
The Pennsylvania State University, University Park, PA

II. Research

Research grants

2024-2028 **Pew Biomedical Scholars Program Grant**
“Developing a unified framework for avian influenza cross-species transmission and risk assessment”
Direct costs: $300,000, Role: PI

2024-2026 **Center of Excellence for Influenza Research and Response Option Project**
“Developing new and improved bioinformatic resources for avian influenza evolution”
Direct costs: $446,304, **Role: PI**

2023-2024 **Scialog: Mitigating Zoonotic Threats**
“To catch a virus: Decoy polymers and influenza’s evolutionary response”
Direct costs: $50,000, **Role: Co-PI** with Dr. Michael Schultz

2023-2024 **Scialog: Mitigating Zoonotic Threats**
“When pigs fly: animal movement networks to project spillovers”
Direct costs: $50,000, **Role: Co-PI** with Dr. Tavis Andersen and Dr. Nicholas DeFelice

2023-2025 **Center of Excellence for Influenza Research and Response Option Project**
“Reconstructing the drivers of H5Nx transmission in North America”
Direct costs: $391,633, **Role: PI**

2023-2025 **Center of Excellence for Influenza Research and Response Option Project**
"Computational Modeling Core"
Direct costs: $60,000, **Role: Co-Investigator**

2023-2024 **Center for Research on Coronaviruses and Other Emerging Pathogens Pilot and Feasibility Grant**
"Developing a framework for H5N1 sequencing and transmission inference in Pennsylvania"
Direct costs: $50,000, **Role: PI**

2022-2024 **Margaret Q. Landenberger Research Foundation Grant**
"Reconstructing the ecological and evolutionary drivers of H5Nx cross-species transmission."
Direct costs: $200,000, **Role: PI**

2022-2025 **CDC Broad Agency Announcement: "Applied Research to Address Emerging Public Health Priorities"**
"Impact of local differences in vaccine uptake on SARS-CoV-2 evolution and spread across three Upper Midwestern states"
Direct costs to lab: $195,277, **Role: Co-Investigator**

2020-2024 **K99/R00 Pathway to Independence Award, NIAID/NIH**, impact score: 10
"Quantifying the genetic and environmental factors driving avian influenza spillover"
Direct costs: $555,962, **Role: PI**

Honors and Awards

2024 **Pew Biomedical Scholar**, *Pew Charitable Trusts* (2024-2028)

2023 **Scialog Fellow – Mitigating Zoonotic Threats**, *Research Corporation for Science Advancement* (2023)

2020 **K99/R00 Pathway to Independence Award,** *NIAID/NIH*, impact score: 10 (2020-2024)

2019 **Life Sciences Research Foundation Post-doctoral Fellowship**, *The Life Sciences Research Foundation* (2019-2020, left early upon receipt of K99/R00)

2019 **Best Poster Award**, *Human Biology Division Annual Retreat,* Fred Hutchinson Cancer Research Center

2016 **Macrae Foundation Young Investigator Award**, *XVIII International Symposium on Respiratory Viral Infections, Lisbon, Portugal*

2016 **Wisconsin Distinguished Graduate Fellowship**, *University of Wisconsin-Madison*

2016 **Student Research Travel Grant**, University of Wisconsin-Madison

2015 **Pasteur Institute Young Investigator Award**, *1st International Meeting on Respiratory Pathogens, Singapore*

2012 **NIH T32 Molecular Biosciences Training Grant**, *University of Wisconsin-Madison* (2012-2016)

2011 **Phi Beta Kappa Honors Society**

2008 **Schreyer Honors College Academic Scholarship**, *The Pennsylvania State University (2008-2012)*

Peer-reviewed publications

Ordered from most to least recent; ‡ denotes corresponding author, * denotes first author, Google Scholar link

1. Ashley Sobel Leonard*,Lydia Mendoza, Alexander G. McFarland, Andrew Marques, John K. Everett, **Louise Moncla**, Frederic D. Bushman, Audrey R. Odom John, Scott E. Hensley*. Within-Host Influenza Viral Diversity in the Pediatric Population as a Function of Age, Vaccine and Health Status. **Virus Evolution**, April 25, 2024, DOI: 10.1093/ve/veae034
2. Miguel I. Paredes*, Amanda C. Perofsky, Lauren Frisbie, **Louise H. Moncla**, Pavitra Roychoudhury, Hong Xie, Shah A. Mohamed Bakhash, Kevin Kong, Isabel Arnould, Tien V. Nguyen, Seffir T. Wendm, Pooneh Hajian, Sean Ellis, Patrick C. Mathias, Alexander L. Greninger, Lea M. Starita, Chris D. Frazar, Erica Ryke, Weizhi Zhong, Luis Gamboa, Machiko Threlkeld, Jover Lee, Jeremy Stone, Evan McDermot, Melissa Truong, Jay Shendure, Hanna N. Oltean, Cécile Viboud, Helen Chu, Nicola F. Müller, Trevor Bedford. "Local-Scale phylodynamics reveal differential community impact of SARS-CoV-2 in metropolitan US county." **PLOS Pathogens**, March 26, 2024, DOI: 10.1371/journal.ppat.1012117
3. Andrew D. Marques, Jevon Graham-Wooten, Layla A. Khatib, Ayannah S. Fitzgerald, Ashley Sobel-Leonard, Emma J. Cook, John Everett, **Louise H. Moncla**, Brendan Kelly, Frederic D. Bushman*, and Ronald G. Collman*. SARS-CoV-2 Evolution During Prolonged Infection in Immunocompromised Patients. ***MBio*,** February 16, 2024, DOI: https://doi.org/10.1128/mbio.00110-24
4. Katarina M. Braun*, Luis A. Haddock III*, Chelsea M. Crooks, Gabrielle L. Barry, Joseph Lalli, Gabriele Neumann, Tokiko Watanabe, Masaki Imai, Seiya Yamayoshi, Mutsumi Ito, **Louise H. Moncla**, Katia Koelle, Yoshihiro Kawaoka, Thomas C. Friedrich. "Avian H7N9 influenza viruses are evolutionarily constrained by stochastic processes during replication and transmission in mammals." **Virus Evolution**, January 19, 2023, 2023, DOI:10.1093/ve/vead004.
5. Claudia P Arevalo, Marcus J Bolton, Valerie Le Sage, Naiqing Ye, Colleen Furey, Hiromi Muramatsu, Mohamad-Gabriel Alameh, Norbert Pardi, Elizabeth M Drapeau, Kaela Parkhouse, Tyler Garretson, Jeffrey S Morris, **Louise H Moncla**, Ying K Tam, Steven HY Fan, Seema S Lakdawala, Drew Weissman, Scott E Hensley. "A multivalent nucleoside-modified mRNA vaccine against all known influenza virus subtypes". **Science**, November 25, 2022, DOI: 10.1126/science.abm0271.
6. Katarina Braun*, Gage Moreno*, Cassia Wagner, Molly A. Accola, William M. Rehrauer, David Baker, Katia Koelle, David H. O'Connor, Trevor Bedford, Thomas C. Friedrich‡, **Louise H. Moncla‡**. "Acute SARS-CoV-2 infections harbor limited within-host diversity and transmit via tight transmission bottlenecks." **PLOS Pathogens**, August 23, 2021, DOI: 10.1371/journal.ppat.1009849. **‡ Corresponding author**
7. **Louise H. Moncla*‡,** Allison Black*, Chas DeBolt, Misty Lang, Nicholas R. Graff, Ailyn C. Pérez-Osorio, Nicola F. Müller, Dirk Haselow, Scott Lindquist, Trevor Bedford‡. "Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State." **eLife**, April 19, 2021, DOI: 10.7554/eLife.66448. ***‡ Co-first and co-corresponding author**
8. Nicola F. Müller‡, Cassia Wagner*, Chris D. Frazar*, Pavitra Roychoudhury*, Jover Lee, **Louise H. Moncla**, Benjamin Pelle, Matthew Richardson, Erica Ryke, Hong Xie, Lasata Shrestha, Amin Addetia, Victoria M. Rachleff, Nicole A. P. Lieberman, Meei-Li Huang, Romesh Gautom, Geoff Melly, Brian Hiatt, Philip Dykema, Amanda Adler, Elisabeth Brandstetter, Peter D. Han, Kairsten Fay, Misja Ilcisin, Kirsten Lacombe, Thomas R. Sibley, Melissa Truong, Caitlin R. Wolf, Michael Boeckh, Janet A. Englund, Michael Famulare, Barry R. Lutz, Mark J. Rieder, Matthew Thompson, Jeffrey S. Duchin, Lea M. Starita, Helen Y. Chu, Jay Shendure, Keith R. Jerome, Scott Lindquist, Alexander L. Greninger‡, Deborah A. Nickerson‡, Trevor Bedford‡. "Viral genomes reveal patterns of the SARS-CoV-2 outbreak in Washington State". **Science Translational Medicine**, May 3, 2021, DOI: 10.1126/scitranslmed.abf0202.

9. Bedford T, Greninger AL, Roychoudhury P, Starita LM, Famulare M, Huang ML, Nalla A, Pepper G, Reinhardt A, Xie H, Shrestha L, Nguyen TN, Adler A, Brandstetter E, Cho S, Giroux D, Han PD, Fay K, Frazar CD, Ilcisin M, Lacombe K, Lee J, Kiavand A, Richardson M, Sibley TR, Truong M, Wolf CR, Nickerson DA, Rieder MJ, Englund JA, Hadfield J, Hodcroft EB, Huddleston J, **Moncla LH**, Müller NF, Neher RA, Deng X, Gu W, Federman S, Chiu C, Duchin J, Gautom R, Melly G, Hiatt B, Dykema P, Lindquist S, Queen K, Tao Y, Uehara A, Tong S, MacCannell D, Armstrong GL, Baird GS, Chu HY, Shendure J, Jerome KR. "Cryptic Transmission of SARS-CoV2 in Washington State." **Science**, October 30, 2020, DOI: 10.1126/science.abc0523
10. **Louise H. Moncla‡,** Trevor Bedford, Philippe Dussart, Srey Viseth Horm, Sareth Rith, Philippe Buchy, Erik A. Karlsson, Lifeng Li, Yongmei Liu, Huachen Zhu, Yi Guan, Thomas C. Friedrich, Paul F. Horwood‡. "Quantifying within-host diversity of H5N1 influenza viruses in humans and poultry in Cambodia." **PLOS Pathogens**, January 17, 2020, DOI: 10.1371/journal.ppat.1008191. **‡ Co-corresponding author**
11. Allison Black*, **Louise H. Moncla***, Katherine Laiton-Donato, Barney Potter, Lissethe Pardo, Angelica Rico, Catalina Tovar, Diana P. Rojas, Ira M. Longini, M. Elizabeth Halloran, Dioselina Peláez-Varvajal, Juan D. Ramírez, Marcela Mercado-Reyes, Trevor Bedford‡. "Genomic Epidemiology supports multiple introductions and cryptic transmission of Zika virus in Colombia." **BMC Infectious Diseases,** November 12, 2019. *** Co-first author**
12. YQ Shirleen Soh, **Louise H. Moncla**, Rachel Eguia, Trevor Bedford, Jesse D. Bloom. "Comprehensive mapping of the avian influenza polymerase protein PB2 to humans." **eLife***,* April 30, 2019.
13. Mauricio A. Salvo, Mathew T. Aliota, **Louise H. Moncla**, ID Velez, AL Trujillo, Thomas C. Friedrich, Jorge E. Osorio‡. "Tracking dengue virus type 1 genetic diversity during lineage replacement in an hyperendemic are in Colombia." **PLOS One**, March 7, 2019.
14. Hirotaka Imai, Jorge M. Dinish, Gongxun Zhong, **Louise H. Moncla**, Tiago J.S. Lopexs, Ryan McBride, Andrew J. Thompson, Wenjie Peng, Mai thi Q. Le, Anthony Hanson, Michael Lauck, Yuko Sakai-Tagawa, Shinya Yamada, Julie Eggenberger, David H. O'Connor, Yasuo Suzuki, Masato Hatta, James C. Paulson, Gabriele Neumann, Yoshihiro Kawaoka‡. "Diversity of influenza A(H5N1) viruses in infected humans, northern Vietnam, 2004-2010." **Emerging Infectious Diseases** *24*, 7, July 2018.
15. Katherine S. Xue, **Louise H. Moncla**, Trevor Bedford, Jesse D. Bloom‡. "Within-host evolution of human influenza virus." **Trends in Microbiology**, March 10, 2018.
16. Maki Kiso, Kiyoko Iwatsuki-Horimoto, Seiya Yamayoshi, Ryuta Uraki, Mutsumi Ito, Eiryo Kawakami, Yuriko Tomita, Satoshi Fukuyama, Tiago J.S. Lopes, Tokiko Watanabe, **Louise H. Moncla**, Thomas C. Friedrich, Gabriele Neumann, Yoshihiro Kawaoka‡. "Emergence of oseltamivir-resistant H7N9 influenza viruses in immunosuppressed cynomolgus macaques." **Journal of Infectious Diseases***, Volume 216, issue 5*, September 1, 2017.
17. **Louise H. Moncla***, Nicholas W. Florek, Thomas C. Friedrich‡. "Influenza evolution: new insights into an old foe." **Trends in Microbiology**, June 25, 2017. PMID: 28478941.
18. **Louise H. Moncla***, Andrea M. Weiler, Gabrielle Barry, Jason Weinfurter, Jorge M. Dinis, Olivia Charlier, Michael Lauck, Adam Bailey, Jens Kuhn, Victoria Wahl-Jensen, Joshua C. Johnson, Peter B. Jahrling, Tony L. Goldberg, David H. O'Connor, Thomas C. Friedrich‡. "Within-host evolution of simian arteriviruses in crab-eating macaques." **Journal of Virology***,* August 12, 2016*.*
19. Elizabeth A. Caine, **Louise H. Moncla**, Monica Ronderos, Thomas C. Friedrich, Jorge E. Osorio‡. "A Single Mutation in the VP1 of Enterovirus 71 is Responsible for Increased Virulence and

Neurotropism in Adult Interferon Deficient Mice." **Journal of Virology**. July 20, 2016. PMID: 27440896.

20. Dudley DM, Aliota MT*, Mohr EL*, Weiler AM, Lehrer-Brey G, Weisgrau KL, Mohns MS, Breitbach ME, Rasheed MN, Newman CM, Gellerup DD, **Moncla LH**, Post J, Schultz-Darken N, Schotzko ML, Hayes JM, Eudailey JA, Moody MA, Permar SR, O'Connor SL, Rakasz EG, Simmons HA, Capuano S, Golos TG, Osorio JE, Friedrich TC, O'Connor DH‡. "A rhesus macaque model of Asian-lineage Zika virus infection." **Nature Communications;** 7:12204. Jun 28, 2016.
21. **Louise H. Moncla***, Gongxun Zhong, Chase W. Nelson, Austin L. Hughes, James Mutschler, Tokiko Watanabe, Yoshihiro Kawaoka, Thomas C. Friedrich‡. "Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus." **Cell Host and Microbe** *19*, 169-190, February 10, 2016. **(Featured Article)**
22. Victoria Wahl-Jensen, Joshua Johnson*, Michael Lauck, Jason Weinfurter, **Louise Moncla**, Andrea Weiler, Olivia Charlier, Oscar Rojas, Russell Byrum, Dan Ragland, Louis Huzella, Erika Zommer, Melanie Cohen, John Bernbaum, Yíngyún Caì, Hannah Sanford, Steven Mazur, Reed Johnson, Gustavo Palacios, Adam Bailey, Peter Jahrling, Tony Goldberg, David O'Connor, Thomas Friedrich, and Jens Kuhn‡. "Divergent simian arteriviruses cause simian hemorrhagic fever of different severity in macaques." **MBio**. 2016 Febraury 23; 7(1).
23. Jorge M. Dinis, Nicholas W. Florek*, Omolayo O. Fatola, **Louise H. Moncla**, James P. Mutschler, Jennifer K. Meece, Edward A. Belongia, Thomas C. Friedrich‡. "Deep sequencing reveals potential antigenic drift variants at low frequency in influenza A-infected humans." **Journal of Virology.** 2016 January 6.
24. Nelson CW, **Moncla LH**, Hughes AL‡. "SNPGenie: estimating evolutionary parameters to detect natural selection using pooled next-generation sequencing data." **Bioinformatics**. 2015 July 29.
25. **Louise H. Moncla***, Ted M. Ross*, Jorge M. Dinis, Jason T. Weinfurter, Tatum D. Mortimer, Nancy Schultz-Darken, Kevin Brunner, Saverio V. Capuano III, Carissa Boettcher, Jennifer Post, Michael Johnson, Chalise E. Bloom, Andrea M. Weiler, Thomas C. Friedrich‡. "A novel nonhuman primate model for influenza transmission." **PLOS One 8**, e78750. November 14, 2013.

Submitted preprints

1. Valerie Le Sage*, Bailee Werner, Grace Merrbach, Sarah Petnuch, Aoife O'Connell, Douglas Reed, **Louise Moncla**, Nicholas Crossland, Anita McElroy, William Duprex, Seema Lakdawala‡. "Pre-existing H1N1 immunity reduces severe disease with cattle H5N1 influenza virus." August 21, 2024.

2. Bernadeta Dadonaite*, Jenny J. Ahn, Jordan T. Ort, Jin Yu, Colleen Furey, Annie Dosey, William W. Hannon, Amy L. Vincent Baker, Richard Webby, Neil P. King, Yan Liu, Scott E. Hensley, Thomas P. Peacock, **Louise H. Moncla**, Jesse D. Bloom‡. "Deep mutational scanning of H5 hemagglutinin to inform influenza virus surveillance." **bioRxiv**, https://doi.org/10.1101/2024.05.23.595634, May 24, 2024

Non-published research/tool development

Developer for nextstrain.org
Nextstrain.org is a website that provides real-time phylogenetic inference for currently circulating viruses. In 2019, I built the avian influenza phylogenies hosted on Nextstrain.org/avian-flu, which includes interactive, real-time displays of circulating avian influenza diversity. We currently track global evolution of H5N1, H5Nx, H7N9, and H9N2. During the H5N1 panzootic of 2022 in North

America, our group built an additional data display that highlights the ongoing evolution of the outbreak in North America, along with an interactive "narrative" that walks through each analysis and interpretation. We rapidly responded to the H5N1 outbreak in cattle with updated data visualizations, enabling real-time inference of outbreak timing and spread, which are critical for public health interventions. We continue to develop and maintain these visualizations and update the data monthly.

- Tracking of global H5N1 evolution: https://nextstrain.org/avian-flu/h5n1/ha/2y
- Narrative of H5N1 evolution in North America, 2022-present: https://nextstrain.org/groups/moncla-lab/narratives/h5nx/north-america-2021-present

During the emergence of the SARS-CoV-2 pandemic in spring of 2020, I maintained and updated the SARS-CoV-2 builds daily. These updates involved curating and cleaning new full-genome sequence data deposited in public databases, running the phylogenetics pipeline, error-checking results, and using the resulting phylogeny to infer new introduction and community transmission patterns. To ensure that data submitters were credited for their contributions and to alert them to noteworthy patterns in the data, I finished each update by tweeting relevant observations from the Nextstrain twitter account (@nextstrain) with data submitters tagged.

Developer for Nextclade
Nextclade is a drag-and-drop tool for viral clade assignment and quality control evaluation. We recently developed and released a dataset to enable clade assignment for circulating H5Nx viruses. This tool enables public health and surveillance labs to rapidly evaluate the genetic lineage of circulating viruses without the need for bioinformatics expertise. These datasets are available at: https://clades.nextstrain.org/ and are in development on our lab github page: https://github.com/moncla-lab/h5nx-Clades/tree/main/jordan-h5-clades

Invited research talks

2024 Phylodynamic approaches for reconstructing outbreaks of new and re-emerging viruses. **Cornell University Department of Microbiology and Immunology Seminar Series on Infections and Immunity**, Ithaca, NY, USA (September 27, 2024) **(*invited talk*)**

2024 Intensive Transmission in Wild, Migrating Birds Drove Rapid Geographic Dissemination and Repeated Spillovers of H5N1 into Mammals and Agriculture in North America. **University of Georgia Symposium on Viral Traits,** Athens, GA, USA (September 10-11, 2024) **(*invited talk*)**

2024 Intensive Transmission in Wild, Migrating Birds Drove Rapid Geographic Dissemination and Repeated Spillovers of H5N1 into Mammals and Agriculture in North America. **Centers of Excellence for Influenza Research and Response National Annual Network Meeting,** New York, NY, USA (July 23, 2024) **(*selected abstract*)**

2024 Highly pathogenic H5Nx avian influenza in North America: how did we get here, and response to the outbreak in cattle. **Invited presentation to NIAID Director, Dr. Jeanne Marazzo, and other NIAID program directors,** virtual, (July 2, 2024) **(*invited talk*)**

2024 Highly pathogenic H5Nx avian influenza in North America: how did we get here, and response to the outbreak in cattle. **Sequencing for Public Health Emergency Response, Epidemiology and Surveillance (SPHERES) Seminar Series.** Virtual seminar series attended by ~200 individuals spanning academia and public health, (May 8, 2024) **(*invited talk*)**

2024 Reconstructing highly pathogenic avian influenza virus transmission in North America. **Workshop on Determinants and dynamics of Viral Emergence and Establishment in Human Populations.** Princeton University, (April 10-12, 2024) ***(invited talk)***

2024 Reconstructing the drivers of highly pathogenic avian influenza virus transmission in North America, and surveillance for the future" **Emory Population Biology, Ecology, and Evolution Graduate Program Seminar Series**, Emory, Atlanta, GA, USA (March 29, 2024) **(*invited talk*)**

2024 "Using genomics to disentangle respiratory virus emergence and transmission" **Pennsylvania State University Center for Infectious Disease Dynamics Seminar Series**, State College, PA, USA (February 29, 2024) **(*invited talk*)**

2024 "Reconstructing highly pathogenic H5Nx avian influenza evolution and transmission" **Dean's Distinguished Visiting Professorship Series**, University of Pennsylvania, USA (February 14, 2024) **(*invited talk*)**

2023 "Plenary event: live podcast recording: Ongoing H5Nx Outbreak Live podcast recording" **Centers of Excellence for Influenza Research and Response Annual Network Meeting**, *Baltimore, MD, USA* (August 28, 2023), ***(invited plenary panelist)***

2023 "Viral genotype and endemic circulation increase risk of H5Nx human infection" **Centers of Excellence for Influenza Research and Response National Annual Network Meeting**, Baltimore, MD, USA (August 29, 2023) **(*selected abstract*)**

2023 "Nextstrain as a toolkit for tracking avian influenza evolution and transmission" **Centers of Excellence for Influenza Research and Response Annual Network Meeting**, *Baltimore, MD, USA* (August 28, 2023) **(*invited talk*)**

2023 "Using multi-scale genomic approaches to disentangle H5Nx evolution and cross-species transmission" **Centers of Excellence for Influenza Research and Response Computational Modeling Core Seminar Series**, *virtual* (August 23, 2023) **(*invited talk*)**

2023 "Using multi-scale genomics to disentangle respiratory virus emergence and transmission" **Colorado State University, Genomics of Disease in Wildlife Workshop Plenary speaker**, *Fort Collins, CO, USA* (June 7, 2023), ***(invited plenary speaker)***

2023 "Using multi-scale genomics to disentangle respiratory virus emergence and transmission" **Princeton University Infectious Disease Group seminar**, *Princeton, NJ, USA* (April 5, 2023) **(*invited talk*)**

2023 "Using multi-scale genomics to disentangle respiratory virus emergence and transmission" **University of Pennsylvania Institute for Infectious and Zoonotic Diseases Symposium** (invited speaker), *Philadelphia, PA, USA* (March 30, 2023) **(*invited talk*)**

2023 "Using multi-scale genomics to disentangle respiratory virus emergence and transmission" **University of Georgia Infectious Disease Seminar series**, *Athens, GA, USA* (February 20, 2023) **(*invited talk*)**

2022 "Using multi-scale genomics to disentangle H5N1 emergence and transmission" **American Society for Virology Annual meeting, Satellite Symposium: "Shaking the Trees: Sequence-Based Inference in Virus Ecology and Evolution"**, *Madison, WI, USA* (July 16, 2022) **(*invited talk*)**

2021 "Nextstrain as a tool kit for tracking avian influenza virus evolution and transmission" **Toward Mitigating Pandemic Influenza Risk: A regional consultation on avian influenza surveillance in Asia,** *virtual* (December 2, 2021) **(*invited talk*)**

2020 "Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State"
UC Berkeley Evolution Seminar Series, *virtual* (December 2, 2020) **(*invited talk*)**

2020 "Harnessing viral genomics to interrogate SARS-CoV2 transmission at the community to individual scale"
Chilean Genetics Society annual meeting, Roche invited speaker, *virtual* (November 25, 2020) **(*invited talk*)**

2020 "Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State"
Virus Evolution Seminar Series, *joint-hosted by University of Wisconsin-Madison and UC Davis, virtual* (November 23, 2020) **(*invited talk*)**

2020 "Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State"
Vaccine and Infectious Disease Departmental Scientific Seminar Series, *Fred Hutchinson Cancer Research Center, Seattle, WA, virtual* (May 5, 2020) **(*invited talk*)**

2018 "Genomic characterization of H5N1 spillover infection in humans and poultry in Cambodia"
Orthomyxovirus 2018 Conference, *Hanoi, Vietnam* (September 12-14, 2018) **(*selected abstract*)**

2018 "Genomic characterization of H5N1 spillover infection in humans and poultry in Cambodia"
Institut Pasteur du Cambodge, *Phnom Pehnh, Cambodia* (September 5, 2018) **(*invited talk*)**

2018 "Genomic reconstruction of a mumps virus outbreak in Washington state"
Models of Infectious Disease Agent Study network meeting, *Washington D.C, USA* (April 3-5, 2018) **(*selected abstract*)**

2016 "Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus"
The Macrae Foundation's XVIII International Symposium on Respiratory Viral Infections, *Lisbon, Portugal* (March 31-April 2, 2016) **(*selected abstract*)**

2015 "Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus"
1st International Meeting on Respiratory Pathogens, *Furama Riverfront, Singapore* (September 2-4, 2015) **(*selected abstract*)**

2013 "A novel nonhuman primate model for influenza transmission."
Joint University of Minnesota-University of Wisconsin Virology Training Grant Symposium, *University of Wisconsin-La Crosse, La-Cross, WI, USA* **(*selected abstract*)**

Poster presentations

2019 "Quantifying within-host evolution of H5N1 viruses in humans and poultry in Cambodia"
Options X for the Control of Influenza, *Singapore*

2016 "Quantifying the limits of accurate and reproducible influenza sequencing"
Options IX for the Control of Influenza, *Chicago, Illinois, USA*

2015 "Selective bottlenecks shape evolutionary pathways during mammalian adaptation of a 1918 like avian virus"
ISIRV workshop on the next-generation sequencing of viruses, *Pasteur Institute, Paris, France*

III. Professional Service

International Committees and activities:

1. World Health Organization Tool for Influenza Pandemic Risk Assessment (TIPRA) Risk Assessment Committee, **Committee Member** (March 2024 – present)

National Committees and activities:

1. National Centers of Excellence for Influenza Research and Response: Phylodynamics Working Group, **Co-Lead** with Dr. Martha Nelson (February 2024 – present)
2. National Centers of Excellence for Influenza Research and Response: Risk Assessment Pipeline Working Group, **Leadership Team Member** (February 2024 – present)
3. National Centers of Excellence for Influenza Research and Response: Bovine H5 Outbreak Response Team, **Core Member** (April 2024 – present)

Ad-hoc peer review service

Paper reviews: Cell, Cell Host and Microbe, Nature Communications, Nature Ecology and Evolution, eLife, PLOS Pathogens, Virus Evolution, MBio, Journal of Virology, Epidemics, Scientific Reports, Cell Reports, Cell Reports Medicine, Infection Genetics and Evolution, PLOS One, Evolution Medicine and Public Health, Communications Medicine, Ecology and Evolution, Virulence, BMC Bioinformatics, Open Forum ID, Journal of Infectious Diseases

Grant reviews:
Natural Sciences and Engineering Research Council of Canada Discovery Grant (Canada)
Genome British Columbia Genesolve Grant Program (Canada)
Medical Research Council Career Development Award (United Kingdom)

Science communication

Podcasts

2023 **This Week in Virology**, live Podcast recording, Centers of Excellence for Influenza Research and Response Annual Network Meeting, August 28, 2023: https://www.microbe.tv/twiv/twiv-1053/

2023 **The Naked Scientist, BBC** Podcast episode, "A Bird Flu Pandemic Hovering on the Horizon", February 14, 2023: https://www.thenakedscientists.com/podcasts/naked-scientists-podcast/bird-flu-pandemic-hovering-horizon

2022 **This Week in Evolution** Podcast episode, "Viruses of a Feather Bottleneck Together", July 29, 2022: https://www.youtube.com/watch?v=UcHmebKO_K4

Media Engagement

Highly pathogenic avian influenza:
2024 National Public Radio: https://www.npr.org/sections/health-shots/2024/04/26/1247479100/bird-avian-flu-cows-cattle-milk-virus-unanswered-questions
2024 National Public Radio: https://www.npr.org/2024/04/02/1242328542/a-strain-of-the-bird-flu-virus-has-been-detected-in-a-human-in-texas
2024 Nature news: https://www.nature.com/articles/d41586-024-01256-5
2024 Vox: https://www.vox.com/even-better/24145304/bird-flu-h5n1-avian-influenza-pandemic

2024 New York Times: https://www.nytimes.com/2024/04/22/health/birdflu-marine-mammals.html
2024 New York Times: https://www.nytimes.com/2024/05/03/health/bird-flu-cows-mutations.html
2023 The Atlantic: https://www.theatlantic.com/science/archive/2023/08/avian-flu-vaccine-wild-bird-transmission-endemic/674903/
2023 Science News: https://www.sciencenews.org/article/bird-flu-mammals-influenza-pandemic
2022 BBC News: https://www.bbc.com/news/science-environment-63464065
2022 Nature News: https://www.nature.com/articles/d41586-022-03322-2

SARS-CoV-2 Pandemic:
2020 Science News: https://www.sciencenews.org/article/coronavirus-covid19-mutations-strains-variants
2020 KNKX Radio: https://www.knkx.org/post/new-research-suggests-nations-first-covid-19-case-was-not-source-washingtons-outbreak
2020 Wall Street Journal: https://www.wsj.com/articles/the-search-is-on-for-americas-earliest-coronavirus-deaths11588597831?shareToken=st53246b5625b043cb89ec5493cb64017a&reflink=article_email_share
2020 Kiro 7 News, Seattle, WA: https://www.kiro7.com/news/local/cdc-first-us-coronavirus-deaths-happened-weeks-before-first-death-kirkland/HCTCEX45XFCRVE5742JWR7ZP44/?_website=cmg-tv-10090

University of Pennsylvania Community Engagement

2024 Research Presentation for Penn Vet Board of Advisors Meeting (February 8, 2024)
2023 Invited Panelist for "The World Today" series, hosted by Perry World House, Topic: Stopping the Next Pandemic: The Role of Animals in Disease Transmission (April 18, 2023)

IV. Teaching, Mentorship and Outreach

Classroom teaching

National, invited teaching:

1. Genomics of Disease in Wildlife Workshop, Fort Collins, CO (2023-): This workshop is an intensive, 8-day course covering computational aspects of studying diseases in wildlife, hosted by Colorado State University. This workshop is attended by national and international participants spanning academic, public health, government, and wildlife health institutions who want to learn about using genomics to study diseases in wildlife. As an invited instructor, I provided 1.5 hours of lecture and 2.5 hours of computer lab instruction covering introductions to phylodynamics and Bayesian phylogenetics, and setting up and interpreting analyses with the BEAST and Nextstrain softwares. I designed each lecture and lab activity, which are publicly available on both the course website and my professional github page (https://github.com/lmoncla/csu-genomics-disease-wildlife-workshop). I have been invited to continue teaching this module in future workshops, and intend to do so.

2. American College of Veterinary Preventive Medicine Exam Preparation Course, Epidemiology and Biostatistics Module, January 26, 2024. This online, virtual preparatory course is intended to provide veterinary students the opportunity to develop deeper knowledge of principles related to veterinary preventive medicine. I provided a 1-hour lecture for the epidemiology and biostatistics module that focused on my research on highly pathogenic avian influenza, and how epidemiology concepts like contact tracing, testing, and genomic epidemiology can be used to detect, trace, and control viral outbreaks.

Teaching in Penn Biomedical Graduate Studies PhD curriculum:

1. Public Health Certificate Program for Biomedical Graduate Studies students. (April 24, 2024). This seminar course gives BGS students the opportunity to earn a certificate in public health while completing a PhD in one of the major BGS programs. This seminar course is designed to expose students to the ways in which research and public health practice can interact and inform each other, and to give examples of public health concepts in action. I gave a 1-hour lecture on combining basic research in viral genomic epidemiology with community outreach to understand a mumps virus outbreak, and how that led to future research directions that are applicable to public health and the study of health disparities and their impacts on disease transmission.

Teaching in Penn Microbiology, Virology, and Parasitology (MVP) PhD program curriculum

The MVP graduate program curriculum at the University of Pennsylvania includes courses designed to cover basic information on virology. I currently teach lectures in two courses.

1. CAMB 617, Emerging Infectious Diseases (2023-): I teach a 1.5 hour lecture with an associated hands-on lab activity that covers an introduction to viral spillover, zoonosis, and new tools for outbreak response.
2. CAMB 706, Virology (2024-): I taught a one hour lecture in February 2024 for CAMB 706, Virology, covering an introduction to the field of viral phylodynamics.
3. CAMB 700, Topics in Microbiology (2023-): Each year, I participate in a 1.5 hour feedback session aimed to help 2nd year MVP students prepare for their preliminary exams. Each session, two faculty listen to practice talks, ask questions and provide feedback on scientific content, presentation skills, and presentation development/organization.

Teaching in Penn Veterinary School curriculum

1. Defense and Barriers (2024-): As part of the Penn Vet first year curriculum, students take a course on “Defense and Barriers”, which covers introductory immunology and infectious diseases of veterinary importance. I teach a 1 hour lecture on influenza viruses, including the viral life cycle, immune responses, antivirals, ecology and evolution, public health, and emerging issues in influenza. This is a one-hour lecture for all first year veterinary students.

Mentorship

Mentored Post-docs in Moncla lab:

Anna Jaeger, post-doctoral research fellow (2023-)
Lambodhar Damodaran, post-doctoral research fellow (2023-)

Mentored PhD students in Moncla lab:

Clara Malekshahi, PhD student, Microbiology Virology and Parasitology Program (2024-)
Maria Maltepes, PhD student, Biology Graduate Program (2023-)
Jordan Ort, PhD student, Microbiology Virology and Parasitology Program (2023-)

Mentored rotation students in Moncla lab:

Sonja Zolnoski, PhD rotation student, Microbiology Virology and Parasitology Program (2023)
Natalie Hagan, PhD rotation student, Microbiology Virology and Parasitology Program (2023)

Thesis and advisory committees:

Andrew Marques, PhD student, Frederic Bushman lab (2023-2024)
Ashley Soebel-Leonard, Pediatric Infectious Disease Fellow, Scott Hensley Lab (2023-)
Olivia Pilling, PhD student, Daniel Beiting lab (2023-2024)

Qianzuan She, PhD student, Paul Planet lab (2023-)

Mentored students during PhD and post-doc:
Cassia Wagner, graduate student (2020-2021)
Gage Moreno, graduate student (2020-2021); *now post-doctoral researcher at the Broad Institute in the laboratory of Pardis Sabeti*
Katarina Braun, MD/PhD student (2015-2021); *now finishing medical training at University of Wisconsin*
Macy Pell, undergraduate research assistant (2015-2017); *now PhD student at Michigan State University in laboratory of Shannon Manning*
Mauricio Salvo, graduate student (2014-2017); *now research scientist at Roche*
Olivia Charlier, undergraduate research assistant (2012-2014); *now a physician's assistant*
Kelsey Florek, Microbiology Doctoral Training Program rotation student (2013); *now lead bioinformatician at the Wisconsin State Lab of Hygiene*

Outreach

Facilitator for Girls Who Code (2017-2022)

Girls who code is an outreach program targeting high-school aged girls who are interested in learning to code. During my post-doc, I have served each year as a course facilitator. As a facilitator, I volunteer with coding sessions during which participants learn fundamentals of coding in python or R, and work towards completing a coding-based project that is showcased for parents and researchers at the end of the semester. During each session, I assist in trouble shooting, answer questions, and provide general support while participants develop coding skills.

Expanding Your Horizons Outreach program (2015-2016)

Expanding Your Horizons is an outreach program intended to promote interest and confidence in middle school girls to pursue STEM fields. During my PhD, I participated as a student volunteer, where I led an activity introducing the participants to programming in python and shared my path to becoming a scientist.

Madison Science Museum Women in STEM Symposium (2016)

The Madison Science Museum Women in STEM Symposium is an event targeted to high school girls who are interested in STEM fields. The event brings in successful women working in STEM fields to speak about their career paths, the challenges they have faced and why it is important to build a diverse work environment. As a volunteer I helped register and direct participants to the talks and activities and discussed my own aspirations as a scientist with the participating young women.